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OM protein - protein search, using sw model

December Run on:

6, 2001, 08:04:02; Search time 184.09 Seconds (without alignments) 3.621 Million cell updates/sec

PEP1-MOD8A Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 SLFEGIDAY 9 Scoring table: Sequence:

522463 seqs, 74073290 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_1101:\*

\*\*Sinssy\_codata/geneseqp/AA1980.DAT:\*\*

\*\*Sinssy\_godata/geneseqp/AA1981.DAT:\*\*

\*\*Sinssy\_godata/geneseqp/AA1992.DAT:\*\*

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\*\*Sinssy\_godata/geneseqp/AA1992.DAT:\*\*

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\*\*Sinssy\_godata/geneseqfy\_eneseqpy\_AA1992.DAT:\*\*

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\*\*Sinssy\_godata/genes

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Heat shock protein	Human heat shock p	Human Hsp72 (heat	Gallus gallus HSP							
ID	AAY44199	AAB97601	AAY44200	AAB97602	AAB97603	AAY88409	AAY88410	AAY88412	AAY88413	AAB23252	AAR03930
DB	21	22	21	22	22	21	21	21	71	71	11
% Duery Match Length DB	6	σ	10	10	10	554	554	554	.554	624	634
% Query Match	89.1	89.1	89.1	89.1	87.0	87.0	87.0	87.0	87.0	87.0	87.0
Score	41	41	41	41	40	40	40	40	40	40	40
Result No.	1	7	m	4	S	9	7	æ	σ	10	11

Homo sapiens HSP ( Human heat shock p	heat	Human neat shock p Mature mouse sperm	Human heat shock 7	Human heat shock p	Human heat shock p		Xenopus laevis HSP	Marmoset intracell	Lung cancer associ	Human secreted pro	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Rat HSP (rathsp70)	Heat shock cognate	Human heat shock c	Mouse heat shock c		Human heat shock p	Human heat shock p	Candida albicans h	GFP-HSC70 fusion p	Mouse SLIP1 homolo	S. avermitilis ORF	B. subtilis dihydr	Zea mays HSP (mzeh	T. gondii antigen	Toxoplasma gondii	Staphylococcus aur	Synthetic human ta
AAR03929 AAW10065	AAY88408	AAY88411 AAR43004	AAW54349	AAB23652	AAB82534	AAB23650	AAR03928	AAW22895	AAB58386	AAG02174	AAG24333	AAG24332	AAG24331	AAR03927	AAW54364	AAY17407	AAY17408	AAB23649	AAB23651	AAB82535	AAW01638	AAB22938	AAR43002	AAB61974	AAU01251	AAR03931	AAY31380	AAB49099	AAW77538	AAU02055
111	21	21	19	21	22	21	11	18	21	21	21	21	21	11	19	20	20	21	21	22	18	21	14	22	22	11	20	22	19	22
640 640	640	640 641	641	641	641	642	647	643	665	91	253	279	342	646	646	646	646	646	646	646	959	890	633	412	558	646	647	647	86	100
87.0 87.0		87.0 87.0	87.0	7.	^	7	•		84.8	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	œ	76.1	9	76.1		9		73.9
044	04	404	40	40	40	40	40	39	39	37	37	37	37	37	37	37	37	37	37	37	37	37	36	35	35	35	32	35	34	34
132	12	16	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAY44199 standard; peptide; 9 AA AAY44199 RESULT

AAY44199;

(first entry) 15-FEB-2000

Heat shock protein 70 amino acid residues 286-294.

Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HIA; immune defence; immunogenicity; specificity; human leucocyte antigen.

Homo sapiens

WO9954464-A1.

28-OCT-1999.

99WO-FR00957 22-APR-1999; 

98FR-0005033. 22-APR-1998;

(INSR ) INST ROUSSY GUSTAVE.

Triebel F, Gaudin C;

WPI; 2000-013251/01.

Identifying mutant peptides from heat-shock protein 70, for treatment of cancer -

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                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                   heat shock protein 70 (hsp70). The invention relates to a method of caentifying peptides, derived from hsp70 that stimulate a tumour-specific caentifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified canced into a vector that can be replicated in bacteria; (iii) sequencian fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the cancer (iii) sequencian fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the cancer (iii) sequenced in each cultured bacterial colony to identify agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic cytotoxic factors (specifically interleukin-2, interferor-gamma and cytotoxic factors (specifically interleukin-2, interferor-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HLAA (human leucocyte continue).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat shock protein 70 (HSP70) peptidic fragment 1.
                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 21;
Pred. No. 4.3e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB97601 standard; peptide; 9 AA.
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 Claim 10; Page 6; 56pp; French
                                                                                                                                                                                                                                                                                                                                                                      89.1%;
88.9%;
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Best Local Similarity 88.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-290909/30.
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                                                                                                                                                                                                                                                                                                                                 Sequence
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This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify
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human, heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP periopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; heat shock protein 70; hsp70; identification; tumour; mutation;
T cell'response; amplification; vector; bacterium; cancer; allale;
cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA:
immune.defence; immunogenicity; specificity; human leucocyte antigen.
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Pred. No. 4.3e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat shock protein 70 amino acid residues 286-295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intracellular infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.1%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic Tymphocytes in a cell culture and/or induce these cells to secrete cytotoxic factors (specifically interleukin-2, interferon-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HLA (human leucocyte antigen) alleles SSSSSSSSSSSSSS

10 AA; Sequence Score 41; DB 21; Length 10; Pred. No. 0.031; ); Mismatches 1; Indels ö 89.1%; 88.9%; Conservative Local Similarity nes 8; Conser 1 SLFEGIDAY 9 Query Match Best Loc Matches õ

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AAB97602 standard; peptide; 10 (first entry) 30-JUL-2001 AAB97602; RESULT

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Heat shock protein 70 (HSP70) peptidic fragment 2.

HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 2.

Homo sapiens

WO200129190-A1

26-APR-2001

29-SEP-2000; 2000WO-EP09530.

(IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

99EP-0120484

15-OCT-1999;

Abastado JP, Bartholeyns J;

WPI; 2001-290909/30.

Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression Claim 8; Page 15; 21pp; English. of heat shock protein -

The amino acid sequence of fragment 2 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to 1 ymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which Kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to HSP and helps direct the immune response to specific cells, (e.g.

intracellular infections by vaccination. The tolerance of the organism to the turnour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or intracellular infected cells.

Sequence

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ö Gaps ö Score 41; DB 22; Length 10; Pred. No. 0.031; 0; Mismatches 1; Indels 89.1%; 88.9%; Best Local Similarity 88.9 Matches 8; Conservative Query Match

1 SLFEGIDAY 9 ŏ g

AAB97603

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Gaps

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AAB97603 standard; peptide; 10 AA.

AAB97603;

(first entry) 30-JUL-2001

Heat shock protein 70 (HSP70) peptidic fragment 3.

HSP: HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.

Homo sapiens.

WO200129190-A1.

26-APR-2001.

29-SEP-2000; 2000WO-EP09530.

99EP-0120484. 15-OCT-1999; (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

Abastado JP, Bartholeyns J;

WPI; 2001-290909/30.

Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of heat shock protein -

Claim 8; Page 15; 21pp; English

the amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP pittopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes or cell pericellular membranes by lymphocytes alicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or infected cells. 

Sequence

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WPI; 2000-264458/23
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AAY88412 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the human heat shock protein SHSP70 amino acid agequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14922-24. The invention relates to the abnormal transcription of further and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
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                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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Score 40; DB 22; Length 10;
Pred. No. 0.05;
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Similarity 88.9%;
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This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNN under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abnormal transcription of intracellular \mbox{HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
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Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress, chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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Pred. No. 4;
0; Mismatches
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Best Local Similarity 88.9%;
Matches 8; Conservative
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sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human heat shock protein SHSP70 amino acid
Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
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Score 40; DB 21; Length 554; Pred. No. 4; 0; Mismatches 87.0%; 88.9%; Conservative 200 slfegidfy 208 Best Local Similarity Matches 8; Conser 1 SLFEGIDAY 9 Query Match õ

Sequence

AAY88413 standard; Protein; 554 AA. AAY88413 

31-JUL-2000 (first entry) AAY88413;

Human heat shock protein SHSP70 amino acid sequence.

Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.

Homo sapiens.

JP2000069999-A.

07-MAR-2000.

99JP-0257146 01-JUN-1995; 95JP-0158581 01-JUN-1995; (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

WPI; 2000-264458/23

Abnormal transcription of intracellular  ${\tt HSP70mRNA}$  under acute and chronic continuous load of stress in a human being and its application

Disclosure; Fig 6; 11pp; Japanese.

sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome. This sequence represents the human heat shock protein SHSP70 amino acid

554 AA; Sequence DB 21; Length 554; 87.0%; Score 40;

Query Match

ö Gaps ö Indels 1; ed. No. 4; Mismatches Pred. No. ; 0 88.98; 8; Conservative Best Local Similarity Matches 8; Conserv

200 slfegidfy 208 σ 1 SLFEGIDAY g õ

10 AAB23252

¥. AAB23252 standard; Protein; 624

AAB23252;

(first entry) 29-JAN-2001

Human Hsp72 (heat shock protein 72).

Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiprolliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.

Homo sapiens.

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Gaps

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1; Indels

WO200054814-A1

21-SEP-2000

17-MAR-2000; 2000WO-US07350.

99US-0125046. 18-MAR-1999;

(PHYL-) PHYLOGENY INC

Volloch VZ, Sherman M;

WPI; 2000-647056/62. N-PSDB; AAA97541 

Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,

Examples; Fig 16B; 77pp; English.

The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.

Conditions to allow the two components to interact and bind, forming a conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNR phosphatase cutivation, comprising ocnacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNR phosphatase activity. The compound inhibitors of Hsp72 or JNR phosphatase activity. The compounds identified as invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNR phosphatase activity. The compounds identified as inhibiting the proliferation of cells. Modulation of the activity of the JNR phosphatase or Hsp72 is used to reach premalignant conditions as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function of cells. The present sequence represents when the present interesents of Hsp72 used

624 Sequence

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AAR03929 standard; Protein; 640 AA.
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289 slfegidfy 297
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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634.
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                                                                                                                                                                                                                                                                                                                                                                  Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                Score 40; DB 21; Length 624;
pred. No. 4.5;
0; Mismatches 1; Indels
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ilarity 88.9%;
Conservative
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Best Local Similarity 88.9
Matches ~ 8; Conservative
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Matches 8; Conserv
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                          Query Match
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2. Bacillus megaterium (Bmehsp70 - AAR03922);
3. E. coli (dnaK - AAR03924);
4. T. cruzi (tc70kd - AAR03925);
5. T. cruzi (tAR03926);
6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapiens (humhsp70 - AAR03928);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03931).
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                                              Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
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Pred. No. 4.7;
0; Mismatches 1;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Homo sapiens HSP (humhsp70)
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Gaps

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1; Indels

DB 11; Length 634;

Score 40; DB 1 Pred. No. 4.6; 0; Mismatches

87.0%;

AAW10065 standard; Protein; 640 AA.

AAW10065

Human heat shock protein 70

Homo sapiens. JP08322577-A.

stress.

24-OCT-1997 (first entry)

AAW10065;

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The present invention describes a fused protein (1) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the Arbase domain of a heat shock protein. Also described are: (1) a drug composition containing (1) as a active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (1) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer -
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88.9%; Pred. No. 4.7;
iive 0; Mismatches 1; Indels
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                                                                                                                                 (SUME ) SUMITOMO ELECTRIC IND
                                                                                            99JP-0041535.
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                                                     18-FEB-2000; 2000WO-JP00941
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                                                                                                                                                                        Udono H,
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                                                                                                                                                                        Shinbara N,
              24-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The cDNA encoding the present sequence, human heat shock protein 70 (HSP70), is located on human chromosome 6p 21.3·22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abhormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained
                                                                                                                                                                                                           Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; tycostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 18; Length 640;
Pred. No. 4.7;
0; Mismatches 1; Indels
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(HOKE-) HOKEN KAGAKU KENKYUSHO KK

WPI; 1997-081088/08. N-PSDB; AAT58086.

95JP-0158581 95JP-0158581

01-JUN-1995; 01-JUN-1995;

10-DEC-1996.

Claim 1; Fig 1; 13pp; Japanese.

AAB23653 standard; protein; 640 AA.

05-JAN-2001 (first entry)

AAB23653;

WO200049041-A1

Homo sapiens

87.08; 88.98;

640 AA;

stress load. Sequence Best\_Local Similarity 88.9 Matches 8; Conservative

Query Match

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This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14922-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                 Abnormal transcription of intracellular \mbox{HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                                                                                   Claim 2; Fig 1; 11pp; Japanese.
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ö Gaps ő Score 40; DB 21; Length 640; Pred. No. 4.7; 0; Mismatches 1; Indels 87.0%; 88.9%; Query Match Best Local Similarity 88.9%; Thes 8; Conservative Sequence 640 AA;

1 SLFEGIDAY 9

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Search completed: December 6, 2001, 08:04:02 Job time: 610 sec

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Ask-type molecular chaperone HSP70a - California sea hare (fragment)
NyAlternate names: heat shock protein 70
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999
C;Accession: A44261
S;Kuhl. D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1992
A;Fitle: Long-term sensitization training in Aplysia leads to an increase in the expra A;Reference number: A44261; MUID:93077669
A;Fatus: preliminary; not compared with conceptual translation
A;Accession: A44261
A;Accession: 
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C;Function:
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                                                                                                      6, 2001, 07:58:26; Search time 88.19 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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DB 2; Length 208; 0.72; 1; Indels

Mismatches Score 40; Pred. No. (

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Query Match Best Local Similarity Matches 8; Conserv

87.0%; 88.9%;

dnaK-type molecula heat shock protein dnaK-type molecula dnaK-type molecula heat shock protein heat shock protein dnaK-type molecula dnaK-type molecula heat-shock protein heat-shock protein dnaK-type molecula heat shock protein dnaK-type molecula heat shock protein dnaK-type molecula heat shock protein heat shock protein heat shock protein heat shock protein	ALIGNMENTS  chaperone HSC70 - California sea hare (fragment) eat shock protein 70 homolog HSC70 alifornica (California sea hare) #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999	Fixuhi, D.; Kennedy, T.E.; Barzallal, A.; Kandel, E.R. J. Cell Biol. 119, 1069-1076, 1992 J. Cell Biol. 119, 1069-1076, 1992 A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr. A;Reference number: A44261; MUID:93077669 A;Recession: B44261 A;Retaus: preliminary; not compared with conceptual translation A;Ketaus: preliminary; not compared with conceptual translation A;Residues: 1-208 <kuh> A;Residues: 1-208 <kuh> C;Genetics: sequence extracted from NCBI backbone (NCBIP:118950)</kuh></kuh>	and assembling/disassembling of protein co
151129 746650 HHXLO S44168 344168 744121 JC74131 14558 14558 745473 745473 745473 745473 745473 745517 JC7132	ALIGNMENTS RESULT 1  And 261  And 261	Kunlı, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.B. K. Kullı, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.B. S. Cell Biol. 119, 1069-1076, 1992. A.;Title: Long-term sensitization training in Aplysis A.;Reference number: A44261; MUID:93077669 A.;Reference number: A44261; MUID:93077669 A.;Ketsison: B44261 A.;Ketsius: preliminary; not compared with conceptual A;Molecule type: nucleic acid A.;Mesidues: 1-208 < KUH> A.;Residues: 1-208 < KUH> C.;Genetics:	olding
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NyAlternate names: heat shock protein 68
C; Species: Mus musculus (house mouse)
C; Species: Jus musculus (house mouse)
C; Species: John 1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Accession: A26283
R; Lowe, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A; Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000
A; Reference number: A26283; MuID:86111900
A; Accession: A26283.
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A; Residues: 1-420 <LOW>
A; Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208
A; Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208
A; Note: the authors translated the codon CTG for residue 173 as Val and CGC for resid
C; Function:
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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
R;Borchiellini, C: Le Parco, Y.
8:Borchiellini, C: Le Parco, Y.
8:Ubmitted to the EMBL Data Library, September 1997
A;Reference number: 222983
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C;Species: Chondrosia reniformis
C;Sate: 31-3an-2000 #sequence_revision 31-3an-2000 #text_change 21-Jul-2000
C;Accession: T#5477
R;Borchiellini, C; Le Parco, Y
submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
A;Reference number: 222983
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0; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
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Pred. No. 1.6;
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                                                                                                                                                                                     dnak-type molecular chaperone - mouse (fragment)
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A;Gene: Hsp70
C;Superfamily: heat shock protein 70
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Matches 8; Conservative
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A; Description: involved in protein folding and assembling/disassembling of protein compl
C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: 151344
R;Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-Kilodalton heat shock polypeptides from rainbow trout: Characterization of A;Reference number: 151344; MUID:85036330
A;Accession: 151344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
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dnak-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)
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A;Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region. A;Reference number: PQ0138; MUID:91099690
A;Accession: PQ0138
A;Molecule type: DNA
A;Residues: 1-372 <ROS>
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                                                                                                                                         Length 209
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1.4;
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                                                                                                                                            DB 2;
                                                                                                                                            Score 40; DB 2
Pred. No. 0.72;
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A; Introns: 68/1; 137/1; 188/3; 281/3
C; Function:
                                                                                                                                            87.0%;
88.9%;
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Best Local Similarity 88.9°
Matches 8; Conservative
                                                                                                                                         Query Match 87.0
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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745A74

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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45476
R;Borchiellini, C:; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
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A;Accession: T45479
X;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
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Pred. No. 1.8;
0; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-468 <BOR>
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A;Molecule type: mRNA
A;Residues: 1-469 <BOR>
A;Cross-references: EMBL:AF026518; PIDN:AAC05363.1
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Pred. No. 1.8;
0; Mismatches
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Pred. No. 1.8;
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C;Genetics:
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C.Genetics: Hsp70
C.Superfamily: heat shock protein 70
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R;Borchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
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C;Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
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Best Local Similarity
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252 SLFEGIDFY 260
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Rytheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hudhes, B.; Hudzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Ji, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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probable heat shock protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: H96605
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Pred. No. 2.4;
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Pred. No. 2.5;
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A,Note: localized to filopodias and c
C,Superfamily: heat shock protein 70
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-617 <STO>
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292 SLFEGIDFY 300
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dnaK-type molecular chaperone - chicken

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A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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Gene 121, 353-358, 1992
A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp
A;Reference number: JC1391; MUID:93077053
      R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible A;Reference number: 136927; MUID:95080396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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N;Alternate names: heat shock protein 70IV; hsp70IV protein
C;Species: paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C;Accession: JC1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917 C;Genetics:
C;Genetics:
A;Gene: hsp701V
A;Intross: 61/2
C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X70684; NID:922781; PIDN:CAA50019.1; PID:922782 A;Experimental source: kidney; cell line COS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
2.5;
                                                                                                                                           A; Accession: 136927
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2;
Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conservative
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A, Molecule type: DNA
A, Residues: 1-639 <SCO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1/111111 1
284 SLFEGIDFY 292
A; Residues: 1-638 <SAI>
                                                                                                                                                                                                                                                      A; Residues: 1-638 <RES>
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                                                                                                                                                                                                                                                                                                                                                                        A; Gene: hsp70
C; Function:
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N;Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S31766; 136927
C;Accession: S17766; 136927
Ssains. T; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
Submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L22736; NID:9433179; PIDN:AAA33219.1; PID:9433180
A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Va
                                                          C; Accession: A25646
R: Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
A; Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene. A; Reference number: A25646; MUID:86304452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein agi
C;Species: Dictyostelium discoideum
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Eddy, R.J.; Sauterer, R.A.; Condeells, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A.Fitle: Adinactin, an agonist-regulated F-actin capping activity is associated with an A;Reference number: A48872; MUID:94043116
A;Accession: A48872
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C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: involved in protein folding and assembling/disassembling of protein comple; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dnaK-type molecular chaperone hspB – slime mold (Dictyostellum discoideum) (fragment)
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   N;Alternate names: heat shock protein 70
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-634 <MOR>
A; Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A; Note: the authors translated the codon TCG for residue 583 as Trp
C; Function:
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Indels

Length 634;

Score 40; DB 2; Pred. No. 2.5; 0; Mismatches

87.0%; 88.9%;

Best\_Local Similarity 88.9 Matches 8; Conservative

Query Match

1 SLFEGIDAY 9

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Indels

Length 636;

DB 2; 2.5;

87.0%; Score 40; DB 88.9%; Pred. No. 2.5; tive 0; Mismatches

Conservative

280 SLFEGIDFY 288

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1 SLFEGIDAY 9

Query Match Best Local Similarity Matches 8; Conserv

A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-636 <EDD>

Accession: A48872

A; Reference number: S31766 A; Accession: S31766 A; Molecule type: mRNA

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

6, 2001, 07:58:27; Search time 88.19 Seconds
(without alignments)
7.774 Million cell updates/sec December

1 SLFEGIDFY 9 PEP1-MOD8F 48 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_68:\* Database:

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	H	dnaK-type molecula		dnaK-type molecula	heat-shock protein	heat-shock protein	heat-shock protein			dnaK-type molecula		dnaK-type molecula	hypothetical prote	dnaK-type molecula	heat shock protein															
COTAMANA	QI	B44261	I51344	A26283	T45477	T45479	T45476	T45478	н96605	T45471	A25646	A48872	S31766	JC1391	S20139	HHKW7A	A29160	S37394	T21394	T43724	S53357	S35718	I54542	A45871	HHBYA1	JH0095	B36590	A45635	$\overline{}$	T46650
	DB	7	7	7	7	7	7	7	~	~	7	7	~	7	7	Н	7	7	7	7	7	~	~	~	-	7	~	~	7	7
	Length	208	278	420	467	467	468	469	617	632	634	636	638	639	639	640	640	640	640	640	641	641	641	641	642	642	642	4	645	4
	Query	0.00	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0.0
æ	Ma	100	10	10	10	ĕ	10	100	10	10	10	10	10	10	10	10	10	Ĭ	10	100	10	10	70	70	Ĭ	70	70	10	20	100
	Score	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48
	Result No.	1	7	e	4	Ŋ	9	7	80	٥.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

dnaK-type molecula	dnaK-type molecula	heat shock protein	heat shock protein	dnaK-type molecula	dnaK-type molecula	heat-shock protein	heat-shock protein	dnaK-type molecula	heat shock protein	dnaK-type molecula	dnaK-type molecula	heat shock protein	heat shock protein	dnaK-type molecula	dnaK-type molecula
ннхг70	S44168	T41121	JC7088	A03309	I46588	T45473	T45474	JN0668	PC7036	S25585	809036	T45517	JC7132	S48024	S48025
7	~	7	7	7	7	7	7	7	7	7	7	7	7	7	7
647	647	647	650	214	379	467	467	641	641	643	643	651	651	209	209
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100	100	100	100	97	97	97	97	97	97	97	97	97	97	93	93
48	48	48	48	47	47	47	47	47	47	47	47	47	47	45	45
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels

Gaps ö 1 SLFEGIDFY 9

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132 SLFEGIDFY 140 qq δ

drak-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)
N;Alternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Accession: 151344
R;Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polyeeptides from rainbow trout: Characterization o
A;Reference number: 151344, MUID:85036330
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-278 <KOT>
A;Residues: 1-278 <KOT>
A;Residues: 1-278 <KOT>
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70

C; Keywords: ATP; molecular chaperone

Query Match

Best Local Similarity 100.0%;

Matches 9; Conservative 0

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1 SLFEGIDFY 9

dnaK-type molecular chaperone - mouse (fragment)
N;Alternate names: heat shock protein 68
C;Species: Mus musculus (house mouse)

A; Accession: A26283

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                  C;Species: Eunicella cavolini
C;Species: Eunicella cavolini
C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
R;Borchhellnin, C; Le Parco, Y.
A;Reference number: 222983
A;Reference number: 222983
A;Accession: T45479
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Atatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-467 <BOR>
A;Residues: 1-467 <BOR>
A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1
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C;Species: Eunicella cavolini
C;Species: Eunicella cavolini
C;Bate: 31-3an-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45478
R;Borchiellini, C.; Le Parco, Y.
S;Borchiellini, C.; Le Parco, Y.
A;Reference number: 222983
A;Accession: T45478
A;Accession: T45478
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)
C;Species: Puniculina quadrangularis
C;Species: Puniculina quadrangularis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45476
R;Borchiellini, C; Le Parco, Y.
B;Rorchiellini, C; Le Parco, Y.
B;Reference number: 222983
A;Reference number: 222983
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-468 <BOR>
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heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
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100.0%; Pred. No. 0.068;
Live 0; Mismatches 0;
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C;Genetics:
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A,Gene: Hsp70
C,Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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Best Local Similarity 100.
Matches 9; Conservative
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A; Residues: 1-469 <BOR>
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252 SLFEGIDFY 260
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C; Accession: A26283
R; Lowe, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A; Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
A; Reference number: A26283; MUID:86111900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-420 <LOM>
A; Cross-references: 6B:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208
A; Cross-references: translated the codon CTG for residue 173 as Val and CGC for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: involved in protein folding and assembling/disassembling of protein compl
C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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C;Species: Chondrosia reniformis
C;Dacession: 13-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45477
R;Borchiellini, C: Le Parco, Y.
Submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
A;Reference number: 222983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                       Score 48; DB 2; Length 278; Pred. No. 0.039; 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.061;
rative 0; Mismatches 0; Indels
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Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative

1 SLFEGIDFY 9

ò g A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-467 < GDR-A;Cross-references: EMBL:AF026517; PIDN:AAC05362.1

A;Gene: Hsp70 C;Superfamily: heat shock protein 70

C;Genetics

Query Match 100. Best Local Similarity 100. Matches 9; Conservative

252 SLFEGIDFY 260

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RESULT T45479

Bright Care

1 SLFEGIDFY 9

Query Match

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dnaK.type molecular chaperone - chicken
N;Alternate names: heat shock protein 70
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C;Accession: A25646 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C;Accession: A25646 #unt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 12692-12699, 1986
A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 ge
A;Fdeference number: A25646; MUID:86304452
A;Accession: A25646
A;Molecule type: DNA
A;Rocsidues: 1-634 <AMOR>
A;Accession: A25646
A;Molecule type: DNA
A;Rocsidues: 1-634 <AMOR>
A;Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A;Note: the authors translated the codon TCG for residue 583 as Trp
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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NiAlternate names: heat shock protein 70
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 48; DB 2; 100.0%; Pred. No. 0.095;
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Best Local Similarity 100.
Matches 9; Conservative
11111111
285 SLFEGIDFY 293
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280 SLFEGIDFY 288
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                                                                                                                                                                                                                                                                            probable heat shock protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: H96605
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.*, Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Sctus: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <STO
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dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostellum discoideum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: heat shock cognate protein 70
C;Species: Dictyostellum discoldeum
C;Sate: 31-7an-2000 #sequence_revision 31-7an-2000 #text_change 18-Feb-2000
C;Accession: 745471
R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Score 48; DB 2; Length 469; 100.0%; Pred. No. 0.069;
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A; Accession: T45471
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-632 <BOV>
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A;Experimental source: strain AX3
C;Genetics:
A;Gene: hscol
A;Note: localized to filopodias and cortex
C;Superfamily: heat shock protein 70
                                                    0; Mismatches
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C;Superfamily: heat shock protein 70
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                                                    9; Conservative
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                   Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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254 SLFEGIDFY 262
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A; Gene: F13N6.9

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Gaps

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Gaps

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A;Gene: hsp70 C;Function:

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A;Cross-references: EMBL:273129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YL A;Experimental source: strain $288C
R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D. submitted to the Protein Sequence Database, May 1996
A;Reference number: $64775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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N.Alternate names: heat shock protein 70 A
C.Species: Genorhabditis elegans
C.Species: Genorhabditis elegans
C.Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
C.Specession: JT0285
R.Snutch, T.P.: Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A.Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri
A.Reference number: JT0285; MUID:88297155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, April 1996
A;Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals mily and a new ABC transporter homologous to the human multidrug resistance protein. A;Reference number: $69380
A;Accession: $69383
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C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000 C;Accession: S20139; S64772; S64775; S69383 R;Stater, M.r.; Craig, E.A. Mucleic Acids Res. 17, 805-806, 1989 A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae. A;Reference number: S20139; MUID:89128457 A;Accession: S20139 A;Ditle: translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007
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R; Goffeau, A.; Purnelle, B.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64761
A; Accession: S64772
A; Molecule, type:
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Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0;
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A;Map position: 12L
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A;Residues: 72-639 <DUE>
A;Cross-references: EMBL:273129; MIPS:YLL024c
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R; Purnelle, B.; Goffeau, A.
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A; Molecule type: DNA; mRNA
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          C;Accession: S31766; I36927
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
Submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein A;Reference number: S31766
A;Accession: S31766
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R;Sconzo, G.; Scardina, G.; Ferraro, M.G.
Resconzo, G.; Scardina, G.; Ferraro, M.G.
A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
A;Reference number: JC1391; MUID:93077053
A;Accession: JC1391
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                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-638 <631.
R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A; Title: The hac'O gene which is slightly induced by heat is the main virus inducible in the factore number: 136927; MUID:95080396
A; Accession: 136927
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N;Alternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
N;Alternate names: heat shock protein 70IV; hsp70IV protein
C;Species: Paracentrotus lividus (common urchin)
C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: involved in protein folding and assembling/disassembling of C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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A;Residues: 1-639 <SCO>
A;Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-638 <RES>
A;Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A;Experimental source: Kidney; cell line COS-1
C;Genetics:
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Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0;
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284 SLFEGIDFY 292
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A; Gene: hsp70IV A; Introns: 61/2

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RESULT S20139

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C;Genetics:
A;Gene: hsp70A
A;Mep position: IV
A;Introns: 69/1; 331/3; 558/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

ő Gaps 0; Query Match

100.0%; Score 48; DB 1; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0; Indels

1 SLFEGIDFY 9

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GenCore version 4 Copyright (c) 1993 - 2000 c in search, using sw model ecember 6, 2001, 08:04:03;	4.0 LLOSUMG2 Gapop 10.0 , Gapext 0.5 522463 seqs, 74073290 residues	f hits satisfying chosen parameters length: 0 length: 0 length: 2000000000 grammatch 0% Maximum Match 100% Listing first 45 summaries	A_Geneseq_1101:*     /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*     /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*     /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*     /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*     /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*     /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*     /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*     /SIDS8/gcgdata/geneseqy/geneseqp/AA1985.DAT:*     /SIDS8/gcgdata/geneseqy/geneseqp/AA1987.DAT:*     /SIDS8/gcgdata/geneseqy/geneseqp/AA1987.DAT:*     /SIDS8/gcgdata/geneseqp/AA1987.DAT:*	10: \SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:* 11: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 11: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 12: \SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* 14: \SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:* 15: \SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:* 15: \SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:* 16: \SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:* 17: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 18: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 19: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 20: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 21: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 22: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 23: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 24: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* 25: \SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*	the number of results predit than or equal to the score is by analysis of the total SUMMARIES	554 21 25 25 21 26 25 21 26 25 21 26 25 21 21 26 26 21 21 26 20 20 20 20 20 20 20 20 20 20 20 20 20
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                                                                    the amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to pumphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes presented on the pericellular membranes by lymphocytes elicits a cytocoxic response which Kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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100.0%; Pred. No. 0.0012;
iive 0; Mismatches 0;
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Claim 8; Page 15; 21pp; English
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Matches 9; Conservative
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N-PSDB; AAA15621.
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                     Length 554;
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                     DB 21; I
0.11;
thes 0;
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                          100.0%; Score 48; 100.0%; Pred. No.
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Query Match
Best Local Similarity 100
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Best Local Similarity 100.
Matches 9; Conservative
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N-PSDB; AAA15622.
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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.
                                                                                                                                                    This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNB under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; NK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukeamia, lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
                                                          Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,
                                                                                                                                                                                                                                                                                                                               21; Length 554;
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100.0%; Pred. No. 0.11;
ive 0; Mismatches 0; Indels
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                                                                                                                          Disclosure; Fig 6; 11pp; Japanese.
 (HOKE-) HOKEN KAGAKU KENKYUSHO KK
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Best Local Similarity 100.
Matches 9; Conservative
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200 slfegidfy 208
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                                                                                                                                                                                                                                                                                                                                                         Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
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chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; SHSP70.
                                                                       Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; SHSP70.
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                                           Human heat shock protein SHSP70 amino acid sequence.
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              31-JUL-2000 (first entry)
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Matches 9; Conserv
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                                                                                                                                       Homo sapiens
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provides an alignment of heat shock proteins from a variety

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Fig. 2
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      complex which is detected. The invention also relates to a method of complex which is detected. The invention also relates to a method of dentifying compounds that inhibit Hsp72-mediated JNK phosphatase activity incomposition contacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The cinvention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity. The compounds identified as inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibitors of Hsp72 or JNK phosphatase activity are useful for as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention.
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                                                                                                                                                                                                                                                                                                                                Gaps
Optionally, Hsp72 is contacted with the test compound under optimum
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                                                                                                                                                                                                                                                                                                     Score 48; DB 21; Length 624;
Pred. No. 0.12;
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634
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Best Local Similarity 100.
Matches 9; Conservative
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Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922); 2. Bacillus megaterium (Emensp70 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T. cruzi (tc70kd - AAR03925);
                                                                                                                                                                                                                                                                                                The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                E. coli (dnaK - AAR03924);
T. cruzi (tc70kd - AAR03925);
T. cruzi (tat03925);
Rat rattus (rathsp70 - AAR03927);
Kenopus laevis (x170 - AAR03928);
Homo sapiens (humhsp70 - AAR03928);
Gallus gallus (chkhsp70 - AAR03930);
O. cae mays (mzehsp70 - AAR03931);
L. Serratia marcescens (smahsp70 - AAR03932).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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M.hyopneumoniae (Mhyhsp70 - AAR03922);
Bacillus megaterium (Bmehsp70 - AAR03923);
E. coli (dnaK - AAR03924);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 48; DB 11; Length 634; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR03929 standard; Protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89WO-0003955.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens HSP (humhsp70)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dragon E, Faulds D,
                                                                                                                                                                                                                                                                                                                                  vaccines and diagnos.
Mycobacteria species
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  of organisms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (copo-) copon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR03929;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ArPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the protein vector of (3). (1) has cytostafic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compositions in preventing and/or treating infectious diseases such as malazia or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a fused protein (I) prepared from a
                                                                                                                                                                                                                                                                                                        ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
                                                                                                                                                                                                                                                                Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 48; DB 21; Length 640; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 49-52; 72pp; Japanese.
                                                                                                                                    AAB23653 standard; protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-2000; 2000WO-JP00941.
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                                                                                                                                                                                                                        (first entry)
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                      05-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2000
                                                                                                                                                                              AAB23653;
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AAY88408
ID AAY81
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AC AAY81
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                                                                                                                  AAB23653
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5. T. cruzi (AAR03926);
6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapiens (humhsp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03932).
having homology to hsp's of T. cruzi can be used in diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
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                                                                                                                                                                                                                                                                                                          Length 640;
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100.0%; Pred. No. 0.12;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.12;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW10065 standard; Protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95JP-0158581
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                  Mycobacteria species
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N-PSDB; AAT58086.
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Matches 9; Conser
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286 slfegidfy 294
                                                                                                                                                                                                                                          640 AA;
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                                                                                                                                                        The proteins
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AAW10065;

stress.

Sequence

888888888888

Query Match

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Gaps

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1 SLFEGIDFY 9

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Sequence

Query Match

31-JUL-2000 (first entry)

99JP-0257146 95JP-0158581

01-JUN-1995; 01-JUN-1995;

07-MAR-2000

JP2000069999-A.

Homo sapiens

WPI; 2000-264458/23. N-PSDB; AAA15620.

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This sequence represents the human heat shock protein LHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                             Abnormal transcription of intracellular \mbox{HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..385
/label= 44kD_ATPase_fragment
/note= "peptides comprising an intact domain from fnote The ATPase fragment of hsp70 are claimed; the peptides are homologous to sequences conserved between SLIP1 and 74.5kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulphoglycolipid immobilising protein 1; sperm plasma membrane; HSC70B; mammalian; infertility; mycoplasma; HSP70.
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                                                                                                                                                                                                                                                                                                                                                                      Length 640;
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100.0%; Pred. No. 0.12;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mycoplasma protein"
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                                                                                                                                         Disclosure; Fig 4; 11pp; Japanese.
(HOKE-) HOKEN KAGAKU KENKYUSHO KK.
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/note= "part"
189..228
/label= IIA
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/note= "part"
40.115
/label= IB
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307..385
/label= IIA
/note= "part"
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                                   WPI; 2000-264458/23
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Best Local Similarity
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286 slfegidfy 294
                                                                                                                                                                                                                                                                                                                           640 AA;
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                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                  Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                        Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 48; DB 21; Length 640; 100.0%; Pred. No. 0.12; ative 0; Mismatches 0; Indels
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                                       Human heat shock protein HSP70 amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 1; 11pp; Japanese.
                                                                                                              depression; nephrotic syndrome
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99JP-0257146. 95JP-0158581

01-JUN-1995;

07-MAR-2000

01-JUN-1995;

1

JP2000069999-A.

Homo sapiens

31-JUL-2000 (first entry)

AAY88411;

Query Match .100.
Best Local Similarity 100.
Matches 9; Conservative

640 AA;

Sequence

RESULT 12

1 SLFEGIDFY 9

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Gaps

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Gaps

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Proteins AAW54349-W54364 are examples of proteins produced in the endometrium during the hyperplastia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the Arpase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.
                                                                                                                                                                                Score 48; DB 19; Length 641; Pred. No. 0.12; 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 46-48; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                              AAB23652 standard; protein; 641 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protozoacide; leukaemia; cancer
                                                                                                                                                                                100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-543748/49.
                                                                                                                                                                                                                                                                                286 slfegidfy 294
                                                                                                                                                                                                                                                1 SLFEGIDFY 9
                                                                                                                                  641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-AUG-2000
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                              AAB23652;
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                                                                                                                                                                                                                                                                                                          The likelihood of mammalian fertilisation is decreased by contacting a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated glyco-molety interfering composition. The interfering compositio is e.g. the heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
2D gel electrophoresis; detection.
                                                                                                                                                                                   Mammalian fertilisation decrease for detecting and treating infertility – using sulpho glyco lipid immobilising protein 1-sulphated-glyco molety interfering compsn., for mycoplasma infection treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 48; DB 14; Length 641; 100.0%; Pred. No. 0.12; 1.1ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemical markers of human endometrium - useful for, e.g.
                                                                                                                                                                                                                                                                           Claim 2 and Clalim 17; Page 60-62; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis of hyperplasia and adenocarcinoma
                                                                                                                                Faulds DH, Lingwood CA, Tanphaichitr N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW54349 standard; protein; 641 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 19; 77pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human heat shock 70 kD protein 1.
                                                                                 (BERL-) BERLEX LAB INC. (OTTA-) OTTAWA CIVIC HOSPITAL.
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                  93WO-US03816.
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96GB-0018600
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                WPI; 1993-368422/46.
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                22-APR-1993;
                                               24-APR-1992;
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AAW54349
ID AAW5
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0; Gaps Query Match 100.0%; Score 48; DB 21; Length 641; Best Local Similarity 100.0%; Pred. No. 0.12; Matches 9; Conservative 0; Mismatches 0; Indels 0

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1 SLFEGIDFY 9 ||||||||| 286 slfegidfy 294 QQ

Search completed: December 6, 2001, 08:04:03 Job time: 611 sec

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Perfect score:

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                                                      P26413 divine max
P1943 divine the P11142 homo sapien
P08109 mus musculu
P87047 paracoccidi
O65719 arabidopsis
 mus musculu
pichia angu
                      schizosacch
                                P53421 pichia angu
P27322 lycopersico
                                                                                                                                                                                                                                                                                                                                            MEDLINE-89201313; PubMed-2704388; MEDLINE-89201313; PubMed-2704388; MEDLINE-89201313; PubMed-2704388; Methstein N.M., Higashi G., Yates J., Rajan T.V.; Rothstein N.M., Higashi G., Yates J., Rajan T.V.; Mollochocerca volvulus hear shock protein 70 is a major immunogen in amicrofilaremic individuals from a filariasis-endemic area."; Mol. Biochem. Parasitol. 33:292-236(1989).

1- DISERSE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.

1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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          P53623
Q10265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35614 MW; 2BA3A2E8155A7180 CRC64;
                                                                                                                                                                                                                                         01-0CT-1989 (Rel. 12, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).
Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 AA
                                                                                                                                                                                                                     322 AA
         HS72_PICAN
HS71_SCHPO
HS71_PICAN
HS72_LIVCES
HS72_LIVCES
HS7C_CHIGR
HS7C_MOUSE
HS7C_MOUSE
HS77_MARAH
HS73_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PR0SITE; PS00297; HSP70_1; PARTIAL.
PR0SITE; PS00329; HSP70_2; PARTIAL.
ATP-binding; Heat shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Matches 9; Conservative
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322 AA;
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1 SLFEGIDFY 9
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HS73_MOUSE
ID HS73_MOUSE
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P11503;
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SEQUENCE
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HS70_ONCVO
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homo sapien
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brugia mala
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blastocladi
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drosophila
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Q92260
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                      Compugen Ltd.
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS70_CHICK
HS71_CERAE
HS72_YEAST
HS74_PARLI
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HS71_MOUSE
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HS76_HUMAN
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HS70_PENCI
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HS7C_DICDI
HS71_BOVIN
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HS70_NEUCR
HS70_XENLA
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDIJINE=86304422; Pubmed=3017985;
MOTIMOTO R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
Morjanization, nucleotide sequence, and transcription of the chicken HSP70 gene.";
                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium
                                                                                                                                                                                                                       Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.; "Molecular cloning and expression of a Penicillium citrinum allergien with sequence homology and antigenic cross-reactivity a hsp?0 human heat shock protein."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 261:12692-12699(1986).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 48; DB 1; Length 503; 100.0%; Pred. No. 0.035; Live 0; Mismatches 0; Indels
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER 1 1 1 SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (HSP70).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 064207; AAB06397.1; -. HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                            Penicillium citrinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 SUFECIDEY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SLFEGIDFY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                   NCBI_TaxID=5077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HS70_CHICK
P08106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
HS70_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONMATYVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
-!- INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                              Lowe D.G., Moran L.A.;
"Molecular cloning and analysis of DNA complementary to three mouse
Mr = 68,000 heat shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 V -> G.
46292 MW; 5DAlC6155C7B16B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00012; HSP70; 1.
PROSITE; PS00297; HSP70_1; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).
HSP70-3 OR HSP70A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 155-420 FROM N.A.
MEDLINE=94357449; PubMed=8076831;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-86111900; PubMed-2868009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M12571; AAA57234.1; -. EMBL; M12572; AAA57235.1; -. HSSP; P19120; lATR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:96244; Hsp70-3.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 146:273-278(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS70_PENCI
Q92260;
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HS70\_PENCI RESULT

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Gaps

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1 SLFEGIDFY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C;
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MEDLINE-95080396; PubMed-7988690;

MEDLINE-95080396; PubMed-7988690;

MEDLINE-95080396; PubMed-7988690;

Radias I., Angelidas C., Pagoulatos G., Lazaridis I.;

Radias I., Angelidas C., Lazaridis I.;

Radias I., Angelidas C., Lazaridis I.;

RADIAS I., Radias I., Angelidas C., Lazaridis I.;

RADIAS I., Radias I., Angelidas I., A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 48; DB 1; Length 634; 100.0%; Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                  Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEAPTO: 1.
PROSITE; PS00391; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
SEQUENCE 634 AA; 69750 WW; 4270FF00B3365ABB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
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PRINTS; PR00301; HEATSHOCK70.
                                                                              EMBL; J02579; AAA48825.1; •. PIR; A25646. HSSP; P19120; 1ATR. InterPro; IPR001023; HSP70.
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Matches 9; Conservative
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Q28222;
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H871_CERAE

115-DEC_20

DT 115-DEC_20

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                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 71-638 FROM N.A. Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garrels J.I., Futcher B., Robayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.

-i- FUNCTION: SSA2 MAY DELAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender E
Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaberone; Heat shock; Multigene family; MHC III.
SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                 ó
                                                                                                                          Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                        RESULT 6
HS72_YEAST
LD HS72_LYEAST
AC P10592,
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 34, Last annotation update)
DF 01-OCT-1996 (Rel. 34, Last annotation update)
DF SA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lectrophoresis 15:1466-1486(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89128457; PubMed-2644626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95203288; PubMed=7895733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 38531 / Y41;
MEDLINE=97089742; Pubmed=8935650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 91-97 AND 325-341.
                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norbeck J., Blomberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 186-195.
                                                                                                                                                                                                                         11111111
284 SLFEGIDFY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88297155; PubMed-2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 64:241-255(1988).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 48; DB 1; Length 640; 100.0%; Pred. No. 0.046; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                              100.0%; Score 48; DB 1; Length 639; 100.0%; Pred. No. 0.046; ative 0; Mismatches 0; Indels
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PRINTS: PRO01012; HSP70: 1.

PRINTS: PRO03012; HSP70: 1.

PROSITE; PS00329; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2.CRC64;
                                                                                   PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 639 AA; 69749 MW; 40EZF29570808DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-FBB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M18540; AAA28078.1; -.
                       HSSP; P19120; 1NGJ.
Interpro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
les 9; Conservative
                                                                                                                                                                                                                                                                  Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JT0285; HHKW7A.
HSSP; P19120; 1NGI.
PIR; JC1391; JC1391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11111111
287 SLFEGIDEY 295
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          1 SLFEGIDEY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           characterization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLFEGIDFY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSP-1 OR HSP70A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS7A_CAEEL
P09446:
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93077053; PubMed=1339375; Sconzo G., Scardina G., Ferraro M.G.; Sconzo G., Scardina G., Ferraro M.G.; Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 gene family and its expression."; Gene 121:333-358(1992).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
    -i- PTM: PHOSPHORYLATED.
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan: PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS001395; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; ATP-binding; Multigene family; Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 AA; 69338 MW; 23BDDD120C194912 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
11-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paracentrotus lividus (Common sea urchin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                         EMBL; X12927; CAA31394.1; -. EMBL; Z73129; CAA97472.1; -. EMBL; X97560; CAA66167.1; -. PIR; S20139; S20139.
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                                                                                                                                                                                                                                                                                                                                   HSSP; P19120; INGJ.
SWISS-2DPAGE; P10592; YEAST
                                                                                                                                                                                                                                                                                                                                                                                      (EPD; 9800; -.
SGD; S0003947; SSA2.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.،
المالية 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 SLFEGIDFY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7656;
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Q06248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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RESULT 7 HS74\_PARLI

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eddy R.J., Sauterer R.A., Condeelis J.S.;
"Aginactin, an agonist-regulated F-actin capping activity is associated with an HS270 in Dictyostelium.";
J. Biol. Chem. 268:22367-23274 (1993).
-!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROFIEN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DEMANDIATED CAP32 AND CAP34.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS OF THE CELL CORTEX AND CELL PROTRUSIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSSIGIDLGTTYSCVGVWQNDRVEIIAND -> IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                           "The heat shock cognate protein from Dictyostelium affects actin polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                    MEDLINE-94008983; PubMed-8404847;
Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
Noegel A.A., Schleicher M.;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                             Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N -> T (IN REF. 2).
N -> A (IN REF. 2).
N -> L (IN REF. 2).
N -> C (IN REF. 2).
                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last annotation update)
HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
                   640 AA
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94043116; PubMed=8226849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X75263; CAA53039.1; -.
EMBL; L22736; AAA33219.1; -.
PIR; 337394; S37394.
HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P36415; DICTY.
DICTYDb; DD01078; hspB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00297; HSP70_1; 1. PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 12:3763-3771(1993).
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 3
352 3
640 AA;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=44689;
                                                                                                                          OR HSC70
                                                                                                                                                                                                                                      STRAIN-AX3;
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-AX3;
                 HS7C_DICDI
P36415;
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HS7C_DICDI
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100.0%; Score 48; DB 1; Length 640;

Query Match

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A ADMIT Genet. 25:196.196.1994).

A Anim. Genet. 25:196.196.196.1994).

- 1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
COF UNEXTY STEAMS AGAINST AGARGATION AND MEDITATE THE POLDING
OF UNEXTY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
COF GANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICLUAD PLAX AN ADDITIONAL ROLE BY PROVIDING A DRIVING PORCE FOR PROTEIN TRANSLACATION. THEY ARE INVOLVED IN SIGNAL TRANSDCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CONFORMATIONS OF SHORK.

- 1- INDUCTION: BY HEAT SHOCK.

- 1- INDUCTION: BY HEAT SHOCK.

- 1- INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                     ö
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ANGUS;
MEDLINE=95030563; PubMed=7943958;
GFOSZ M.D., Skow L.C., Stone R.T.;
"An AluI polymorphism at the bovine 70 kD heat-shock protein-1
                       ö
                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaperone; Heat shock; Multigene family.
 Pred. No. 0.046;
                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1)
                                                                                                                                                                                      641 AA.
                       Mismatches
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-95126904; PubMed-7826329;
                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641 AA; 70250 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE OF 212-641 FROM N.A.
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U09861; AAA73914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U02891; AAA03450.1; -.
                       9; Conservative
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
   Best Local Similarity
                                                                              11111111
284 SLFEGIDFY 292
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                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HSP70-1) locus.
                                                                                                                                                                                    HS71_BOVIN
Q27975; Q27964;
                                                         1 SLFEGIDFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                 HSP70-1
                                                                                                                                                   RESULT 10
HS71_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                     Matches
                                                                                                                                                 RESULT
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DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        641 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D-structure.
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CONFLICT
SEQUENCE
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HS71_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells."; Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).
ROWEN L., QIN S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
LOTELZ C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
"Human major histocompatibility complex contains genes for the major
heat shock protein HSP70".
Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
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MEDLINE=99234376; PubMed=10216320;
Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
"Structure of a new crystal form of human hsp70 ATPase domain.";
Acta Crystallogr. D 55:1107(1999).
-!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hunt C., Morimoto R.I.; "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70."; Proc. Natl. Acad. Sci. U.S.A. 82:6459(1985).
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
                                                                             ;;
                              100.0%; Score 48; DB 1; Length 641; 100.0%; Pred. No. 0.046;
                                                                             0; Indels
                                                                                                                                                                                                                                                                                              HS71_HUMAN STANDARD; PRT; 641 AA. P08107; P19790; O9UGMO; O9UGUB; 001-AUG-1988 (Rel. 08, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HEAT SHOCK 70 ROA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2). (HSPAIA OR HSPAI) AND HSPAIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                             0; Mismatches
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                                                    Best Local Similarity 100.
Matches 9; Conservative
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286 SLFEGIDFY 294
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                                                                                                                             1 SLFEGIDFY
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HS71_HUMAN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
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"Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
N -> S (IN REF. 3; AAD21815).
STRESS-INDUCED DAMAGE.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 48; DB 1; Length 641; 100.0%; Pred. No. 0.046;
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P17879; 061689;
01-MUG-1990 (Rel. 15, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
HSPA1 OR HSP70-1 OR HSP70-1 OR HCP70.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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MEDLINE=90236310; Pubmed=2332169;
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110
370
459
70052 MW; '
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                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF134726; AAD21816.1; -. EMBL; AF134726; AAD21815.1; -.
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Pfam; PF00012; HSP70; 1.
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SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                           -i- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEMLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED DEPTIDES EGGENITS WITH A NET HYDROHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metázoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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MEDILNE-92175874; PubMed-1339404;
Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
Bouquet Y.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 48; DB 1; Length 641; 100.0%; Pred. No. 0.046; hismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-289(1992).
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
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                                                           TISSUE=Liver;
MEDLINE=94357449; PubMed=8076831;
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                            Gene 146:273-278(1994).
Gene 87:199-204(1990)
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286 SLFEGIDFY 294
                                        FROM N.A.
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                                                                                                                                         Mus musculus.
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SEQUENCE
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P34930;
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HS71_PIG
DD HS71_PIG
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FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PEREXISENT PROTETINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPARE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES EGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLACTION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN=LEW.IM/GUN,
MEDIAINE=B9.012453: PubMed=7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
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Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.; Masse S.M., Sharp F.R.; CobNa cloning and expression of stress-inducible rat hsp70 in normal
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS71_RAT STANDARD; PRT; 641 AA. 007439; P42853; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
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J. Neurosci. Res. 36:325-335(1993).
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InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
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Best Local Similarity 100.

Matches 9; Conservative
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database.";
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                                                Gaps
                 Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.; "Cloning, nucleotide sequence and expression of rat heat inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS01039; HSP70_3; 1.

ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 48; DB 1; Length 641; 100.0%; Pred. No. 0.046; Live 0; Mismatches 0; Indels
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D -> H (IN REF. 2 AND 3).
G -> A (IN REF. 3).
; D02D96751C868583 CRC64;
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1-CT-1994 (Rel. 30, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).
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 MEDLINE=94368874; PubMed=8086479;
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EMBL; X77208; CAA54423.1; -.
EMBL; X77207; CAA54422.1; -.
EMBL; X74271; CAA52328.1; -.
HSSP; P19120; 1NCC.
InterPro; IPR001023; HSP70.
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Best Local Similarity 100.
Matches 9; Conservative
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SEQUENCE FROM N.A.
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286 SLFEGIDFY 294
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SEQUENCE FROM N.A.
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P10591;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
Norbeck J., Blomberg A.;
"Protein expression during exponential growth in 0.7 M NaCl medium of
STRAIN=S288C / AB972;
MEDLINE=95028152; PubMed=7941740;
Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
Delaney S., Ouellette B.F.F. , Barton A.B., Kaback D.B., Bussey H.;
"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 42 kbp SP07-CENI-CDC15 region.";
Yeast 10:535-541(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.

-!- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYBEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND IMPO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
-!- SUBCELLULAR LOCATION. CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.; "Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                Ogden R.C., Lee M.-C., Knapp G.; "Transfer RNA splicing in Saccharomyces cerevisiae: defining the
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PIR; 542164; 542164.
HSSP; P19120; 1ATR.
SWISS-2DPAGE; P10591; YEAST.
YEPD; 9788; ---
SSD; SOUGOOO04; SSA1.
InterPro; 1PR001023; HSP70.
PFMTX; PR00301; HSP70.1.
PROSITE; PS00329; HSP70.2; 1.
PROSITE; PS00329; HSP70.2; 1.
PROSITE; PS01036; HSP70.2; 1.
ROSITE; PS01036; HSP70.2; 1.
ROSITE; PS01036; HSP70.3; 1.
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Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996)
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EMBL; L22015; AAC04952.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 590-641 FROM N.A. MEDLINE-85087943; Pubmed=6096826;
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SEQUENCE OF 91-97 AND 325-341.
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SQ SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;

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pep1-mod8f.rsp
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0; Gaps
Query Match
100.0%; Score 48; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels
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Human heat shock p Mature mouse sperm Human heat shock 7 Human heat shock p Human heat shock p

AAB23652 AAB82534

Rat heat shock pro Xenopus laevis HSP Heat shock protein Heat shock protein Heat shock protein

Pyrobacullum aerop Marmoset intracell

AAR03928 AAY4199 AAB97601 AAY4200 AAB97602 AAW24255 AAW24255 AAW24858

Title:

Lung cancer associ Arabidopsis thalia Human secreted pro C glutamicum prote Corynebacterium gl Arabidopsis thalia Arabidopsis thalia

AAG02174 AAG9267 AAG45253 AAG45252 AAG45252 AAG4323 AAG2433 AAG2433 AAG2433 AAG2433 AAG3927 AAW54364 AAW31408

Human heat shock p Candida albicans h GFP-HSC70 fusion p H. pylori cytoplas

AAB82535 AAW01638 AAB22938 AAB22938

ALIGNMENTS

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26-APR-2001.
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 RESULT
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Human heat shock p
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Gallus gallus HSP
Homo saplens HSP
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Human heat shock p
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of heat shock protein -HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3. Heat shock protein 70 (HSP70) peptidic fragment 3. (IDMI-) IDM IMMUNO-DESIGNED MOLECULES Ą. AAB97603 standard; peptide; 10 Abastado JP, Bartholeyns J; 29-SEP-2000; 2000WO-EP09530 99EP-0120484 (first entry) WPI; 2001-290909/30. WO200129190-A1. Homo sapiens. 15-OCT-1999;

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554 AA;

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Sequence
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                                        the amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membranes. Recognition of increased numbers of HSP epitopes presented on the pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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        Claim 8; Page 15; 21pp; English.
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N-PSDB; AAA15621.
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Pred. No. 19;
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Best Local Similarity 88.9
Matches 8; Conservative
                                                 Conservative
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N-PSDB; AAA15622.
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        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                  200 slfegidfy 208
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                                                                                           1 SLFEGIDGY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995;
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ID AAY8
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AC AAY8
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XX.

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(HOKE-) HOKEN KAGAKU KENKYUSHO
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                                                                                                                                                                                                                                                                               sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14g22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                      This sequence represents the human heat shock protein SHSP70 amino acid
                                                                                                                                                                                                               Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                          Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; SHSP70.
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                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 21; Length 554;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                        Human heat shock protein SHSP70 amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY88413 standard; Protein; 554 AA.
                                                                                                                                                                           (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                    Disclosure; Fig 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                            81.2%;
88.9%;
                                                                                                                                       99JP-0257146
                                                                                                                                                        95JP-0158581
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      JUL-2000 (first entry)
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            200 slfegidfy 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                Homo sapiens
                                                                                                                                      01-JUN-1995;
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                                                                                                                   07-MAR-2000
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                                                                                                                                                                                                                                         This sequence represents the human heat shock protein SHSP70 amino acid asquence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14922-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
                                                          Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,
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Pred. No. 19;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB23252 standard; Protein; 624 AA.
                                                                                                                                                                                     Disclosure; Fig 6; 11pp; Japanese.
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHYL-) PHYLOGENY INC
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WPI; 2000-264458/23.
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Best Local Similarity
Matches 8; Conserv
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200 slfegidfy 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000.
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Optionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase cativity compounds in inhibit Hsp72-mediated JNK phosphatase cativity. The expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity. The compounds identified as inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibiting the proliferation of cells. Modulation of the activity of the inhibiting the proliferation of cells. Modulation of the activity of the as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit ways a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents buman Hsp72 used in the exemplifications of the invention.
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Sequence

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                           Gaps
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Score 39; DB 21; Length 624; Pred. No. 22;
                            1; Indels
                           0; Mismatches
   81.2%;
88.9%;
   Query Match 81.2
Best Local Similarity 88.9
Matches 8; Conservative
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AAR03930 standard; Protein; 634 AA. Gallus gallus HSP (chkhsp70). 30-AUG-1990 AAR03930; AAR03930 

(first entry)

Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

Gallus gallus.

/note= "residue given as "O" in specification" Location/Qualifiers Misc-difference

WO9002564-A

22-MAR-1990

12-SEP-1989;

88US-0243474 12-SEP-1988;

89WO-0003955

(CODO-) CODON

Dragon E, Faulds D,

Sias S;

WPI; 1990-115820/15

Proteins homologous to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

Disclosure; Fig 2.1-2.14; 86pp; English.

According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, <u>inc</u>luding "O" (?) at position 634.

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in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                                                                                                                                                                          Gaps
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Fig. 2 provides provides to the sequence (Mhyhsp70 - AAR03922); of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922); 2. Bacillus megaterium (Bmehsp70 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T. cruzi (tc70kd - AAR03925);
Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (RM)HySPO - AAR03922);
3. Bacillus megaterium (Bmehsp70 - AAR03923);
3. E. coli (dnaK - AAR03924);
                                         3. E. coll (dnaK - AAR03924);
4. T. cruzi (Lc70kd - AAR03925);
5. T. cruzi (AAR03926);
6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapiens (humhsp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03932);
proteins having homology to hsp's of T. cruzi can be used in cines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
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                                                                                                                                                                                                                                                                               11; Length 634;
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22;
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                                                                                                                                                                                                                                                                               Score 39;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR03929 standard; Protein; 640 AA.
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                         Mycobacteria species
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289 slfeqidfy 297
                                                                                                                                                                                                                                       634 AA;
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                                                                                                                                                                                              vaccines and
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peptide containing a CTL (Cytotoxic Tlymphocyte) epitope recognised by cytotoxic T cells and a protein containing the AFPase domain of a heat shock protein. Also described are: (1) a drug composition containing (1) as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the protein vector of (3). (1) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a fused protein (I) prepared from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                   Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 49-52; 72pp; Japanese
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                     AAB23653;
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ID AAY8
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AC AAY8
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                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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5. T. cruzi (AAR03926);
6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (X170 - AAR03928);
8. Homo sapiens (humhsp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03932).
The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 11; Length 640;
Pred. No. 22;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW10065 standard; Protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.2%;
88.9%;
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95JP-0158581
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 81.2
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                      Mycobacteria species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-081088/08.
N-PSDB; AAT58086.
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286 slfegidfy 294
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                                                                                                                                                                                                                                                                                                                                                                  640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLFEGIDGY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1996.
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Gaps

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07-MAR-2000

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This sequence represents the human heat shock protein LHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                           Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "peptides comprising an intact domain from the ATPase fragment of hsp70 are claimed; the peptides are homologous to sequences conserved between SLIP1 and 74.5kD mycoplasma protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sulphoglycolipid immobilising protein 1; sperm plasma membrane; HSC70B; mammalian; infertility; mycoplasma; HSP70.
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                                                                                                                                                                                                                                                                                                                                            21; Length 640;
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                                                                                                                                                                                                                                                                                                                                                                             1;
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1..385
/label= 44kD_ATPase_fragment
                                                                                                                                                                                                                                                                                                                                            Score 39; DB
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mature mouse sperm 70kD heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR43004 standard; protein; 641 AA.
                                                                                                                              Disclosure; Fig 4; 11pp; Japanese.
(HOKE+) HOKEN KAGAKU KENKYUSHO KK
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/label= IA
/note= "part"
40..115
/label= IB
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189..228
/label= IIA
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88.9%;
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/label= IIA
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/label= IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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/label- I
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                WPI; 2000-264458/23
                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             1 SLFEGIDGY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                Sequence
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14922-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                               Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; LHSP70.
                                                             Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human heat shock protein LHSP70 amino acid sequence.
                                  Human heat shock protein HSP70 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                  KK.
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Best Local Similarity 88.9%;
Matches 8; Conservative
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   (first entry)
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N-PSDB; AAA15620.
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                                                                                                                                                                  JP2000069999-A
                                                                                                                                   Homo sapiens.
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 31-JUL-2000
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Sequence

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AAY88411 RESULT

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Proteins AAW54349-W54364 are examples of proteins produced in the endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                                                                                                                                                           AAB23652 standard; protein; 641 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
                                                                                                                                                                                                                                                                                                                                                                protozoacide; leukaemia; cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUME ) SUMITOMO ELECTRIC IND
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                                                                                                                      81.2%;
88.9%;
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                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Udono H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-543748/49.
                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     641 AA;
                                                                                                                                                                                ||||||| |
286 slfegidfy 294
                                                                                       641 AA;
                                                                                                                                                                 1 SLFEGIDGY 9
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                  AAB23652;
                                                                                         Sequence
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                                                                                                                                                                                                         The likelihood of mammalian fertilisation is decreased by contacting a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated glyco-moiety interfering composition. The interfering compos. is e.g. the heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
                                                                                                                               Mammalian fertilisation decrease for detecting and treating infertility - using sulpho glyco lipid immobilising protein 1-sulphated-glyco moiety interfering compsn., for mycoplasma infection treatment
                                                                                                                                                                                                                                                                                                                     DB 14; Length 641;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemical markers of human endometrium - useful for, e.g. diagnosis of hyperplasia and adenocarcinoma
                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                    Claim 2 and Clalim 17; Page 60-62; 77pp; English.
                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                      Faulds DH, Lingwood CA, Tanphaichitr N;
                                                                                                                                                                                                                                                                                                                     Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW54349 standard; protein; 641 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 19; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2D gel electrophoresis; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CLIN-) CENT CLINICAL & BASIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human heat shock 70 kD protein 1.
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                                                                (OTTA-) OTTAWA CIVIC HOSPITAL
                                                                                                                                                                                                                                                                                                                     81.2%;
88.9%;
                                  92US-0873961.
            93WO-US03816
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Matches 8; Conservative
                                                       (BERL-) BERLEX LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fey SJ,
                                                                                                            WPI; 1993-368422/46.
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286 slfegidfy 294
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           22-APR-1993;
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06-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1998
                                                                                                                                                                                                                                                                                       Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer -
                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPase: Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.
                                                                                               1; Indels
Score 39; DB 19;
Pred. No. 22;
); Mismatches 1
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0; Gaps

Query Match
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels

1 SLFEGIDGY 9 ||||||| | 286 slfegidfy 294

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Search completed: December 6, 2001, 08:04:03 Job time:  $611\ sec$ 

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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		Description	Heat shock protein	Human heat shock p	Human Hsp72 (heat	Gallus gallus HSP							
COTTANTANOC		a.	AAY44199	AAB97601	AAY44200	AAB97602	AAB97603	AAY88409	AAY88410	AAY88412	AAY88413	AAB23252	AAR03930
		 	21	22	21	22	22	71	21	21	21	21	11
	a Query	Length	6	6	10	10	10	554	554	554	554	624	634
	a Query	Match	95.7	95.7	95.7	95.7	91.3	91.3	91.3	91.3	91.3	91.3	91.3
		Score	44	44	44	44	42	42	42	42	42	42	42
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640 11 AAR03929 640 18 AAW10065 640 21 AAR83653 640 21 AAY88401 641 21 AAY83004 641 19 AAR53004 641 22 AAB25534 642 21 AAB2553 643 18 AAW52895 644 22 AAB2534 223 21 AAG22174 223 21 AAG22174 224 2 1 AAG2433 21 AAG2433 22 21 AAG2433 22 AAG2333 246 20 AAY17408 646 20 AAY17408 646 20 AAY17408 646 21 AAB25649 646 22 AAB25649 646 22 AAB22651 646 22 AAB22651 646 22 AAB2263 890 21 AAB2263 890 21 AAB2263 890 21 AAB2263 890 21 AAB2263 891 22 AAB61974 633 14 AAR4002 134 22 AAG72333 188 21 AAG4338 841 22 AAG7333 188 21 AAG4338		Human heat shock p	mouse sper	heat shock	heat shock	ar snoc	xar near snock pro Xenonus laevis HSP	t intrac	Lung cancer associ	¥	Arabidopsis thalia		Arabidopsis thalia	Rat HSP (rathsp70)	Heat shock cognate	Human heat shock c	Mouse heat shock c	u	Human heat shock p	Human heat shock p	Candida albicans h	GFP-HSC70 fusion p	S. avermitilis ORF	Mouse SLIP1 homolo	Human olfactory re	Human OR-like poly	Human ORFX ORF174	thal	thal	Arabidopsis thalia
	AAR0392 AAW1006 AAB2365	AAY8840 AAY8841	AAR4300	AAW5434						AAG0217	AAG2433							AAB2364	-				AAB6197	-		AAG7233	AAB4041		AAG4138	
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### ALIGNMENTS

Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immunne defence; immunogenicity; specificity; human leucocyte antigen. Identifying mutant peptides from heat-shock protein 70, for treatment of cancer -Heat shock protein 70 amino acid residues 286-294. AAY4199 standard; peptide; 9 AA. 99WO-FR00957. 98FR-0005033. (INSR ) INST ROUSSY GUSTAVE. (first entry) Gaudin C; WPI; 2000-013251/01. Homo sapiens WO9954464-A1. 22-APR-1999; 22-APR-1998; 15-FEB-2000 28-OCT-1999 Triebel F, AAY44199; AAY44199 RESULT 

Claim 10; Page 6; 56pp; French.

This peptide corresponds to amino acid residues 286-294 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour specific T cell response. Identification of the hsp70 peptides that have at least a tumour specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (ii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an each culture sequencing colony contact in the peptides optionally formulated with an each culture sequencing the immunogenicity of the matant peptides identified. The peptides, optionally formulated with an each culture colony contact in the peptides in the peptides optionally formulated with an each culture colony. particularly solid cancers (carcinoma, saccoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumnour specific cytotoxic cytotoxic factors (specifically interleukin 2, interferon-gamma and tumour necrosis factor), particularly where the calls are used to stimulate immune defences. The method identifies peptides with high immunocity and high specificity for particular HLA (human leucocyte antigen) alleles.

Sequence

Gaps ; Score 44; DB 21; Length 9; Pred. No. 4.3e+05; 1; Mismatches 0; Indels 95.7%; 88.9%; Query Match Best Local Similarity 88.5

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1 SLFEGIDLY 9

q ð

AAB97601 standard; peptide; 9 AA.

AAB97601;

30-JUL-2001 (first entry)

Heat shock protein 70 (HSP70) peptidic fragment 1.

HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 1.

Homo sapiens

WO200129190-A1.

26-APR-2001

29-SEP-2000; 2000WO-EP09530.

15-OCT-1999;

(IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

Abastado JP, Bartholeyns J;

WPI; 2001-290909/30.

Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of heat shock protein –

Claim 8; Page 15; 21pp; English.

√The amino acid sequence of fragment 1 relating to position 286-294 of

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human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSP spitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; heat shock protein 70; hsp70; identification; tumour; mutation; r cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HIA; immune defence; immunogenicity; specificity; human leucocyte antigen.
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Pred. No. 4.3e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                     intracellular infected cells.
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88.9%;
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les 8; Conservative
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Matches 8,
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The amino acid sequence of fragment 2 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to 1 ymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to HSP and helps direct the immune response cancer cells). HSP70 fragments are useful for treating cancer or any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic T jumphocytes in a cell culture and/or induce these cells to secrete cytotoxic factors (specifically interleuwin-2, interferon-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HLA (human leucocyte Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 2. Score 44; DB 21; Length 10; Pred. No. 0.013; 1; Mismatches 0; Indels Heat shock protein 70 (HSP70) peptidic fragment 2. (IDMI-) IDM IMMUNO-DESIGNED MOLECULES. AAB97602 standard; peptide; 10 AA. Claim 8; Page 15; 21pp; English. 95.7%; 88.9%; Abastado JP, Bartholeyns J; 29-SEP-2000; 2000WO-EP09530 99EP-0120484 (first entry) 8; Conservative of heat shock protein WPI; 2001-290909/30. Query Match Best Local Similarity 10 AA; σ 6 antigen) alleles WO200129190-A1. 1 SLFEGIDLY Homo sapiens. 15-OCT-1999; 30-JUL-2001 26-APR-2001. Sequence AAB97602; Matches RESULT g 

ó The amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3. Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression Gaps ; Score 44; DB 22; Length 10; Pred. No. 0.013; 1; Mismatches 0; Indels Heat shock protein 70 (HSP70) peptidic fragment 3. (IDMI-) IDM IMMUNO-DESIGNED MOLECULES. AAB97603 standard; peptide; 10 AA. Claim 8; Page 15; 21pp; English intracellular infected cells. 95.7%; 88.9%; 29-SEP-2000; 2000WO-EP09530. Abastado JP, Bartholeyns J; 99EP-0120484 (first entry) Best Local Similarity 88.9 Matches 8; Conservative of heat shock protein -WPI; 2001-290909/30. 1 SLFEGIDLY 9 WO200129190-A1. Homo sapiens. 15-OCT-1999; 30-JUL-2001 26-APR-2001. Sequence Query Match Ŋ RESULT AAB97603 g 8à

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Gaps

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cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or

.ntracellular infected cells.

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the human heat shock protein SHSP70 amino acid asquence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-34. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                              Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                  Gaps
                                                                                                                                                                    Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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Score 42; DB 22; Length 10;
Pred. No. 0.032;
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                  1; Indels
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                                                                                                                                                     Human heat shock protein SHSP70 amino acid sequence.
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Pred. No. 2.3;
0; Mismatches
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                                                                                                  AAY88409 standard; Protein; 554 AA.
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Best Local Similarity 88.9
Matches 8; Conservative
                   8; Conservative
                                                                                                                                                                                                                                                                                                                      WPI; 2000-264458/23.
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 Query Match
Best Local Similarity
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                                    1 SLFEGIDLY 9
                                               N-PSDB; AAA15621
                                                                                                                                                                                                                              JP2000069999-A.
                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                 01-JUN-1995;
                                                                                                                                      31-JUL-2000
                                                                                                                                                                                                                                                07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                     AAY88409;
                                                                                  9
                   Matches
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This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-34. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
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Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                              (HOKE-) HOKEN KAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.3%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                       Homo sapiens
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sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP/OmRNA under acute and chronic stress load in a human. The abnormal transcription of HSP/O can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of
                                                                                                                 This sequence represents the human heat shock protein SHSP70 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the human heat shock protein SHSP70 amino acid
            . transcription of intracellular {\rm HSP70mRNA} under acute and continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; SHSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human heat shock protein SHSP70 amino acid seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY88413 standard; Protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 6; 11pp; Japanese.
                                                                                 Disclosure; Fig 5; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                        91.3%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                          8; Conservative
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Best Local Similarity
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200 slfegidfy 208
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                                                                                                                                                                                                                                                        554 AA;
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               Abnormal
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                                 chronic
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DB 21; Length 554;

91.3%; Score 42;

Query Match

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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell and witch overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.

Optionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase certivation, comprising ocnacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and cetermining if the compound inhibits JNK phosphatase activity. The compound inhibitors of Hsp72 or JNK phosphatase activity. The compounds identified as invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity. The compounds identified as inhibiting the proliferation of cells. Modulation of the activity of the conflict or Hsp72 or JNK phosphatase activity. The compounds that inhibit conflict as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient chaving a disease or disorder mediated by an increase of Hsp72 expression cor activity relative to normal levels. The present sequence represents thum Hsp72 used in the exemplifications of the invention.
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                                                                                                                                                                                                                                                                                                                                                                    Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiprolliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; prostate cancer; prostate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,
                     Gaps
                     ó
                       Indels
                     1;
  Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                Human Hsp72 (heat shock protein 72)
                                                                                                                                                                                                       AAB23252 standard; Protein; 624 AA.
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88.98;
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                                                                                                                                                                                                                                                                                       (first entry)
                       8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PHYL-) PHYLOGENY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-647056/62.
Best Local Similarity
Matches 8; Conserv
                                                                                                   200 slfegidfy 208
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                                                             1 SLFEGIDLY
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                                                                                                                                                                                                                                               AAB23252;
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Gaps

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Score 42; DB 21; Length 554; Pred. No. 2.3; 0; Mismatches 1; Indels

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AAR03929 standard; Protein; 640 AA.
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289 slfegidfy 297
1 SLFEGIDLY 9
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                                                                                                                                                                                                                                                                                                                                                                                        Proteins homologous to heat shock proteins from Trypanosoma cruzi – use in vaccines and diagnosis for species of eg Mycoplasma or Mycobacterla.
                                                                                                                                                                                                                                                                                                                                                                                                                                  According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634.

Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyoponeumoniae (Mhyhsp?0 - AAR03922);

C. Bacillus megaterium (Bmehsp?0 - AAR03923);
3. E. coli (dnak - AAR03924);
4. T. cruzi (tc70kd - AAR03925);
5. T. cruzi (AAR03926);
6. Rat rattus (rathsp?0 - AAR03928);
7. Xenopus laevis (rathsp?0 - AAR03929);
9. Gallus gallus (chkhsp?0 - AAR03939);
10. Zea mays (mzchsp?0 - AAR03931);
11. Serratia marcescens (smahsp?0 - AAR03932).
The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                            Gaps
                                                                                                                                                                                                                                          /note= "residue given as "O" in specification"
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                                                                                                                                                                                     Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
          Length 624;
                            1; Indels
          DB 21;
         Score 42; DB 21
Pred. No. 2.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                              AAR03930 standard; Protein; 634 AA.
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                                                                                                                                                                    Gallus gallus HSP (chkhsp70)
            91.3%;
88.9%;
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                                                                                                                                                  (first entry)
                              Conservative
                                                                                                                                                                                                                                                                                                                                                       Dragon E, Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacteria species
  Query Match
Best Local Similarity
8; Conserv
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                                                           1 SLFEGIDLY 9
                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                         Gallus gallus
                                                                                                                                                                                                                                                                                                                                     (copo-) copon
                                                                                                                                                                                                                                                                                                 12-SEP-1989;
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                                                                                                                                                 30-AUG-1990
                                                                                                                                                                                                                                                             WO9002564-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins homologous to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           According to the legend of Fig 2, the H. sapiens HSP sequence has 641 amino acid residues, the sequence itself has only 640, including "O" (?) at position 640.
Fig. 2 provides are positionent of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. M. hyopneumoniae (Mhyhsp70 - AAR03922);
2. Bacillus megaterium (Bmehsp70 - AAR03922);
3. E. coli (dnaK - AAR03924);
4. T. cruzi (tc70kd - AAR03925);
5. T. cruzi (tc70kd - AAR03925);
6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (x170 - AAR03927);
8. Homo saplens (x170 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03929);
10. Zea mays (mzehsp70 - AAR03930);
11. Serratia marcescens (smahsp70 - AAR03931).
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                                                                                                                                                                                                                                                                /note= "residue given as "O" in specification"
                                                                                                                           Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
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                                                                                                                                                                                                     Location/Qualifiers
640
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                                                                                   Homo sapiens HSP (humhsp70)
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Best Local Similarity 88.3.
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacteria species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-115820/15.
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                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CODO:) CODON
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-1988;
                                        30-AUG-1990
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                       WO9002564-A.
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AAR03929
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Gaps

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1; Indels

DB 11; Length 634;

Score 42; DB 1. Pred. No. 2.7; 0; Mismatches

91.3%; 88.9%;

Query Match 91.3 Best Local Similarity 88.9 Matches, , 8; Conservative

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A CONTRACTOR OF THE PARTY OF TH

AAW10065 standard; Protein; 640 AA.

13

AAW10065 RESULT

Human heat shock protein 70

24-OCT-1997 (first entry)

AAW10065;

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The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the Arpase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 640; 2.7;
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Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                            Claim 3; Page 49-52; 72pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY88408 standard; Protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.3%;
88.9%;
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                                                      18-FEB-2000; 2000WO-JP00941.
                                                                                          99JP-0041535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 86.5.
امر 8; Conservative
                                                                                                                                                                     Shinbara N, Udono H,
                                                                                                                                                                                                           WPI; 2000-543748/49.
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N-PSDB; AAA15620.
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286 slfegidfy 294
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                                                                                          19-FEB-1999;
                24-AUG-2000
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AAY88408
ID AAY8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The cDNA encoding the present sequence, human heat shock protein 70 (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained
                                                                                                                                                                                                         Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
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Pred. No. 2.7;
0; Mismatches 1; Indels
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(HOKE-) HOKEN KAGAKU KENKYUSHO KK.

WPI; 1997-081088/08. N-PSDB; AAT58086.

95JP-0158581 95JP-0158581

01-JUN-1995; 01-JUN-1995;

JP08322577-A. Homo sapiens

stress.

10-DEC-1996

Claim 1; Fig 1; 13pp; Japanese.

AAB23653 standard; protein; 640 AA.

05-JAN-2001 (first entry)

AAB23633
AAB23633
XX
XX
AC AAB2
XX
XX
DT 05-J
XX
KW ATPa
KW AT

AAB23653;

WO200049041-A1

Homo sapiens.

91.3%; 88.9%;

Query Match Best Local Similarity 88.9°, .-hea 8; Conservative

õ

640 AA;

Sequence

ö

This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome. Sequence 640 AA;

Query Match

91.3%; Score 42; DB 21; Length 640;
Best Local Similarity 88.9%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 1; Indels 1 SLFEGIDLY 9 ŏ

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Search completed: December 6, 2001, 08:04:02 Job time: 610 sec

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Heat shock protein
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shock p
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Human Hsp72 (heat
Gallus gallus HSP
                                                                                       6, 2001, 08:04:02; Search time 184.09 Seconds (without alignments)
3.621 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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	12	41	89.1	640	11	AAR03929	Homo sapiens HSP (
	13	41		4	18	AAW10065	
•	14	41		4	21	AAB23653	
·	15	41		4	21	AAY88408	Human heat shock p
	16	41		4	21	AAY88411	Human heat shock p
,	17	41		4	14	AAR43004	Mature mouse sperm
	18	41	٠	4	19	AAW54349	Human heat shock 7
	19	41	٠	4	21	AAB23652	Human heat shock p
	50	41		4	22	AAB82534	Human heat shock p
	21	41		4	21	AAB23650	Rat heat shock pro
	22	41		4	11	AAR03928	Xenopus laevis HSP
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•	59	38		4	11	AAR03927	athsp70
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. ,	31	38		4	20	AAY17407	t shock
. ,	32	38		4	20	AAY17408	heat shock
	33	38		4	21	AAB23649	heat
	34	38	•	4	21	AAB23651	heat shock
	35	38		4	22	AAB82535	
	36	38		S	18	AAW01638	lbicans
	37	38		9	21	AAB22938	FP-HSC70 fusion
	38	37		$\vdash$	19	AAY85808	der
	39	37		2	19	AAW80645	
-	40	37	•	Н	22	AAB61974	S. avermitilis ORF
-	41	37		3	14	AAR43002	Mouse SLIP1 homolo
-	42	35	•	4	11	AAR03931	mays
-	43	35	76.1	647	20	AAY31380	T. gondii antigen
-	44	35		4	22	AAB49099	Toxoplasma gondii
•		34		a	21	AAG27768	Arabidopsis thalia
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RESULT AAY44199	LT 1						
<u>a</u>	AAY44199		standard;	peptide;	de;	9 AA.	
A A	AAY44199	66;					
××							
E	1	000		1	•		

AAY44199 standard; peptide; 9 AA.

AAY44199;

15-FEB-2000 (first entry)

Heat shock protein 70 amino acid residues 286-294.

Human; heat shock protein 70; hsp70; identification; tumour; mutation;

T cell response; amplification; vector; bacterium; cancer; allale;

Cytotoxic factor; interlaukin; interferon; tumour necrosis factor; interlaukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen.

S Homo sapiens.

WO9954464-A1.

28-OCT-1999.

22-APR-1999; 99WO-FR00957.

22-APR-1998; 98FR-0005033.

(INSR ) INST ROUSSY GUSTAVE.

Triebel F, Gaudin C;

WPI; 2000-013251/01.

I identifying mutant peptides from heat-shock protein 70, for treatment of cancer -

RESULT ŏ g This peptide corresponds to amino acid residues 286-294 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, darived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplifying hsp70 encoding pNA from one or more tumours; (ii) cloning the amplifying hsp70 encoding pNA from one or more tumours; (iii) sequencing fragments in each cultured bacterial colony to identify can pyp70 mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly widney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic T lymphocytes in a cell culture and/or induce these cells to secrete tumour necrosis factor), particularly where the cells are used to tumour necrosis factor), particularly where the cells are used to timnunde immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HLA (human leucocyte ö HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 1. Gaps .; 0 Score 45; DB 21; Length 9; Pred. No. 4.3e+05; Ordels 0; Indels Heat shock protein 70 (HSP70) peptidic fragment 1. 1; Mismatches (IDMI-) IDM IMMUNO-DESIGNED MOLECULES. AAB97601 standard; peptide; 9 AA Claim 10; Page 6; 56pp; French. 97.8%; 88.9%; Abastado JP, Bartholeyns J; 29-SEP-2000; 2000WO-EP09530 99EP-0120484 30-JUL-2001 (first entry) Query Match 97.8° Best Local Similarity 88.9° Matches 8; Conservative 1 SLFEGIDVY 9 antigen) alleles WO200129190-A1. Homo sapiens. 15-0CT-1999; 26-APR-2001 AAB97601; Sequence N AAB97601 õ

Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression

The amino acid sequence of fragment 1 relating to position 286-294 of

Claim 8; Page 15; 21pp; English

of heat shock protein

WPI; 2001-290909/30.

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to lymphocytes which recognise cells of a patient in which overexpression of HSP heads to a substantial cof HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increase allicits a cytotoxic pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSPVO epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to specific cells, (e.g. cancer cells). HSPVO fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or intracellular infected cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen.
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Pred. No. 4.3e+05;
Mismatches 0; Indels
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              Sequence
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pepl-mod8v.rag

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any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic T ymphocytes in a cell culture and/or induce these cells to secrete cytotoxic factors (specifically interleuwin-2, interferon-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high farminogenicity and high specificity for particular HLA (human leucocyte
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            55555555555555x&
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Sequence

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Score 45; DB 21; Length 10;
Pred. No. 0.0046;
1; Mismatches 0; Indels
 97.8%;
88.9%;
           Local Similarity 88.5
hes 8; Conservative
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                                           SLFEGIDVY
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 Query Match
Best Local S
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AAB97602 standard; peptide; 10 AA. (first entry) 30-JUL-2001 AAB97602; 

Heat shock protein 70 (HSP70) peptidic fragment 2.

HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 2.

Homo sapiens

WO200129190-A1.

26-APR-2001,

29-SEP-2000; 2000WO-EP09530

99EP-0120484 15-OCT-1999; (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

Bartholeyns J; Abastado JP,

WPI; 2001-290909/30.

Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of heat shock protein -Claim 8; Page 15; 21pp; English.

The amino acid sequence of fragment 2 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to 1 ymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to Specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or

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intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
                                                                                                                                                                                                                                                           HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.
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                                                                          97.8%; Score 45; DB 22; Length 10; 88.9%; Pred. No. 0.0046;
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                                                                                                                                                                                                                                           Heat shock protein 70 (HSP70) peptidic fragment 3.
                                                                                             1; Mismatches
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                            intracellular infected cells.
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                                                                                    Best Local Similarity 88.9
Matches 8; Conservative
                                              10 AA;
                                                                                                               1 SLFEGIDVY 9
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The amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP heads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which Kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or intracellular infected cells. 10 AA;

Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression

Claim 8; Page 15; 21pp; English

of heat shock protein

(IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

Abastado JP, Bartholeyns J;

WPI; 2001-290909/30.

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WPI; 2000-264458/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
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    Score 41; DB 22; Length 10;
Pred. No. 0.031;
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0; Mismatches
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Matches 8; Conservative
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This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The apnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
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Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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Pred. No. 2.6;
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88.98;
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AAY88413 standard; Protein; 554 AA.
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AAY88413
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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses HSP72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of HSP72.

Optionally, HSP72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a comparation, comprising contacting a test compound with a cell which expresses HSP72, exposing the cell to a heat induced stress and cettracting if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of HSP72 or JNK phosphatase activity. The compounds identified as invention additionally encompasses compositions comprising an inhibitor of HSP72 or JNK phosphatase activity. The compounds identified as inhibitors of HSP72 or JNK phosphatase activity are useful for on thibitors of HSP72 or JNK phosphatase activity are useful for inhibitors of HSP72 or JNK phosphatase activity are useful for as cancers (e.g., leukaenia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit the HSP72 activity can also be administered to treat premalignant conditions and to prevent progression to a neophastic or malignant state. The compounds that inhibit HSP72 function are administered to a patient condition and alsease or disorder mediated by an increase of HSP72 expression or activity relative to normal levels. The present sequence represents thuman HSP72 used in the exemplifications of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
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  Pred. No.
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Best Local Similarity
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                                                                                                                                                                                              sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSPOMRNA under acute and chronic stress load in a human. The abnormal transcription of HSPO can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
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                                                                                                                                                                           This sequence represents the human heat shock protein SHSP70 amino acid
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                  Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
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88.9%;
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Sequence

DB 21; Length 554;

89.1%; Score 41;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                        Proteins homologous to heat shock proteins from Trypanosoma cruzi – used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyopneumoniae (Mhyhap70 - AAR03922);
2. Bacillus megaterium (Bmehsp70 - AAR03923);
3. E. coli (dnaK - AAR03924);
4. T. cruzi (tc70kd - AAR03925);
5. T. cruzi (AR03926);
6. Rat ratius (rathap70 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapiens (humhsp70 - AAR03929);
9. Gallus gallus (chkhap70 - AAR03939);
10. Zea mays (mzehsp70 - AAR03930);
11. Serratia marcescens (smahsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03932).
The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  According to the legend of Fig 2, the G gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634.
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                                                                                                                                                                                                                                                    /note= "residue given as "O" in specification"
                                                                                                                                                                                            Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
         Length 624;
                              1; Indels
          Score 41; DB 21;
Pred. No. 2.9;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                   AAR03930 standard; Protein; 634 AA.
                                                                                                                                                                                                                                                                                                                                                                     Sias S;
                                                                                                                                                                           Gallus gallus HSP (chkhsp70).
            89.1%;
88.9%;
                                                                                                                                                                                                                                                                                                            89WO-0003955
                                                                                                                                                                                                                                                                                                                               88US-0243474
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                     Dragon E, Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacteria species
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-115820/15
                   Local Similarity
es 8; Conserv
                                                                    286 slfegidfy 294
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                                                                                                                                                                                                                                                                                                             12-SEP-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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             Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           Proteins homologous to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
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                                                                                                         Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2.1-2.14; 86pp; English
                                                                                                                                                            Location/Qualifiers
AAR03929 standard; Protein; 640 AA.
                                                                                                                                                                                                                                                                                                     88US-0243474
                                                                                                                                                                                                                                                                          89WO-0003955
                                                                               Homo sapiens HSP (humhsp70)
                                                                                                                                                                                                                                                                                                                                                            Sias
                                                      30-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacteria species.
                                                                                                                                                                                                                                                                                                                                                         Dragon E, Faulds D,
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DB 11; Length 634;

Score 41; DB 1 Pred. No. 3; 0; Mismatches

Query Match
Best Local Similarity 88.3%;
Matches 8; Conservative

7

AAW10065;

13

RESULT 1

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In present investigation with the properties of the present investigation of the properties of the protein containing the ATPase domain of a heat cytotoxic T cells and a protein containing the ATPase domain of a heat as brock protein. Also described are: (1) a drug composition containing (1) as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the protein vector of (3). (1) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence respresents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                            Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a fused protein (I) prepared from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome.
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                                                                                                                                                                                                                                                                                                                             Claim 3; Page 49-52; 72pp; Japanese.
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                                                                                                                                (SUME ) SUMITOMO ELECTRIC IND CO.
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N-PSDB; AAA15620.
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                                                                                                                                                                                      Human; heat shock protein 70; HSP70; primer; probe; detection; intracellular; abnormal transcription; acute; chronic; sustained; stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The cDNA encoding the present sequence, human heat shock protein (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Trimers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 18; Length 640;
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                                                    AAW10065 standard; Protein; 640 AA.
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88.9%;
                                                                                                                                                                    Human heat shock protein 70
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AAB23653;

Query Match

Matches

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Gaps

This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 1462-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome. Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application Claim 2; Fig 1; 11pp; Japanese. 640 AA; Sequence 

Score 41; DB 21; Length 640; Pred. No. 3; 0; Mismatches 1; Indels Query Match
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Homo sapiens HSP (
Human heat shock p
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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### ALIGNMENTS

Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen. Heat shock protein 70 amino acid residues 286-295. AAY44200 standard; peptide; 10 AA 99WO-FR00957. 98FR-0005033 (INSR ) INST ROUSSY GUSTAVE. (first entry) Triebel F, Gaudin C; W09954464-A1 22-APR-1999; Homo sapiens 22-APR-1998; 15-FEB-2000 28-OCT-1999 AAY44200; -AAY44200

Identifying mutant peptides from heat-shock protein 70, for treatment

WPI; 2000-013251/01.

of cancer

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This peptide corresponds to amino acid residues 286-295 of the human clear shock protein 70 (hsp70). The invention relates to a method of clentifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least a tumour-specific T-cell response, comprises: (i) amplifying hsp70 cone mutation or alteration compared with the native sequence, and induce coding DNA from one or more tumours; (ii) cloning the amplified coding DNA from one or more tumours; (ii) cloning the amplified coding DNA from one or more tumours; (ii) cloning the amplified coding DNA from ovector that can be replicated in bacterial.

CC (iii) sequencing fragments in each cultured bacterial colony to identify mutant peptides identified. The peptides, optionally formulated with an expensive that induces cellular stress, are used for treatment of cancer. Cancers of head and neck, particularly kidney cancer. The peptides may concers of head and neck, particularly kidney cancer. The peptides may concers of bead eto increase the proportion of tumour specific cytotoxic cytotoxic factors (specifically interleukin-2, interferon-gamma and cytimmulate immune defences. The method identifies peptides with high antiment allows allowed the antiment letter concerns the antiment of antiment letter consist factors (specifically for particular HLA (human leucocyte
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Pred. No. 0.0031;
0; Mismatches 1; Indels
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 Claim 10; Page 6; 56pp; French.
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90.0%;
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Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of heat shock protein -

The amino acid sequence of fragment 2 relating to position 286-295 of

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buman heat shock protein 70 (HSP70) is given. The new invention relates to thuman heat shock protein 70 (HSP70) is given. The new invention relates of HSP has been induced. Overexpression of HSP leads to a substantial forchase in the numbers of HSPs and HSP epitopes presented on the numbers of HSPs and HSP epitopes presented on the pericellular membranes by lymphocytes elicits a cytotoxic on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the presenting cells. This has the effect of increasing the immune response to HSP70 epitopes are mutated prior to being loaded into antigen to HSP and helps direct the immune response to specific cells, (e.g. intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic intracellular infected cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The amino acid sequence of fragment 3 relating to position 286-295 of human hear shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.
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Pred. No. 0.0031;
0; Mismatches 1; Indels
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90.0%;
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Best Local Similarity
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Human heat shock protein SHSP70 amino acid sequence.

(first entry)

31-JUL-2000

AAY88410; AAY88410

standard; Protein; 554 AA

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RESULT
AAY88410
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presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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Pred. No. 0.005;
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90.0%;
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sequence. Human heat shock proteins are located on chromosomes 5p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSPTOMRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
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Matches 9; Conservative
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Human Hsp72 (heat shock protein 72)
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90.0%;
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N-PSDB; AAA97541.
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Best Local Similarity
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Pred. No. 0.49;
0; Mismatches 1; Indels
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90.0%;
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Matches 9; Conservative
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JP2000069999-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1995;
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                                                                                    01-JUN-1995;
                                                                                                                                01-JUN-1995;
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                                          07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY88413;
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AAY88413

ò a This sequence represents the human heat shock protein SHSP70 amino acid

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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with carelia which overexpresses HSP2 (heat shock protein 71), and determining if the test compound inhibits activity or expression of HSP72.

Optionally, HSP72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a conditions to allow the two components to interact and bind, forming a computity of compounds that inhibit HSP72-mediated JNK phosphatase compounds the compound at the a cell which expresses HSP72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of HSP72 or JNK phosphatase activity. The compound stress and character activity are useful for inhibitors of HSP72 or JNK phosphatase activity are useful for inhibiting the proliferation of cells. Modulation of the activity of the
                                                                                                                                                                                                                                                                                 ö
sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiprolliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                   rheumatisms, schizophrenia, depression and nephrotic syndrome
                                                                                                                                                                                                                                   DB 21; Length 554;
                                                                                                                                                                                                                                                                                 1; Indels
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Pred. No. 0.49;
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JNK phosphatase or Hsp72 is used to treat a proliferative disorder such as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins homologous to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634.

Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03922);

S. Bacillus megaterium (Bmehsp70 - AAR03923);

B. coli (dnaK - AAR03924);

T. cruzi (tc70kd - AAR03924);

S. T. cruzi (tc70kd - AAR03925);

Kanopus laevis (x170 - AAR03928);

M. Momo saplens (humbsp70 - AAR03929);

Gallus gallus (chkhsp70 - AAR03930);

10. Zea mays (mzehsp70 - AAR03931);
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                   DB 21; Length 624;
                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                 Score 45; DB 21
Pred. No. 0.56;
); Mismatches
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                                                                                                                                                                                                 88.2%;
90.0%;
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                                                                                                                                                                                  Query Match
Best Local Similarity 90.uv,
Post 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-115820/15.
                                                                                                                                                                                                                                                                                          286 slfegidfyt 295
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                                                                                                                                                       624 AA;
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Proteins homologous to heat shock proteins from Trypanosoma cruzi – used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                          Gaps
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Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03922); 2. Bacillus megaterium (Bmehsp70 - AAR03922); 3. E. coli (dnaK - AAR03924); 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6. Rat rattus (rathsp70 - AAR03927);
7. Kenopus laevis (x170 - AAR03929);
9. Homo sapiens (humhsp70 - AAR03929);
10. Zea mays (mzehsp70 - AAR03930);
11. Serratia marcescens (smanhsp70 - AAR03931);
11. Serratia marcescens (smanhsp70 - AAR03932).
12. AAR03931);
13. Serratia narcescens (smanhsp70 - AAR03932).
14. AAR03931);
15. Serratia narcescens (smanhsp70 - AAR03932).
16. AAR03931);
17. Serratia marcescens (smanhsp70 - AAR03932).
18. AAR03931);
19. AAR03931);
10. Zea mays (mzehsp70 of T. cruzi can be used in diagnosis involving e.g. Trypanosoma, Mycoplasma and
11. Serratia marcescens (smahsp70 - AAR03932). The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "residue given as "O" in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                          Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                             Length 634;
                                                                                                                             DB 11;
                                                                                                                                          0.57;
                                                                                                                           Score 45; DB
Pred. No. 0.57
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                AAR03929 standard; Protein; 640 AA.
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                                                                                                                           88.2%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens HSP (humhsp70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88US-0243474.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                             Query Match
Best Local Similarity 90.v.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dragon E, Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The proteins having by vaccines and diagnosimy cobacteria species.
                                                   Mycobacteria species
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                                                                                                                                                                                                          1 SLFEGIDAYT 10
                                                                              634 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1988;
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                                                                                                                                                                                                                                                                                                                               AAR03929;
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Sequence

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peptide containing a CTL (cytoxic I lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the Arpase domain of a heat shock protein. Also described are: (1) a drug composition containing (1) as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome.
                                                               ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a fused protein (I) prepared
            Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human heat shock protein HSP70 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 49-52; 72pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY88408 standard; Protein; 640 AA.
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-543748/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            !uman; heat shock protein 70; HSP70; primer; probe; detection;
Intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
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pred. No. 0.58;
0; Mismatches 1; Indels
                                                                              Score 45; DB 11; Length 640;
Pred. No. 0.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; heat shock protein 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.2%;
90.0%;
                                                                                           88.2%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                          Conservative
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N-PSDB; AAT58086.
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286 slfegidfyt 295
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Matches 9; Conserv
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      640
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JP08322577-A

10-DEC-1996

24-OCT-1997

AAW10065;

AAW10065

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01-JUN-1995; 01-JUN-1995;

Sequence

AAB23653;

12 RESULT 1

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8

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Gaps

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Score 45; DB 21; Length 640; Pred. No. 0.58;

0; Mismatches

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Human heat shock proteins are located on chromosomes 6p21.3-22
sequence. Human heat shock proteins are located on chromosomes 6p21.3-2: and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "peptides comprising an intact domain from
the Arpase fragment of hsp70 are claimed;
the peptides are homologous to sequences
conserved between SLIP1 and 74.5kD
                                                                                                                                                                                                                                                                                                                                                                                                             plasma membrane;
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                                                                                                                                     Score 45; DB 21; Length 640; Pred. No. 0.58;
                                                                                                                                                                  1; Indels
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HSC70B; mammalian; infertility; mycoplasma; HSP70.
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/label= 44kD_ATPase_fragment
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/label= IA
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189..228
/label= IIA
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(OTTA-) OTTAWA CIVIC HOSPITAL.
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Best Local Similarity
Matches 9; Conserv
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chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; LHSP70.
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Pred. No. 0.58;
0; Mismatches
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                                                                                            (HOKE-) HOKEN KAGAKU KENKYUSHO KK
                                                                                                                                                                                                                        Claim 2; Fig 1; 11pp; Japanese.
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N-PSDB; AAA15620.
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286 slfegidfyt 295
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                                       01-JUN-1995;
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Mammalian fertilisation decrease for detecting and treating infertility - using sulpho glyco lipid immobilising protein 1-sulphated-glyco molety interfering compsn., for mycoplasma infection treatment
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The likelihood of mammalian fertilisation is decreased by contacting a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated glyco-moiety interfering composition. The interfering compositios is e.g. the heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).
Claim 2 and Clalim 17; Page 60-62; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 641 AA;
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Query Match 88.2%; Score 45; DB 14; Length 641; Best Local Similarity 90.0%; Pred. No. 0.58; Matches 9; Conservative 0; Mismatches 1; Indels 1 SLFEGIDAYT 10 ò g

Search completed: December 6, 2001, 08:04:04 Job time: 612 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Result		Query					
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П	53	100.0	10	22	AAB97603	Heat shock protein	
7	53	100.0	554	21	AAY88409	Human heat shock p	
e	53	100.0	554	21	AAY88410	Human heat shock p	
4	53	100.0	554	21	AAY88412	Human heat shock p	
5	53	100.0	554	71	AAY88413	Human heat shock p	
9	53	100.0	624	21	AAB23252	Human Hsp72 (heat	
7	53	100.0	634	1	AAR03930	Gallus gallus HSP	
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6	53	100.0	640	18	AAW10065	Human heat shock p	
10	53	100.0	640	21	AAB23653	Human heat shock p	
11	53	100.0	640	21	AAY88408	Human heat shock p	

Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of heat shock protein -

WPI; 2001-290909/30.

Human heat shock Mature mouse sper Human heat shock Human heat shock Rat heat shock Rat heat shock Rat man secreted pr Human secreted pr Rat HSP (rathsp70	Hea Mou Mou Hum Hum Hea Ara Ara Ara Ara Ara Ara Ara Ara	dic fragment 3.  cancer; chronic infectious disease;  r; peptidic fragment; lymphocyte;  in presenting cell; fragment 3.  ES.
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                       the amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP leads to a substantial concease in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSPs epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cencer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRM under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including **rheumatisms*, schizophrenia, depression and nephrotic syndrome.
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Pred. No. (
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    Claim 8; Page 15; 21pp; English.
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100.0%;
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100.0%; Score 53; DB 21; Length 554;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels
Length 554;
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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.
                                                                                                                                                                                              This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leuksemia, lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
                                                                            Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
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                                                                                                                                                            Disclosure; Fig 6; 11pp; Japanese.
(HOKE-) HOKEN KAGAKU KENKYUSHO KK
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Best Local Similarity 100.
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
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                                                                                             Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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                                                       Human heat shock protein SHSP70 amino acid sequence.
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compilarly, map: 15 contacted with the test compound under optiming a compilations to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of dentifying compounds that inhibit Hsp72-mediated JNK phosphatase activation. Comprising contacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and etermining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity are useful for inhibiting the proliferation of cells. Modulation of the activity of the inhibiting the proliferation of cells. Modulation of the activity of the UNK phosphatase or Hsp72 is used to treat a proliferative disorder such as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and ascancers and to preast cancer, prostate cancer). The compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention.
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Optionally, Hsp72 is contacted with the test compound under optimum
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Pred. No. 0.027;
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100.0%;
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Matches 10; Conservative
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Misc-difference
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Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922);
2. Bacillus megaterium (Bmehsp70 - AAR03923);
3. E. coli (dnaK - AAR03924);
4. T. cruzi (tc70kd - AAR03925);
5. T. cruzi (tc70kd - AAR03925);
6. Rat rattus (rathsp70 - AAR03929);
7. Kenopus laevis (x170 - AAR03928);
8. Homo sapiens (x170 - AAR03928);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (meaksp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03931);
The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                    Gaps
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Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03922);
2. Bacillus megaterium (Bmehsp70 - AAR03923);
3. E. coli (dnaK - AAR03924);
4. T. cruzi (tc70kd - AAR03925);
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Best Local Similarity 100.
Matches , 10; Conservative
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cruzi (AAR03926);

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shock protein. Also described are: (1) a drug composition containing (1) as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (1) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a fused protein (I) prepared from a
                                                                                                                                                                                                                                                                                                 ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 53; DB 21; Length 640; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                            Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 49-52; 72pp; Japanese.
                                                                                                                              AAB23653 standard; protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                    protozoacide; leukaemia; cancer
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                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-543748/49.
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                                                                                                                                                                        AAB23653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The cDNA encoding the present sequence, human heat shock protein 70 (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained
                 6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Home sapiens (humhsp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03932).
proteins having homology to hsp's of T. cruzi can be used in class and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
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                                                                                                                                                                                                                                                                                                 100.0%; Score 53; DB 11; Length 6
100.0%; Pred. No. 0.027;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.027;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW10065 standard; Protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95JP-0158581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                              Mycobacteria species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-081088/08.
N-PSDB; AAT58086.
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Best Local Similarity
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                                                                                                                                                                                                                                      640 AA;
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10.
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                                                                                                                                                                        vaccines and
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AAW10065;

stress.

RESULT
XX AAW10065
XX AAW10
XX AAW10
DT 24-04
DT 24-04
DY 24-04
XX HUMBA
XX HUMBA
XX HOME
XX CHOK
XX C

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Gaps

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Indels

AAY88408;

1 SLFEGIDFYT 10

Matches

(first entry)

31-JUL-2000

99JP-0257146. 95JP-0158581

01-JUN-1995;

01-JUN-1995;

JP2000069999-A

07-MAR-2000.

Homo sapiens

WPI; 2000-264458/23

N-PSDB; AAA15620

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This sequence represents the human heat shock protein LHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14422-34. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                           Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..385 / Jabel= 44kD_ATPase_fragment
/label= 44kD_ATPase_fragment
/note= "peptides comprising an intact domain from
the ATPase fragment of hsp70 are claimed;
the peptides are homologous to sequences
conserved between SLIP1 and 74.5kD
mycoplasma protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
HSC70B; mammalian; infertility; mycoplasma; HSP70.
                                                                                                                                                                                                                                                                                                                                              100.0%; Score 53; DB 21; Length 640; 100.0%; Pred. No. 0.027; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mature mouse sperm 70kD heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR43004 standard; protein; 641 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                             Disclosure; Fig 4; 11pp; Japanese.
(HOKE-) HOKEN KAGAKU KENKYUSHO KK
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40..115
/label= IB
116..188
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/note= "part"
229..306
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307..385
/label= IIA
/note= "part"
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Best Local Similarity 100.
Matches 10; Conservative
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/label= 1
                               WPI; 2000-264458/23.
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                                                                                                                                                                                                                                                                                                Sequence
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the human heat shock protein HSP70 amino acid and 1492-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of FFR abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                          Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                           Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; LHSP70.
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             Human heat shock protein HSP70 amino acid sequence.
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99JP-0257146. 95JP-0158581

01-JUN-1995; 01-JUN-1995;

07-MAR-2000

JP2000069999-A.

Homo sapiens

(first entry)

31-JUL-2000

AAY88411;

RESULT AAY88411

Query Match Best Local Similarity 100.

640 AA;

Sequence

1 SLFEGIDFYT 10

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Gaps

pep2-mod8f.rag

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The likelihood of mammalian fertilisation is decreased by contacting a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated givo-molety interfering composition. The interfering composition is e.g. the heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
                                                                                                                                               Mammalian fertilisation decrease for detecting and treating infertility - using sulpho glyco lipid immobilising protein 1-sulphated-glyco moiety interfering compsn., for mycoplasma infection treatment
                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 53; DB 14; Length 641; 100.0%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemical markers of human endometrium – useful for, e.g. diagnosis of hyperplasia and adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                          Claim 2 and Clalim 17; Page 60-62; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                               Faulds DH, Lingwood CA, Tanphaichitr N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 19; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW54349 standard; protein; 641 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human heat shock 70 kD protein 1.
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                                                           (BERL-) BERLEX LAB INC.
(OTTA-) OTTAWA CIVIC HOSPITAL.
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           93WO-US03816
                                    92US-0873961
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                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
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                                                                                                                        WPI; 1993-368422/46.
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          22-APR-1993;
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Proteins AAW54349-W54364 are examples of proteins produced in the endometrium during the hyperplasta, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the Arbase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.
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Pred. No. 0.027;
Mismatches 0; Indels (
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                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 100
Matches 10; Conservative
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Human heat shock p Mature mouse sperm Human heat shock 7 Human heat shock p Human heat shock p

AAY88411 AAR43004 AAW54349 AAB23652 AAB82534 AAB82560 AAR3928

Rat heat shock pro Xenopus laevis HSP Heat shock protein Heat shock protein Marmoset intracell

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GEP-HSC70 fusion p Mouse SLIP1 homolo Heat shock protein Pyrobacullum aerop Hepatitis C virus Hepatitis C virus Protein encoded by Protein encoded by Protein encoded by Hepatitis C virus Non-A non-B hepati Arabidopsis thalia JH-1 E2/NS1 protei

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The amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membranes Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response cancer cells. This has the effect of increasing the immune response cancer cells. HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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Claim 8; Page 15; 21pp; English,
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chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; SHSP70.
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                                                                                                                     Homo sapiens
                                                                                                                                                                                                    01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                               01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1995;
                                                                                                                                                                          07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY88413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                          This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
                                                                                                                        Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Hsp72 (heat shock protein 72).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB23252 standard; Protein; 624 AA.
                                                                                                                                                                                                                                                        Disclosure; Fig 6; 11pp; Japanese.
(HOKE-) HOKEN KAGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples; Fig 16B; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-2000; 2000WO-US07350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.0°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PHYL-) PHYLOGENY INC.
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200 slfegidfyt 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA97541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200054814-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /olloch VZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Optionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase activation, comprising contacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The compounds is identified as invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity. The compounds identified as inhibitions of Hsp72 or JNK phosphatase activity are useful for inhibiting the proliferation of cells. Modulation of the activity of the as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient or arrivity relative to a disorder mediated by an increase of Hsp72 expression or arrivity and activity or a patient or arrivity relative to an increase of Hsp72 expression or arrivity and activity or a patient or arrivity relative to an increase of Hsp72 expression or arrivity or a patient or arrivity or allored to a patient or arrivity or arrivity or allored to a patient or arrivity or arrivity or allored to a patient or arrivity or arrivity or an arrivity or arrivity or arrivity or arrivity or arrivity or arrivity or allored to a patient or arrivity or arrivi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "residue given as "O" in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR03930 standard; Protein; 634 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89WO-0003955.
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||||| ||
286 slfegidfyt 295
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AAR03930
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According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634.

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Gaps

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Mismatches

DB 21; Length 624; 1; Indels

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Proteins homologous to heat shock proteins from Trypanosoma cruzi – used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                                                                                                                                                                       Gaps
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Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922);
2. Bacillus megaterium (Mensp70 - AAR03922);
3. E. coli (dnaK - AAR03924);
4. T. cruzi (tc70kd - AAR03925);
 provides an alignment of heat shock proteins from a variety
                                                                                                                                                                         having homology to hsp's of T. cruzi can be used in diagnosis involving e.g. Trypanosoma, Mycoplasma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "residue given as "O" in specification"
                M.hyopneumoniae (Mhyhsp70 - AAR03922);
Bacillus megaterium (Bmehsp70 - AAR03923);
E. coli (dnaK - AAR03924);
                                                                                                                                                             11. Serratia marcescens (smahsp70 - AAR03932).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                                                                                                                                                         Score 44; DB 11; Length 634;
Pred. No. 3.9;
); Mismatches 1; Indels
                                                                                                                Homo sapiens (humhsp70 - AAR03929);
Gallus gallus (chkhsp70 - AAR03930);
Zea mays (mzehsp70 - AAR03931);
                                           E. coli (dnak - AAR03924);
T. cruzi (tc70kd - AAR03925);
T. cruzi (AAR03926);
Rat raftus (rathsp70 - AAR03927);
Xenopus laevis (x170 - AAR03928);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 2.1-2.14; 86pp; English.
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                                                                                                                                                                                                                                                                         83.0%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                    Mycobacteria species
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                                                                                                                                                                                                                                                                                                                                               289 slfegidfyt 298
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                                                                                                                                                                                                                                                                                                                                1 SLFEGIDGYT 10
                                                                                                                                                                                                                                  634 AA;
                of organisms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CODO-) CODON
                                                                                                                                                                          proteins
                                                                                                                                                                                         vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                  Sequence
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represent invention describes a larged protein (1) prepresent invention of a protein containing and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence regerosciel is a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a fused protein (I) prepared from a
                                                                                                                                                                                                                                                                              ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
                                                                                                                                                                                                                                           Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 21; Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 49-52; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY88408 standard; Protein; 640 AA.
                                                                                                                      AAB23653 standard; protein; 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                              protozoacide; leukaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.0%;
90.0%;
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                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Udono H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-543748/49.
      111111 | 1
286 slfegidfyt 295
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286 slfegidfyt 295
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                                                                                                                                                                                                                                                                                                                                                                                                                          WO200049041-A1
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-1999;
                                                                                                                                                                                                    05-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinbara N,
                                                                                                                                                               AAB23653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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AAY88408
ID AAY8
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AC AAY8
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                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The cDNA encoding the present sequence, human heat shock protein 70 (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained
5. T. cruzi (AAR03926);
6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapiens (humhsp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03931);
having homology to hsp's of T. cruzi can be used in diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
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Pred. No. 3.9;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              Score 44; DB 11; Length 640; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW10065 standard; Protein; 640 AA.
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                                                                                                                                                                                                                                                                                83.0%;
90.0%;
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95JP-0158581
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                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                    Mycobacteria species.
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N-PSDB; AAT58086.
                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            1 SLFEGIDGYT 10
                                                                                                                                                                                                                       640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 AA
                                                                                                                                           The proteins
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                                                                                                                                                                  vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1995;
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AAW10065;

RESULT AAW10065

stress.

Sequence

8888888888888

Query Match

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Gaps

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AAY88408

1 SLFEGIDGYT 10

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Matches

Sequence

pep2-mod8g.rag

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This sequence represents the human heat shock protein LHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                            Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "peptides comprising an intact domain from the APPase fragment of hap70 are claimed; the peptides are homologous to sequences conserved between SLIP1 and 74.5kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
HSC70B; mammalian; infertility; mycoplasma; HSP70.
                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 21; Length 640;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- 44kD_ATPase_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mycoplasma protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mature mouse sperm 70kD heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR43004 standard; protein; 641 AA.
                                                                                                                                    Disclosure; Fig 4; 11pp; Japanese.
(HOKE-) HOKEN KAGAKU KENKYUSHO KK
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/note= "part"
229. 306
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40..115
/label= IB
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/label= IIA
/note= "part"
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189..228
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90.0%;
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/label= IA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116..188
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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286 slfeqidfyt 295
                              WPI; 2000-264458/23
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                        640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR43004;
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                           Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; LHSP70.
                                                                 Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Length 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human heat shock protein LHSP70 amino acid sequence.
                                      Human heat shock protein HSP70 amino acid sequence.
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Pred. No. 3.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                            (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
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90.0%;
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       31-JUL-2000 (first entry)
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Best Local Similarity 90.0
Matches 9; Conservative
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N-PSDB; AAA15620.
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286 slfegidfyt 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640 AA;
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                                                                                                                                                                         JP2000069999-A.
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                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                            01-JUN-1995;
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Gaps

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6p21.3-22

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The likelihood of mammalian fertilisation is decreased by contacting a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated glyco-molety interfering composition. The interfering composition is e.g. the heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
                                                                                                                                             Mammalian fertilisation decrease for detecting and treating infertility - using sulpho glyco lipid immobilising protein 1-sulphated-glyco molety interfering compsn., for mycoplasma
                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 14; Length 641; Pred. No. 3.9;
                                                                                                                                                                                                           Claim 2 and Clalim 17; Page 60-62; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemical markers of human endometrium - adiagnosis of hyperplasia and adenocarcinoma
                                                                                               Faulds DH, Lingwood CA, Tanphaichitr N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW54349 standard; protein; 641 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human heat shock 70 kD protein 1.
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                                                                       (OTTA-) OTTAWA CIVIC HOSPITAL
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90.0%;
                                  92US-0873961.
           93WO-US03816
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96GB-0018600
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                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 90.0
nes 9, Conservative
                                                          (BERL-) BERLEX LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fey SJ,
                                                                                                                       WPI; 1993-368422/46.
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                                                                                                                                                                                     infection treatment
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286 slfegidfyt 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9810291-A1.
          22-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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06-SEP-1996;
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                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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Proteins AAW54349-W54364 are examples of proteins produced in the endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the Afpase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (1) has cytostaic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer -
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.
                                                                                                                                                                                                      Score 44; DB 19; Length 641; Pred. No. 3.9;
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                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAB23652 standard; protein; 641 AA
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useful for, e.g.

Query Match
Best Local Similarity 90.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 1; Indels

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Search completed: December 6, 2001, 08:04:05 Job time: 613 sec

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Heat shock protein
Heat shock protein
Human heat shock p
Human Hsp72 (heat
Gallus gallus HSP
Homo sapiens HSP (
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    522463 seqs, 74073290 residues
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88777777777777777777777777777777777777	residue 670; ide ecfor; de ecfico pecific
AAB23653 AAX88408 AAX88408 AAX43004 AAB23652 AAB23650 AAB23650 AAB23650 AAB23650 AAB23650 AAB97401 AAG02174 AAB022938 AAB022938 AAB022938 AAB022938 AAB022938 AAB022938 AAB022938 AAG02333 AAG02333 AAG02333	ALIGNMENT AA.  G residue sp70; ide tvector; invector specific specific
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11111111112222222222222222222222222222	RESULT 1 AAY44200 ID AAY44200 sta XX AC AAY44200; XX DT 15-FEB-2000 XX XX XX Human; heat XX YX T cell respo XW T cell respo XX XX Homo sapiens XX YX

Tue Dec 11 08:46:00 2001

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This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific confunction of a tensor of the hsp70 peptides that have at least confunction or alteration compared with the native sequence, and induce concorred to more tumours; (ii) amplifying hsp70 confunction or more tumours; (ii) cloning the amplified concorred into a vector that can be replicated in bacteria; (iii) sequences into a vector that can be replicated in bacteria; (iii) sequences into a vector that can be replicated in bacteria; (iii) sequences into a vector that can be replicated in bacteria; (iii) sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify of the mutant peptides identified. The peptides, optionally formulated with an each particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, also be used to increase the proportion of tumour specific cytotoxic factors (specifically interleukin-2, interferon-gamma and cytotoxic factors (specifically interleukin-2, interferon-gamma and cytotoxic factors (specifically where the cells are used to immunogenicity and high specificity for particular HLA (human leucocyte antimum) alledes.
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Pred. No. 0.0015;
1; Mismatches 0; Indels
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Claim 10; Page 6; 56pp; French
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Best Local Similarity 90.0%
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Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression

Abastado JP, Bartholeyns J;

WPI; 2001-290909/30.

The amino acid sequence of fragment 2 relating to position 286-295 of

Claim 8; Page 15; 21pp; English.

transformed human cell of heat shock protein

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to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSPs and HSP pericels presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the periceilular membrane. Recognition of increased numbers of HSP epitopes on cell, periceilular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.
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                                                                                                                                                                                                                                                                                                                                                                                   96.1%; Score 49; DB 22; Length 10; 90.0%; Pred. No. 0.0015; ive 1; Mismatches 0; Indels
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Matches 9; Conservative
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presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14g22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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Pred. No. 0.0038;
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Pred. No. 0.29;
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                                                                                                                                                                                                                                                                                                                                                    AAY88409 standard; Protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Examples; Fig 2; 11pp; Japanese.
                                                                                             intracellular infected cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.2%;
90.0%;
                                                                                                                                                                           92.2%;
90.0%;
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                                                                                                                                                                                                        9; Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-264458/23
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Best Local Similarity
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                                                                                                                                                                                                                                                           1 SLFEGIDLYT 10
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                                                                                                                            10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA15621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2000069999-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1995;
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                   AAY88409;
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AAY88409
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sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP7OmRNA under acute and chronic stress load in a human. The abnormal transcription of HSP7O can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the human heat shock protein SHSP70 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
                                                                                                                             Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                          chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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                                                                                                Human heat shock protein SHSP70 amino acid sequence.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
             AAY88410 standard; Protein; 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.2%;
90.0%;
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N-PSDB; AAA15622.
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200 slfegidfyt 209
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        554 AA;
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                                                                                                                                                                                     Homo sapiens
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                                        AAY88410;
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AAY88410
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This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 1462-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                   Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                            Score 47; DB 21; Length 554;
Pred. No. 0.29;
); Mismatches 1; Indels
                                                                             (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
                                                                                                                                                          Disclosure; Fig 5; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                           92.2%;
90.0%;
                                        99JP-0257146.
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0.
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                                                                                                                                                                                                                                                                                                                                            200 slfegidfyt 209
                                                                                                                                                                                                                                                                                                                                 1 SLFEGIDLYT 10
                                                                                                                                                                                                                                                              , 554 AA;
JP2000069999-A.
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                                        01-JUN-1995;
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                    07-MAR-2000
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Gaps

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1; Indels

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Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; SHSP70.
                                                                                                                                                                                                                       Human heat shock protein SHSP70 amino acid sequence.
AAY88413 standard; Protein; 554 AA.
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(HOKE-) HOKEN KAGAKU KENKYUSHO KK WPI; 2000-264458/23

Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application

This sequence represents the human heat shock protein SHSP70 amino acid Disclosure; Fig 6; 11pp; Japanese.

ö sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14922-24. The invention relates to the abnormal transcription of intracellular HSP70mRA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome. Gaps ö Score 47; DB 21; Length 554; Pred. No. 0.29; 1; Indels 0; Mismatches 92.2%; 90.0%; Conservative 200 slfeqidfyt 209 1 SLFEGIDLYT 10 554 AA; Sequence 8염 à

Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition. Human | Hsp72 (heat shock protein 72). AAB23252 standard; Protein; 624 AA. 29-JAN-2001 (first entry) AAB23252; 

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AAB23252

WO200054814-A1. Homo sapiens 21-SEP-2000

99US-0125046. 17-MAR-2000; 2000WO-US07350 (PHYL-') PHYLOGENY INC 18-MAR-1999;

Volloch VZ, Sherman M; 2000-647056/62. AAA97541. N-PSDB;

Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia, 1 ymphoma

Examples; Fig 16B; 77pp; English.

The invention relates to a novel method of identifying compounds that inhibit prollferation of cells comprising contacting a test compound with a cell.which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.

Optionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNR phosphatase activation, comprising contacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNR phosphatase activity. The compound all pencengasses compositions comprising an inhibitor of Hsp72 or JNR phosphatase activity are useful for inhibiting the proliferation of cells. Modulation of the activity of the

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WO9002564-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dragon E,
                                                        Sequence
                                                                                        Query Match
                                                                                                                                                                                                                                 AAR03929;
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         as carcers (e.g., lengtaenia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or discorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention.
phosphatase or Hsp72 is used to treat a proliferative disorder such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins homologous to heat shock proteins from Trypanosoma cruzi - use in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634.

E including "O" (?) at position 634.

E fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922);

C B E coli (dnaK - AAR03224);

C T cruzi (tc70kd - AAR0324);

S T cruzi (AAR03226);

C Rat ratius (rathsp70 - AAR03928);

C Rat ratius (rathsp70 - AAR03928);

C Honopus laevis (x170 - AAR03928);

C Gallus gallus (chkhsp70 - AAR03929);

C Gallus gallus (ckkhsp70 - AAR03929);
                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "residue given as "O" in specification"
                                                                                                                                                                                                                                                                                                                                                    Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                           DB 21; Length 624; 0.33;
                                                                                                                                                                 1; Indels
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2.1-2.14; 86pp; English
                                                                                                                                           Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                               AAR03930 standard; Protein; 634 AA.
                                                                                                                                                                                                                                                                                                                               Gallus gallus HSP (chkhsp70).
                                                                                                                                           92.2%;
90.0%;
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                                                                                                                                           Query Match 92.2
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dragon E, Faulds D,
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286 slfegidfyt 295
                                                                                                                                                                                     1 SLFEGIDLYT 10
                                                                                                            624 AA;
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                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
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                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         According to the legend of Fig 2, the H. sapiens HSP sequence has 641 amino acid residues, the sequence itself has only 640, cincluding "O" (?) at position 640.

Erg. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03922);

C. Bacillus megaterium (Bmehsp70 - AAR03923);

B. coli (dnaK - AAR03924);

C. T. cruzi (LC70kd - AAR03927);

S. T. cruzi (AAR03926);

C. Rat rattus (rathsp70 - AAR03927);

Xenopus laevis (x170 - AAR03928);

C. Hondon sapiens (humbsp70 - AAR03930);

G. Gallus gallus (chkhsp70 - AAR03930);

C. Lea mays (mzehsp70 - AAR03931);
                                                                                                                                                                                                                                                                                            Gaps
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The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and Mycobacteria species.
11. Serratia marcescens (smahsp70 - AAR03932). The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP
                                                                                                                                                                                                                                 Score 47; DB 11; Length 634;
Pred. No. 0.34;
0; Mismatches 1; Indels
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640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR03929 standard; Protein; 640 AA.
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens HSP (humhsp70)
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                                                                                                                                                                                                                                                               Best_Local Similarity 90.0
Matches 9; Conservative
                                                                                           Mycobacteria species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-115820/15.
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289 slfegidfyt 298
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                                                                                                                                                 634 AA;
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The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (1) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response protozoacide activities, and can be used as a cellular immune response compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                 Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                 ATPase, Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
                        Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                 Claim, 3; Page 49-52; 72pp; Japanese.
                                                                                                                                                                                                                                                    (SUME') SUMITOMO ELECTRIC IND CO.
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                                                                                                                                                                                                18-FEB-2000; 2000WO-JP00941
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                                                                                                                                                                                                                                                                              Shinbara N, Udono H,
                                                                                                                                                                                                                                                                                                      WPI; 2000-543748/49.
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Best Local Similarity
Matches | 9; Conserv
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                                                                                                                                            WO200049041-A1.
                                                                                                                     Homo sapiens.
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                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The cDNA encoding the present sequence, human heat shock protein 70 (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained
                                                                                                                                                                                                                                                                                         Human; heat shock protein 70; HSP70; primer; probe; detection; intracellular; abnormal transcription; acute; chronic; sustained;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                           Score 47; DB 11; Length 640;
Pred. No. 0.34;
0; Mismatches 1; Indels
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Pred. No. 0.34;
); Mismatches 1; Indels
                                                                      1; Indels
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                                                                                                                                                                                  AAW10065 standard; Protein; 640 AA.
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                                       92.2%;
90.0%;
                                                                                                                                                                                                                                                                  Human heat shock protein 70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.28;
90.08;
                         Query Match
Best Local Similarity 90.0%;
..... 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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286 slfegidfyt 295
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N-PSDB; AAT58086.
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  640 AA
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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 Sequence
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92.2%; Score 47; DB 21; Length 640; 90.0%; Pred. No. 0.34; 1. Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Human heat shock protein HSP70 amino acid sequence.
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21; Length 640; 1; Indels

DB 21 0.34;

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sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "peptides comprising an intact domain from
the ArPase fragment of hsp70 are claimed;
the peptides are homologous to sequences
conserved between SLIP1 and 74.5KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
HSC70B; mammalian; infertility; mycoplasma; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..385
/label- 44kD_ATPase_fragment
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                                                                                                                                                                                               Mismatches
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Pred. No. (
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OTTAWA CIVIC HOSPITAL.
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/label= IA
/note= "part"
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/note= "part"
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/note= "part"
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90.0%;
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/label= IA
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286 slfegidfyt 295
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les 9; Conserv
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                                                                                                                640 AA;
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the human heat shock protein LHSP70 amino acid
                                                                                                                                                                                            Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l transcription of intracellular {\tt HSP70mRNA} under acute and continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; LHSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.2%; Score 47; DB 21; Length 640; 90.0%; Pred. No. 0.34;
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                                                                                                                                                                                                                                                            Claim 2; Fig 1; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0257146.
                                                99JP-0257146
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N-PSDB; AAA15620.
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nes 9; Conser
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                                                01-JUN-1995;
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                07-MAR-2000
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Matches
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ò g Mammalian fertilisation decrease for detecting and treating PT infertility - using sulpho glyco libid immobilising protein 1-sulphated-glyco moiety interfering compsn., for mycoplasma pr infection treatment

XX

Claim 2 and Clalim 17; Page 60-62; 77pp; English.

XX

CR

The likelihood of mammalian fertilisation is decreased by contacting companies with a sulphoglycolipid immobilising protein 1 (SLIP1)/

CC

Sulphated glyco-moiety interfering composition. The interfering compsn. is e.g. the heat shock 70kD protein, SLIP1 (or analogues CC

Such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid composition and composition or the 74.5kD mycoplasma protein (AAR43003).

XX

Sequence 641 AA;

Query Match 92.2%; Score 47; DB 14; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SLFEGIDLYT 10

1 SLFEGIDLYT 10 ||||||| || 286 slfegidfyt 295

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Search completed: December 6, 2001, 08:04:04 Job time: 612 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		8 Ouerv			SUMMARIES		
O	Score	Match	e Match Length DB	DB	ID	Description	
-	50	98.0	10	21		Heat shock protein	
7	20	98.0	10	22	AAB97602	Heat shock protein	
m	46	90.3		22	AAB97603	Heat shock protein	
4	46	90.2		21	AAY88409	Human heat shock p	
S	46	90.5		21	AAY88410	Human heat shock p	
9	46	90.2	554	21	AAY88412	Human heat shock p	
7	46	90.5		21	AAY88413	Human heat shock p	
œ	46	90.5		21	AAB23252	Human Hsp72 (heat	
0	46	90.2		11	AAR03930	Gallus gallus HSP	
10	46	90.2		11	AAR03929	Homo sapiens HSP (	
11	46	90.2		18	AAW10065	Human heat shock p	

Human heat shock p Human heat shock p Human heat shock p	e mous heat	Human heat shock p Human heat shock p	Rat heat shock pro	Xenopus laevis HSP	Heat shock protein	set in	Lung cancer associ	Human secreted pro	Rat HSP (rathsp70)	Heat shock cognate	Human heat shock c			Human heat shock p	Human heat shock p		GFP-HSC70 fusion p	Φ	S. pneumoniae prot	ĕ				lis OR	mays	Zea mays protein f	Human pancreatic c	Serratia marcescen
AAB23653 AAY88408 AAY88411	AAR43004 AAW54349	AAB82534	AAB23650	AAR03928	AAB97601	AAW22895	AAB58386	AAG02174	AAR03927	AAW54364	AAY17407	AAY17408	AAB23649	AAB23651	AAB82535	AAW01638	AAB22938	AAY85808	AAW80645	AAR43002	AAG24333	AAG24332	AAG24331	AAB61974	AAG44951	AAG44949	03	AAR03932
21 21 21	14	27 22	21	115	22	18	21	21	11	19	20	20	21	21	22	18	21	19	19	14	21	21	21	22	21	21	21	11
640 640 640	641 641	041 641	642	647	n on	643	999	91	646	646	646	646	646	646	. 646		890	214	221	633	253	279	342	412	91	126	187	620
90.2 90.2 90.2	000		0			8	8	4.	4	4	4	4	4.	4	4.3	4.3	₹.	82.4	$^{\circ}$	$^{\circ}$	9	9	9	72.5	œ	æ	œ	æ
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12 13 14	15	18	19	20 10	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen. Heat shock protein 70 amino acid residues 286-295. AAY44200 standard; peptide; 10 AA. (first entry) 15-FEB-2000 AAY44200; AAY44200 

Homo sapiens. W09954464-A1

28-OCT-1999.

98FR-0005033. 99WO-FR00957 22-APR-1999; 22-APR-1998; (INSR ) INST ROUSSY GUSTAVE.

Triebel F, Gaudin C;

WPI; 2000-013251/01.

Identifying mutant peptides from heat-shock protein 70, for treatment of cancer

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This peptide corresponds to amino acid residues 286-295 of the human care shock protein 70 (hsp70). The invention relates to a method of clear shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 compared to more tumours; (ii) cloning the amplifying hsp70 compared to more tumours of colony to identify sequencing fragments in each cultured bacterial colony to identify any hsp70 mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic corrects (carcinoma, neuropeacific cytotoxic cancers (secrete cytotoxic factors), particularly where the cells are used to through the colls are used to stimulate immune defences. The method identifies peptides with high companients and high specifically for particular HLA (human leucocyte).
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Claim 10; Page 6; 56pp; French
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90.0%;
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The amino acid sequence of fragment 2 relating to position 286-295 of

Claim 8; Page 15; 21pp; English.

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human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSP and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; SHSP70.
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Pred. No. 0.33;
0; Mismatches 1; Indels
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sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
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Pred. No. 0.33;
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AAY88410 standard; Protein; 554 AA.
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Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5; 11pp; Japanese.
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                                                                                                                                                                   (HOKE-) HOKEN KAGAKU KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%;
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Best Local Similarity 90.0
Matches 9; Conservative
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200 slfegidfyt 209
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JP2000069999-A
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                                                                                                                         01-JUN-1995;
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                                                                                01-JUN-1995;
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                                       07-MAR-2000
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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.

Coptionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a conditions to allow the two components to interact and bind, forming a conditions to allow the two components to interact and bind, forming a condition of method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase corresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity are useful for inhibiting the proliferation of cells. Modulation of the activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRN under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 21; Length 554;
Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB23252 standard; Protein; 624 AA.
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                                                                                                                                                                                                                                                                                                                                                                                   90.2%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0125046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Volloch VZ, Sherman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PHYL-) PHYLOGENY INC
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200 slfegidfyt 209
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SLFEGIDVYT 10
                                                                                                                                                                                                                                                                           554 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000,
                                                                                                                                                                                                                                                                               Sequence
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JNK phosphatase or Hsp72 is used to treat a proliferative disorder such as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostete cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins homologous to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.hyopneumoniae (Mhyhsp70 - AAR03922);
Bacillus megaterium (Bmehsp70 - AAR03923);
E. coli (dnak - AAR03924);
T. cruzi (tc70k4 - AAR03925);
T. cruzi (AAR03926);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                                                                                       DB 21; Length 624; 0.38;
                                                                                                                                                                                                                                     1; Indels
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Xenopus laevis (x170 - AAR03928);
Hemo sapiens (humhsp70 - AAR03929);
Gallus gallus (chkhsp70 - AAR03930);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays (mzehsp70 - AAR03931);
                                                                                                                                                                                                       Score 46; DB 2
Pred. No. 0.38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2.1-2.14; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus HSP (chkhsp70).
                                                                                                                                                                                                       90.2%;
90.0%;
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                                                                                                                                                                                                                                    9; Conservative
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286 slfegidfyt 295
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                  1 SLFEGIDVYT 10
                                                                                                                                                          624 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus
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                                                                                                                                                           Sequence
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Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03922);

C forganisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03923);

E coli (dnaK - AAR03924);

A T. cruzi (tc70kd - AAR03925);

C Rat ratius (rathsp70 - AAR03927);

Xenopus laevis (x170 - AAR03927);

Xenopus laevis (x170 - AAR03929);

C Hallus gallus (chkhsp70 - AAR03930);

C G Hallus gallus (chkhsp70 - AAR03930);
                                                                                                                                   Gaps
               in
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11. Serratia marcescens (smahsp70 - AAR03932). having homology to hsp's of T. cruzi can be used in diagnosis involving e.g. Trypanosoma, Mycoplasma and
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "residue given as "O" in specification"
11. Serratia marcescens (smahsp70 - AAR03932). having homology to hsp's of T. cruzi can be used diagnosis involving e.g. Trypanosoma, Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                          DB 11; Length 634;
                                                                                                                                   Indels
                                                                                                                       Pred. No. 0.39
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                          Score 46;
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640
                                                                                                                                                                                                                                                        AAR03929 standard; Protein; 640 AA.
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                                                                                                         90.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens HSP (humhsp70).
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                                                                                                                       Local Similarity 90.0
Les 9; Conservative
                                           Mycobacteria species.
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289 slfegidfyt 298
                                                                                                                                                            1 SLFEGIDVYT 10
                                                                    634 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                The proteins
                              vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The proteins
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1989;
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                                                                     Sequence
                                                                                                                                                                                                                                                                                  AAR03929
                                                                                                          Query Match
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RESULT 13
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                                            Gaps
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                                                                                                                                                                   Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                         The cDNA encoding the present sequence, human heat shock protein (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained stress load.
                                           ö
                                                                                                                                                                                                                                                                                                              Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
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                       90.2%; Score 46; DB 11; Length 640; 90.0%; Pred. No. 0.39; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 18; Length 640;
Pred. No. 0.39;
0; Mismatches 1; Indels
                                                                                                       AAW10065 standard; Protein; 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB23653 standard; protein; 640 AA.
                                                                                                                                                                                                                                                                          (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                      90.2%;
90.0%;
                                                                                                                                                    Human heat shock protein 70
                                                                                                                                                                                                                                                             95JP-0158581
                                                                                                                                       (first entry)
               Query Match
Best Local Similarity 90.0.
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Best Local Similarity 90.0
Matches 9; Conservative
                                                             286 slfegidfyt 295
                                                     1 SLFEGIDVYT 10
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N-PSDB; AAT58086.
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286 slfegidfyt 295
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                                                                                                                                                                                                                                                                                                                                                                                                               640 AA;
 640
                                                                                                                                                                                                               JP08322577-A
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                              01-JUN-1995;
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                                                                                                                                     24-OCT-1997
                                                                                                                                                                                                                              10-DEC-1996.
Sequence
                                                                                                                       AAW10065;
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AAB23653
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The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) containing the INA of (2); and (4) a transformant which can retain the protozoacide activities, and can be used as a cellular immune response protozoacide activities, and can be used as a cellular immune response compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                       ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
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Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%; Score 46; DB 21; Length 640; 90.0%; Pred. No. 0.39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 49-52; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY88408 standard; Protein; 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUME: ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yui K;
                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2000; 2000WO-JP00941.
                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0041535,
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Matches 9; Conserv
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                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      9-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shinbara N,
                                                                                                                                                                                                                                                                                                                       24 - AUG - 2000.
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(BERL-) BERLEX LAB INC.
(OTTA-) OTTAWA CIVIC HOSPITAL.
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/note= "part"
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90.0%;
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/label- IB
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/label= IA
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Best Local Similarity
...hos 9; Conserv?
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                                                                                                                             640 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09321954-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAR43004;
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Region
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                                                                                                                                                                                                                                                                                                                                               sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human heat shock protein LHSP70 amino acid
                                                                                                                                                                                                                   Abnormal transcription of intracellular HSP7OmRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                              This sequence represents the human heat shock protein HSP70 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 21; Length 640;
Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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                                                                                                                             (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
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                                                                                                                                                                                                                                                                                          Claim 2; Fig 1; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOKE-) HOKEN KAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%;
90.0%;
                                                     99JP-0257146
                                                                                       95JP-0158581
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Matches 9; Conservative
                                                                                                                                                              WPI; 2000-264458/23.
N-PSDB; AAA15620.
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286 slfegidfyt 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SLFEGIDVYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 AA;
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                                                   01-JUN-1995;
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                 07-MAR-2000
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AAY88411
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sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // 1.385
/label= 44kD_ATPase_fragment
/note= 'peptides comprising an intact domain from
the ATPase fragment of hsp70 are claimed;
the peptides are homologous to sequences
conserved between SLIP1 and 74.5kD
                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sulphoglycolipid immobilising protein 1; sperm plasma membrane; HSC70B; mammalian; infertility; mycoplasma; HSP70.
                                                                                                                                                                                                                                                                                                                         Score 46; DB 21; Length 640;
Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mature mouse sperm 70kD heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR43004 standard; protein; 641 AA
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The likelihood of mammalian fertilisation is decreased by contacting a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated glyco-moiety interfering composition. The interfering composition is e.g. the heat shock 70kb protein, SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid sequence AAR43002) or the 74.5kb mycoplasma protein (AAR43003). Mammalian fertilisation decrease for detecting and treating infertility - using sulpho glyco lipid immobilising protein 1-sulphated-glyco moiety interfering compsn., for mycoplasma infection treatment Claim 2 and Clalim 17; Page 60-62; 77pp; English. Sequence 641 AA; 

Query Match

90.2%; Score 46; DB 14; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 1 SLFEGIDVYT 10

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Gaps ; 0

Search completed: December 6, 2001, 08:04:04 Job time: 612 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

6, 2001, 07:53:52 ; Search time 88.19 Seconds
(without alignments)
7.774 Million cell updates/sec December

US-09-673-795-1 46 Perfect score: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 SLFEGIDIY 9 Scoring table: Sequence:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	H	dnaK-type molecula			heat-shock protein		heat-shock protein	heat-shock protein	욛	dnaK-type molecula	dnaK-type molecula	dnaK-type molecula		dnaK-type molecula	hypothetical prote	dnaK-type molecula	heat shock protein													
	ΙΩ	B44261	I51344	A26283	T45477	T45479	T45476	T45478	H96605	T45471	A25646	A48872	S31766	JC1391	S20139	HHKW7A	A29160	S37394	T21394	T43724	S53357	S35718	154542	A45871	HHBYA1	JH0095	B36590	A45635	151129	T46650
	DB	7	7	7	7	~	7	~	7	~	7	7	7	~	ď	-	~	7	7	7	ď	7	~	7	П	7	7	7	7	7
	Length	208	278	420	467	467	468	469	617	632	634	636	638	639	639	640	640	640	640	640	641	641	641	641	642	642	4	644	4	646
de	Ouery Match	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	$\vdash$	91.3	91.3	-	-	_	91.3	н	-	91.3	91.3	91.3
	Score	42	42	42	42	42	42	42	42	42	42	42	42	42	43	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
	Result No.	i	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

dnaK-type molecula	dnaK-type molecula	heat shock protein	heat shock protein	dnaK-type molecula	dnaK-type molecula	dnaK-type molecula	dnaK-type molecula	heat-shock protein	heat-shock protein	dnaK-type molecula	heat shock protein	dnaK-type molecula	dnaK-type molecula	heat shock protein	heat shock protein
HHXL70	S44168	T41121	JC7088	A44261	A03309	PQ0138	146588	T45473	T45474	JN0668	PC7036	S25585	809036	T45517	JC7132
1	7	2	7	7	7	7	7	2	7	7	~	2	2	7	7
647	647	647	650	200	214	372	375	467	467	64]	64]	643	643	651	651
91.3	91.3	91.3	91.3	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1
42	42	42	42	41	41	41	41	41	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

daak-type molecular chaperone HSC70 - California sea hare (fragment) MiAlternate names: heat shock protein 70 homolog HSC70 MiAlternate names: heat shock protein 70 homolog HSC70 C:Species: Aplysia californica (California sea hare) C:Species: Aplysia californica C:Species: Aplysia californica J: Cen Biol. 119, 1069-1076, 1992 J: Cell Biol. 119, 1069-1076, 1992 J: Cell Biol. 119, 1069-1076, 1992 A:Attle: Long-term sensitization training in Aplysia leads to an increase in the exprancement on number: A44261; MUID:93077669 A:Attle: Long-term sensitization training in Aplysia leads to an increase in the exprancesion: B44261 A:Accession: B44261
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Gaps ö Score 42; DB 2; Length 208; Pred. No. 0.42; 0; Mismatches 1; Indels Query Match 91.3%; Best Local Similarity 88.9%; Matches 8; Conservative

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dnaK-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)
N;Alternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 21-Feb-1937 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999
C;Accession: 151344
NO1. Cell. Biol. 4, 1785-1791, 1984
NA1. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o
A;Reference number: 151344
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o
A;Reference number: 151344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-278 <KOT>

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C; Keywords: ATP; molecular chaperone

91.3%; 88.9%;

Query Match Best Local Similarity 88.9%, Conservative

156 SLFEGIDFY 164

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1 SLFEGIDIY 9

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heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C;Species: Eunicella cavolini
C;Dacte: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Dactession: T45479
R;Borchiellini, C; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
A;Reference number: 222983
A;Accession: T45479
A;Actersion: T45479
A;Actus: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Funiculina quadrangularis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
c;species: Bunicella cavolini
c;species: Bunicella cavolini
c;pacetes: 131-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
c;Accession: T45478
R;Borchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
A;Reference number: 222983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 467;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule| type: mRNA
A;Residues: 1-468 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 2;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: AF026520; PIDN: AAC05364.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T45476 ...
K; Barchlatlini, C; Le Parco, Y.
Submitted to the EMBL Data Library, September 1997
A; Reference number: Z22983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: AF026516; PIDN: AAC05361.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: Hsp70
C;Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-467 <BOR>
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A; Residues: 1-469 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLFEGIDIY 9
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                                                                                                                                                                                                                                                                                 A26283
dhaM-Type molecular chaperone - mouse (fragment)
NALternate names: heat shock protein 68
G.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: A26883
S.Lowe, D.G.; Moran, D.L.A
J. 2102-2112, 1986
A;Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1.420 cLOW>
A; Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208
A; Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: involved in protein folding and assembling/disassembling of protein compl
C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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C;Species: Chondrosia reniformis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45477
                                                                                                                              Gaps
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                                                                     Score 42; DB 2; Length 278;
Pred. No. 0.58;
0; Mismatches 1; Indels
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Pred. No. 1;
0; Mismatches 1; Indels
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Pred. No. 0.91;
0; Mismatches 1
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A;Molecule type: mRNA
A;Residues: 1.467 < GBOF.
A;Cross.references: EMBL:AF026517; PIDN:AAC05362.1
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91.3%; 88.9%;

Best Local Similarity 88.9 Matches 8; Conservative

Query Match

A; Accession: A26283

SLFEGIDEY 73

65

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A;Gene: Hsp70 C;Superfamily: heat shock protein 70

C; Genetics

Ouery Match
Best Local Similarity 88.9%;
Matches 8; Conservative

111111 | 252 SLFEGIDFY 260

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1 SLFEGIDIY 9

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C,Accession: A25646
C,Accession: A25646
R;Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 1269-12569, 1986
A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 ge
A;Reference number: A25646; MUID:86304452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Blol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with
A;Reference number: A48872; MUID:94043116
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                                                                                                                                                                            N,Alternate names: heat shock protein 70
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Dictyostelium discoideum
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C;Accession: A48872
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N;Alternate names: heat shock protein 70
C;Species: Carcopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: 1-634 <MOR>
A, Cross-references: GB.J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A, Note: the authors translated the codon TCG for residue 583 as Trp
C, Function:
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Pred. No. 1.4;
0; Mismatches
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Pred. No.
                                                                                                                                                            dnaK-type molecular chaperone - chicken
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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285 SLFEGIDFY 293
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289 SLFEGIDFY 297
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                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                           Probable heat shock protein [imported] - Arabidopsis thaliana c'Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: H96605
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurcs, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rohartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tiles Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H96605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dnak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)
N;Alternate names: heat shock cognate protein 70
C;Species: Dictyostelium discoideum
C;Date: 31-3n-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
C;Accession: T45471
R;Boves, H:, Mintert, U:; Dittrich, W.; Faix, J.; Gerisch, G.
A;Reference number: 222980
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     Length 469
                                                        1; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A; Cross-references: EMBL:AF025951; PIDN:AAB81865.1
A; Experimental source: strain AX3
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Pred. No. 1.4;
  DB 1;
                                                     0; Mismatches
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  Score 42;
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A; Residues: 1-617 <STO>
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292 SLFEGIDFY 300
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C; Superfamily: hex
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ò Q C; Genetics:

Matches

A; Accession: S31766

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drawf-type molecular chaperone hsp70A - Caenorhabditis elegans
N.Alternate names: heat shock protein 70 A
C;Species: Caenorhabditis elegans
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
C;Accession: JT0285
R;Snutch, T.P.: Heschi, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri
A;Reference number: JT0285; MUID:88297155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352 A; Note: genomic clones representing six distinct members of the hsp70 gene family wer A; Note: transcripts of hsp70A are abundant in control worms and also increase two- to A; Note: one of the three introns in hsp70A is in a position similar to an intron in D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: 273129; NID: 91360201; PIDN: CAA97472.1; PID: 91360202; MIPS: YL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, April 1996
A; Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals mily and a new ABC transporter homologous to the human multidrug resistance protein. A; Reference number: $69380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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A;Residues: 1-639 <PUR>
A;Cross-references: EMBL:X97560; NID:91297003; PIDN:CAA66167.1; PID:91297007
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000 C;Accession: S20139; S64772; S64775; S69383 R;Slater, M.R.; Craig, E.A. Nucleic Acids Res. 17, 805-806, 1989 A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae. A;Reference number: S20139; MUID:89128457 A;Accession: S20139 A;Accession: S20139 A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: involved in protein folding and assembling/disassembling of C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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R; Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, submitted to the Protein Sequence Database, May 1996
A; Reference number: $64775
A; Accession: $64775
                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:X12927; NID:94545; PIDN:CAA31394.1; PID:94546
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submitted to the Protein Sequence Database, May 1996
A;Reference number: S64761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 72-639 GDUE>
A; Cross-references: EMBL: 273129; MIPS: YLL024c
A; Experimental source: strain S288C
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283 SLFEGIDFY 291
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A; Residues: 1-639 <GOF>
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R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein
A;Reference number: S31766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 A;Reference number: JC1391; MUID:93077053 A;Accession: JC1391
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N;Alternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Spacies: £accharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dnaK-type molecular chaperone 701V - sea urchin (Paracentrotus lividus)
N;Alternate names: heat shock protein 701Y, hsp701V protein
C;Species: Paracentrotus lividus (common urchin)
C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 %sequence_revision 10-Jun-1993 %text_change 20-Aug-1999
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DB 2;

Score 42; DB 2 Pred. No. 1.5; 0; Mismatches

91.3%; 88.9%;

Query Match 91.3 Best Local Similarity 88.9 Matches 8; Conservative

1111111 | 286 SLFEGIDFY 294

RESULT 14

1 SLFEGIDIY 9

Indels

DB 2; 1.5;

Score 42; DB 2 Pred. No. 1.5; 0; Mismatches

91.3%; 88.9%;

Query Match 91.3 Best Local Similarity 88.5 Matches 8; Conservative

1 SLFEGIDIY 9

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C;Accession: JC1391 R;Sconzo, G.; Scardina, G.; Ferraro, M.G. Gene 121, 353-358, 1992

A; Residues: 1-639 <SCO>

A; Gene: hsp70IV A; Introns: 61/2

C; Function:

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us-09-673-795-1.rpr
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C;Genetics:
A;Gene: hsp70A
A;Map position: IV
A;Map position: IV
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels
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287 SLFEGIDFY 295
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Search completed: December 6, 2001, 07:58:26 Job time: 274 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 6, 2001, 07:53:52; Search time 50.21 Seconds (without alignments) 6.572 Million cell updates/sec Run on:

US-09-673-795-1 46 1 SLFEGIDIY 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

(LES		Description	P11503 on		092260	P08106	Q28222 cercop	P10592	00624					P17879 mus n		Q07439 rattus norv			P22202	P27541	091233		Q01233 neurospo			689n60		P22623		P9190			004967	
SUMMAKIES		ΩI	HS70_ONCVO	HS73_MOUSE	HS70_PENCI	HS70_CHICK	HS71_CERAE	HS72_YEAST	HS74_PARLI	HS7A_CAEEL	HS7C_DICDI	HS71_BOVIN	HS71_HUMAN	HS71_MOUSE	HS71_PIG	HS71_RAT	HS71_YEAST	HS72_BOVIN	HS74_YEAST	HS70_BRUMA	HS70_ONCTS	HS70_PLEWA	HS70_NEUCR	HS70_XENLA	HS70_BLAEM	HS7D_MANSE	HS7A_DROSI	HS72_PARLI	HS7X_PIG	HS70_CERCA	HS7A_DROME	HS76_HUMAN	HS76_PIG	HS71_PUCGR
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Gaps

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Score 42; DB 1; Length 322; Pred. No. 0.38; 0; Mismatches 1; Indels

Query Match 91.3%; Best Local Similarity 88.9%; Matches 8; Conservative

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STANDARD;

RESULT 2 HS73\_MOUSE ID HS73\_MOUSE

P34931 homo sapien P16627 mus musculu P55623 pichia angu Q10265 schizosacch P57341 pichia angu P77322 lycopersico P26413 glycine max P19738 cricetulus P11142 homo sapien P08109 mus musculu P87047 paracoccidi O65719 arabidopsis	AA.	e) late) ENT). 1; Spirurida; Filarioidea;	UENCE FROM N.A.  LINE-89201313; PubMed-2704388;  hstein N.M., Higashi G., Yates J., Rajan T.V.;  hstein N.M., Higashi G., Yates J., Rajan T.V.;  crofilareanic individuals from a filariasis-endemic area.";  Biochem. Parasitol. 33:229-236(1989).  DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.  SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.	ed through and the EMB eno restri s content i uge by and //www.isb-si	IAL. IAL. 2BA3A2E8155A7180 CRC64;
HS7H_HUMAN HS77_MOUSE HS77_MOUSE HS71_SCHPO HS71_PICAN HS72_LYCES HS70_SOYBN HS7C_CRIGR HS7C_HUMAN HS7C_HUMAN HS7C_HUMAN HS7C_HUMAN HS7C_MOUSE HS7C_MOUSE HS70_MOUSE	ALIGNMENTS PRT; 322	(Rel. 12, Created) (Rel. 33, Last sequence update) (Rel. 33, Last annotation update) 70 KDA PROTEIN (HSP70) (FRAGMENT). volvulus. Metazoa; Nematoda; Chromadorea; Spae; Onchocerca.	J., J., a fi 36(1 0 IS	This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There are use by non-profit institutions as long as it modified and this statement is not removed. Use entities requires a license agreement (See http: or send an email to license@isb-sib.ch).	RI
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\$ 0 \$ \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$ 0 \$	T 1 ONCVO HS70_ONCVO	P11503. 01-OCT-1989 (Rel. 12, Cre 01-FEB-1996 (Rel. 33, Las 01-FEB-1996 (Rel. 33, Las HEAT SHOCK 70 KDA PROTEIN Onchocerca volvulus. Eukaryota; Metazoa; Nemat Onchocercidae; Onchocerca	GEOUENCE FROM N.A. Dubmed-2704388; SEQUENCE-69201313; Pubmed-2704388; Rothstein N.M., Higashi G., Yates Tochocerca volvulus heat shock pamicrofilaremic individuals from Mol. Biochem. Parasitol. 33:229-21-2 DISEASE: HEAT SHOCK PROTEIN 7 MICROFILAREMIC INDIVIDUALS FREST. SIMILARITY: BELONGS TO THE HE	tis SWISS tween the European by modified a control of the control	SSI - PER COLLEGE
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBL_TaxID=5077;
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                        Penicillium citrinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS70_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@illowing.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-86111900; Pubmed-2868009;
LOWE D.G., Moran L.A.;
"Molecular cloning and analysis of DNA complementary to three mouse
Mr = 68,000 heat shock protein mRNAs.";
                                                                                                                                                                                                                                SEQUENCE OF 155-420 FROM N.A. MEDILINE-04357449; Pubmed-8076831; Petry M.D., Aujame L., Shtang S., Moran L.A.; Structure and expression of an inducible HSP70-encoding gene from
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.3%; Score 42; DB 1; Length 420; 88.9%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 V -> G.
46292 MW; 5DA1C6155C7B16B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:56244; HSP70-3.
InterPro; IPR001023; HSP70.
PROMIZ: HSP70: 1.
PROSITE; PS00297; HSP70-1; PARTIAL.
PROSITE; PS00329; HSP70-2; PARTIAL.
PROSITE; PS01036; HSP70-2; PARTIAL.
ATP-binding; Chaperone; Heat shock; Multigene family.
                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).
HSP70-3 OR HSP70A1.
                                                                                                                                                                                             Mr = 68,000 heat shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M12571; AAA57234.1; -.
EMBL; M12572; AAA57235.1; -.
HSSP; P19120; lATR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
8; Conserv
                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 1
420 AA;
                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
Shen H.D., Au L.C.,
Molecular cloning and expression of a Penicillium citrinum
allergen with sequence homology and antigenic cross-reactivity
a hap? O human heat shock protein ";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
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J. Biol. Chem. 261:12692-12699(1986).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 1;
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
AEAT SHOCK 70 KDA PROTEIN (HSP70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         634 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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MEDLINE=86304452; Pubmed=3017985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U64207; AAB06397.1; -. HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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Best Local Similarity
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P08106;
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Gaps

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1; Indels

Mismatches

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Conservative

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HS70\_PENCI STANDARD; PRT; 503 AA. 02-260; Caug-2014 (Rel. 40, Created) 20-40G-2001 (Rel. 40, Last sequence update)

HS70\_PENCI ID HS70\_P AC Q92260 DT 20-AUG

RESULT

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NCBI_TaxID=4932;
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                                                        ATP-binding;
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                                                                                                                                                                                                                                                                                                                    HS72_YEAST
P10592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            database."
   PROSITE;
PROSITE;
                                                                        SEQUENCE
                                      PROSITE;
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                                                                                                                                                                                                                                                                                   RESULT
     DR DR S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saints I., Angelidis C., Pagoulatos G., Lazaridis I.;
"The hsc70 gene which is slightly induced by heat is the main virus
inducible member of the hsp70 gene family.";
FEBS Lett. 355.282-286(1994).

--- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREAKISTENDY PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEMLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN WITTOCHOWDRIA AND THE ENDOPLASMIC.

RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
PROCESSES THROUGH THEIR ABILLITY TO RECOGNIZE NONNATIVE
CONFORMATIONS OF OTHER PROPEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CONFORMATION OF OTHER PROPEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CONFORMATION OF OTHER PROPEINS. THEY BIND EXTENDED PEPTIDE
STRESS-INDUCED DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops (Green monkey) (Grivet).

Ekaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
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                                                                                                                                                                                                                                                                   Length 634;
                                                                                  InterPro; IRFO1023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR000301; HEATSHOCK70.
PROSITE; PS000397; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;
                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                     0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               638 AA.
                                                                                                                                                                                                                                                                                                       Mismatches
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send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95080396; PubMed=7988690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                 91.3%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X70684; CAA50019.1; -.
                                EMBL; J02579; AAA48825.1;
PIR; A25646; A25646.
                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 88.5.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                      PIR; A25646; A25640
HSSP; P19120; 1ATR
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 71-638 FROM N.A. Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garrels J.T., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- FUNCTION: SAA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSAI AND SAAS PROTEINS IS PEDETED.
ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95203288; PubMed-7895733;
Garrels J.I., Putcher B., Kobayashi R., Latter G.I., Schwender B
Volpe T., Warner J.R., McLaughlin C.S.;
Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                      ö
                                                   Heat shock; Multigene family; MHC III.
                                                                                                                     Score 42; DB 1; Length 638;
Pred. No. 0.79;
                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                       01-JUL 1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                         638 AA.
                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electrophoresis 15:1466-1486(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89128457; PubMed-2644626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACETYLATION, AND PHOSPHORYLATION.
                                                     Chaperone; Heat s
38 AA; 69920 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 91-97 AND 325-341.
PS00297; HSP70_1; 1.
PS00329; HSP70_2; 1.
PS01036; HSP70_3; 1.
                                                                                                                     91.3%;
88.9%;
                                                                                                  Query Match
Best Local Similarity 88.9°,
Best Local Similarity 88.9°,
                                                                                                                                                                                                                                                                                                                                                                                       HEAT SHOCK PROTEIN SSA2.
SSA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norbeck J., Blomberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 186-195.
                                                                   638 AA;
                                                                                                                                                                                                        284 SLFEGIDFY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                       1 SLFEGIDIY 9
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Gaps

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Length 639;

us-09-673-795-1.rsp

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HSSP; P19120, 1MGJ.

InterPro; IPR01023; HSP70.

Fram; PF00012; HSP70.1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS01036; HSP70_2; 1.

PROSITE; PS01006; HSP70_2; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;
                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1;
Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                      91.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M18540; AAA28078.1; -. PIR; JT0285; HHKW7A. HSSP; P19120; 1NG1. IncrePro; IPR001023; HSP70. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                PIR; UC1391; JC1391.
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286 SLFEGIDFY 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
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P09446;
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                   DR DR DR SO RW KW
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=93077053; PubMed=1339375;
Sconzo G., Scardina G., Ferraro M.G.;
"Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 gene family and its expression.";
Gene 121:353-358(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
-!- PTM: PHOSPHORYLATED.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paracentrotus lividus (Common sea urchin).
Sukaryota: Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinoidea; Echinoide; Echinoidee;
Paracentrotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.3%; Score 42; DB 1; Length 638; 88.9%; Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00397; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
Heat shock; APP-binding; Multigene family; Acetylation;
Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLATION. 23BDDD120C194912 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                      EMBL; X12927; CAA31394.1; -. EMBL; X3129.0; CAA97472.1; -. EMBL; X97560; CAA66167.1; -. PIR; S20139; S20139. SWISS-2DPAGE; P10592; XEAST. YEPD; 9800; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     638 AA; 69338 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEFU; 98000; ...
SGD; S0003947; SSA2.
INTERPRO; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
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Matches 8; Conservative
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MOD_RES
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HS74_PARLI
HS74_PARLI
AC Q0624B
DT 01-JUN
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                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE-88297155; PubMed-2841196;
Snutch T.P., Heschi M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterization.";
Gene 64:241-255(1988).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01239; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN A.
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RESULT 10
HS71_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                 Eddy R.J., Sauterer R.A., Condeelis J.S.;

*Aginactin, an agonist-regulated F-actin capping activity is associated with an HSC70 in Dictyostelium.";

J. Biol. Chem. 268:22367-23274 (1993).

-I. FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROPEIN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.

-I. SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS OF THE CELL CORPEX AND CELL PROTRUSIONS.

-I. DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL DEVELOPMENT.

-I. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSSIGIDLGTTYSCVGVWQNDRVEIIAND -> IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
                                                                                                                                                                                                                                                  Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F., Moegel A.A., Schleicher M.;
"The heat shock cognate protein from Dictyostelium affects actin polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
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V -> A (IN REF. 2).
S -> A (IN REF. 2).
S -> A (IN REF. 2).
V -> A (IN REF. 2).
V -> A (IN REF. 2).
I -> L (IN REF. 2).
I -> P (IN REF. 2).
K -> P (IN REF. 2).
K -> P (IN REF. 2).
W; ZEGBDCZDB96A9FSD CRC64;
                                                                                                                          Dictyostellum discoldeum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
                                                                   (Rel. 29, Last sequence update) (Rel. 35, Last annotation update)
                    640 AA
                                                                                                HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
HSPB OR HSC70
                    PRT;
                                                                                                                                                                                                                                    MEDLINE-94008983; PubMed-8404847;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94043116; PubMed=8226849;
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EMBL; 1.22736; AAA33219.1; --
HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P36415; DICTY.
DictyDb; DD01078; hspB.
InterPro; IPR001023; HSP70.
Pfam; PP00012; HSP70: 1.
PROSITE; PS00297; HSP70.1; PROSITE; PS00299; HSP70.1; 1.
                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sem
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240 V
341 I
352 F
70499 MW;
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                    STANDARD;
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640 AA;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                   01-NOV-1997
                   HS7C_DICDI
P36415;
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Length 640;

DB 1;

91.3%; Score 42;

Query Match

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           Gaps
                                                                                                                                                                                                                                                                                                                           Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat shock protein (18970) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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EMBL; U02891; AAA03450.1; -.

HSSP; P19120; 1NGC.

R InterPro; IPR001023; HSP70.

R Pfam; PF00012; HSP70; 1.

R PROSTE; PS00329; HSP70_1; 1.

R PROSITE; PS00329; HSP70_2; 1.

R PROSITE; PS01036; HSP70_2; 1.

R PROSITE; PS01036; HSP70_3; 1.

RW ATP-binding; Chaperone; Heat shock; Multigene family.
           Indels
           1;
                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                  TISSUE-Skeletal muscle;
MEDLINE-95126904; PubMed-7826329;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 212-641 FROM N.A.
88.98;
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos
                                                   111111 | 284 SLFEGIDEY 292
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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PIR; A45871; A45871
PIR; A25773; A25773
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286 SLFEGIDFY 294
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HS71_MOUSE
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**X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.

**REDINE-99234376; PubMed-10216320;

**REDINE-99234376; PubMed-10216320;

**REDINE-99234376; PubMed-10216320;

**Acta Crystallogr. D 55:1105-1107(1999).

**CACTA Crystallogr. D 55:1105-1107(1999).

**CACTA Crystallogr. D 55:1105-1107(1999).

**PREXISTENT PROYELLY AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OF NEWLY TRANSLOCATION IN MITOCHOWDRIA AND THE ENDOPELASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PROTEINS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES

**COMPORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES

**COMPORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).
ROWEN L., QIN S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-99184548; PubMed-2538825;
Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
"Human major histocompatibility complex contains genes for the major heat shock protein HSP70."
Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hunt C., Morimoto R.I.; "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70."; Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                              Gaps
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                            Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
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               Score 42; DB 1; Length 641;
Pred. No. 0.8;
0; Mismatches 1; Indels
                                                                                                                                                                                HS71_HUMAN STANDARD; PRT; 641 AA.
P08107, P19790; 09UGMD9; 09UGMD9;
01-AUG-1988 (ReL. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 ROA PROTEIN I (HSP70.1) (HSP70-1/HSP70-2).
(HSPAIA OR HSPAI) AND HSPAIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=91055806; Pubmed=1700760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-86016721; PubMed-3931075;
                 91.3%;
88.9%;
                                               8; Conservative
                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                             Best Local Similarity
Matches 8; Conserv
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286 SLFEGIDFY 294
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                    Query Match
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE. INDUCTION: BY HEAT SHOCK.
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
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Hunt C., Calderwood S.;
"Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
W; 78F513118C96DE66 CRC64;
                                                                           -!- INDICTION: BY HEAT SHUCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 1; Length 641; Pred. No. 0.8; 0; Mismatches 1; Indels
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P17879.2 Q61689;
01-A0G-1990 (Rel. 15, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY.2000 (Rel. 39, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
HSPAI OR HSP70-1 OR HSP70-1 OR HCP70.1.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M59828; AAA63226.1; -.
EMBL; M59830; AAA6327.1; -.
EMBL; AF134726; AAD21816.1; -.
EMBL; AF134726; AAD21815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M1717; AAA52697.1; EMBL; M24743; AAA59844.1; EMBL; M24744, AAA59845.1; EMBL; X04676; CAA28381.1; EMBL; X04677; CAA28382.1; PIR; A29160; A29160.
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
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88.9%;
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SWISS-2DPAGE; P08107; HUMAN.
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Best Local Similarity 88.2.
Local 8; Conservative
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FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and injured rat brain.";
J. Neurosci. Res. 36:325-335(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M69100; -; NOT_ANNOTATED_CDS. PIR; S35718; S35718.
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MEDLINE=95012453; Pubmed=7927536;
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Pfam. PF00012; HSP70. 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
ATP-binding; Chaperone; Heat sh
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88.9%;
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Best Local Similarity 88.5
المالية 8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 AA;
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                                                                                                                                                                                                                                      -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEXLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEDRANE TRANSLOCATION, OF FOLLOWING STRESS-INDUCED DAMAGE.
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                                                                                                                                     Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene from Mus musculus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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SEQUENCE FROM N.A.
BEDLINE-92175874; PubMed=1339404;
Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
Bouquet Y.H.;
"Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-289(1992).
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HS71_PIG
ID HS71_PIG
C STANDARD; PRT; 641 AA.
P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN I (HSP70.1).
GN HSPA1.
CS Sus scrofa (Pig).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Marmalia; Eutheria; Cetartiodactyla; Suina; Suidac OX NCBI_TaxID=9823;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-92175874; PubMed=1339404;
RX MEDLINE-92175874; PubMed=1339404;
RA Bouquet Y.H.;
RT "Complete nucleotide sequence of a porcine HSP70 Immunogenetics 35:286-289(1992).
                                                                                                         MEDLINE=94357449; PubMed=8076831;
                                                                                                                                                                                                                  Gene 146:273-278(1994)
Gene 87:199-204(1990)
                            [2]
SEQUENCE FROM N.A.
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286 SLFEGIDFY 294
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PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLTY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXPENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
"CDNA cloning and expression of stress-inducible rat hsp70 in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 0.8;
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ACETYLATION.
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HEW REARTS AND SERVED BY THE SERVE SERVER SE
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                                                                                                                     HISPOOR JUNE . ACTA 1219:64-72(1994).

BIOCHIM. BIOCHIM. BIOPHYS. ACTA 1219:64-72(1994).

-!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISEPRET PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL. AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLTY TO RECOGNIZE NONMATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXPONED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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                               Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.; *Cloning, nucleotide sequence and expression of rat heat inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89128457; PubMed=2644626;
Slater M.R., Craig E.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    -i - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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D -> H (IN REF. 2 AND 3).
G -> A (IN REF. 3).
; D02D96751C868583 CRC64;
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01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSAI (HEAT SHOCK PROTEIN YG100).
SSAI OR YAL005C.
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      MEDLINE=94368874; PubMed=8086479;
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X77207; CAA54422.1; -. EMBL; X74271; CAA52328.1; -. HSSP; P19120; INGC.
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Pfam; PF00012; HSP70; 1.
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Best Local Similarity 86...
احد 8; Conservative
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286 SLFEGIDFY 294
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P10591;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norbeck J., Blomberg A.; Norbeck J., Blomberg A.; Protein expression during exponential growth in 0.7 M NaCl medium of
STRAIN=S288C / AB972;
MEDLINE=95028152; PubMed=7941740;
Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
Delandey S., Ouchlette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
the 42 kbp SP07-CENI-CDC15 region.";
Yeast 10:535-541(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 590-641 FROM N.A.
MEDLINE-95087943; PubMed-6096826;
Ogden R.C., Lee M.-C., Knapp G.;
"Transfer RNA splicing in Saccharomyces cerevisiae: defining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95203288; PubMed-7895733;
Garrels J.I., Putcher B., Kobayashi R., Latter G.I., Schwender E
Volpe T., Warner J.R., McLaughlin C.S.;
*protein identifications for a Saccharomyces cerevisiae protein
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                                                                                                                                                                                                                                                                                                                                              substrates.";
Nucleic Acids Res. 12:9367-9382(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
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EMBL; L22015; AAC04952.1; ALT_SEQ
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STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
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PRINTS; PR00301; HEATSHOCK70.
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SWISS-2DPAGE; P10591; YEAST.
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PIR; $42164; $42164.
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Ouery Match 91.3%; Score 42; DB 1; Length 641; Best Local Similarity 88.9%; Pred. No. 0.8; Matches 8; Conservative 0; Mismatches 1; Indels
SQ SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;
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Search completed: December 6, 2001, 08:00:50 Job time: 418 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q93146 botryllus s O15766 dictyosteli Q98900 fugu rubrip Q918f9 oryzias lat O93601 caenorhabdi	093240 paralichthy 063256 rattus norv Q9qqy5 mus musculu 096541 setaria diq	Q9njb7 wuchereria Q9ngk9 wuchereria Q48563 brassica na	09177 stylophora 09177 stylophora 09255 arabidopsis		7
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## ALIGNMENTS

090667; 090667; 01-MAY-2000 (TrE 01-MAY-2000 (TrE 01-JUN-2001 (TrE HEAT-SHOCK PROTE	11 71 man	
UI-JUN-ZUUI (TFE HEAT-SHOCK PROTE HSC70	(TrEMBLrel. 13, Created) (TrEMBLrel. 13, Last sequence update)	
HSC70	EMBLrei. 1/, Last annotation update) SIN (FRAGMENT).	
Littorina plena.		
Eukaryota; Metaz	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;	
Neotaenioglossa;	Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.	
NCBI_TaxID=31219;		
[1]		
SEQUENCE FROM N.A.	Α.	
Hohenlohe P.A.;		
"Heat-shock gene	"Heat-shock genes in the heat-stressed genus Littorina.";	
Submitted (OCT-1999)	1999) to the EMBL/GenBank/DDBJ databases.	
EMBL; AF191828; AAF12787.1;	AAF12787.1;	
HSSP; P19120; 1BA1.	3A1.	
InterPro; IPR001	IPR001023; HSP70.	
PROSITE; PS01036	PS01036; HSP70_3; 1.	
	-1	
NON_TER 146	146	
SEQUENCE 146 AA;	Aa; 16607 MW; C3F3556AlAF438BB CRC64;	
Query Match Rest Local Similarity	91.3%; Score 42; DB 5; Length 146;	
8,	vative 0; Mismatches 1; Indels 0;	Gaps 0;
1 SLFEGIDIY 9		
79 SLFEGIDFY 8	87	
RESULT 2		
Q9U670		
90670	PRELIMINARY; PRT; 153 AA.	
03-08/0; 01-MAY-2000 (TrE	(TrEMBLrel, 13, Created)	
	13,	

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Bukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
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88.9%; Pred. No. 1.3;
tive 0; Mismatches 1; Indels
                                                 Littorina plena.
Sukaryota, Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
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                                                                                                                                                                                                             Hohenlohe P.A.; "Heat-shock genes in the heat-stressed genus Littorina."; "Heat-shock genes in the heat-stressed genus Littorina."; submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191830; AAF12789.1; --
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157 AA: 17834 MW; E8F743382B285EB2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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88.9%; Pred. No. 1.3;
ative 0; Mismatches
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
HEAT-SHOCK PROTEIN (FRAGMENT)
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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Matches 8; Conservative
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Matches 8; Conserv
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Bukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglosas Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
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                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
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                                                                                                                                                                                                                Hohenlohe P.A.;
Hohenlohe P.A.;
Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (CT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAF12784.1;
EMSP; P19120; 118A1.
InterPro, IPROJ01033; HSP70.
PROSITE; PS01036; HSP70.]
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NON_TER 155 155
SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;
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09U665; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROFEIN (FRAGMENT).
     01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT_SHOCK PROTEIN (FRAGMENT).
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Matches 8; Conservative
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                                                                                          Littorina scutulata.
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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80 SLFEGIDFY 88
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NON_TER
SEQUENCE
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RESULT Q90669

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RESULT Q90665 ID Q91 AC Q91 DT 01 DT DT

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Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                               01-NOV-1996 (TIEMBLrel. 01, Created)
01-NOV-1996 (TIEMBLrel. 01, Last sequence update)
01-NOV-2001 (TIEMBLrel. 17, Last annotation update)
01-JUN-2001 (TIEMBLREL. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota: Metazoa: Chordata: Crenidata: Vertebrata: Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protecanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                    24684 MW; FA8557F2BB85C37A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E4C745DE5484C17A CRC64;
  01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Score 42;
88.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.3%; Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=85036330; Pubmed=6092938;
                                                                                                                                                                                                                                                                 Principal Proposition (1970)
PRINTS; PR00301; HSP70; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
Heat shock; Multigene family.
NON_TER 1 1
NON_TER 220 220
SEQUENCE 220 AA; 24684 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 278
278 AA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 SLFEGIDFY 146
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SLFEGIDIY 9
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Q90520;
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Q90520
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
                                                   Eukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neotaenloglossa, Littorinoidea, Littorinidae, Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Heat shock genes in the heat stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191829; AAF12788.1;
HSSP; P19120; 1BAL.
InterPro; IPR001023; HSP70.
PROSTITE; PS01030; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 5; Length 158;
Pred. No. 1.3;
                                                                                                                      Hohenlohe P.A.; "Heat-shock genes in the heat-stressed genus Littorina."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191827; AAF12786.1; -. HSSP; P19120; LBAL. IDBJ. LBAL. IDBJ.
                                                                                                                                                                                                                                                                                                 Score 42; DB 5; Length 158 Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                            158 158 MW; D2ECE71042EC44CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 AA; 17891 MW; B41E5356BCECAD2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AA
                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                     PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                 91.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.38;
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Best Local Similarity 88.5.
                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Hohenlohe P.A.;
                                                                                               [1]
SEQUENCE FROM N.A.
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                                         Littorina plena
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NON_TER
SEQUENCE
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RESULT Q9U666

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P81159

RESULT P81159 ID P8 AC P8 DT 01

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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 8; Conserv
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252 SLFEGIDFY 260
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                                                                                                                                                                                                             NCBI_TaxID=68578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLFEGIDIY 9
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NON_TER
SEQUENCE
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SEQUENCE
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044352
AC 044352
AC 044352
DT 01-JUN
DT 01-JUN
DE HEAT-SI
GN HSPP0.
CC Betrob
CC Betrob
CC Petrob
CC ROBLE
CN NCBLT
RN [1]
RP SEGUEN
RN [1]
RR SEGUEN
RN SEG
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ID 04
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rattus corvegicus (Rat).
Rattus norvegicus (Rat).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                           Gaps
                                                                                                                                                                                                                                                                                                                                                Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.
D'Ambrosio E.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; 227118; CAA81642.1; -.
HSSP; P08107; 1HJO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.3%; Score 42; DB 13; Length 367;
88.9%; Pred. No. 3.6;
tive 0; Mismatches 1; Indels
                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, Y08578; CAA69892.1; -.
HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR001023; HSP70.
Pfam: PF00012; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70.1; 1.
PROSITE; PS01036; HSP70.3; 1.
Heat shock.
NON TER 367 AA; 40405 MW; RCD3DDBDF6E3C2CA CRC64;
                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 AA.
                                                                                                                                                                                                               367 AA
        88.9%; Pred. No. 2.6;
                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS000301; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.2.
Best Local 8; Conservative
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                             8; Conservative
                                                                                                                                                                                                                 PRELIMINARY;
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268 SLFEGIDFY 276
          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Lim E.H.;
                                                                                                             156 SLFEGIDFY 164
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                                                                    1 SLFEGIDIY 9
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                                                                                                                                                                                                                                       098899;
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Q63718
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Q98899
                             Matches
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Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
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Chondrosida; Chondrillidae; Chondrosia.
NCBI_TaxID=68574;
                                                                                                   Query Match 91.3%; Score 42; DB 11; Length 455; Best Local Similarity 88.9%; Pred. No. 4.7; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borchiellini C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026520; AAC05364.1; -.
HSSP; P08109; ICKR.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Decorbielling C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, ARCO5362.1;
HSSP; POBLO9; LCKR.
Interpro; IPR001023; HSP70.
Pfam; PR00012; HSP70;
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
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467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;
1 1
455 455
455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      044350;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5, Last sequence update)
7, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 5;
Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 AA
                                                                                                                                                                                                                                                                                                                                                    467 AA
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                                                                                                                                                                                                                                                                                                                                                    PRT;
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88.9%;
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01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Funiculinidae;
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0
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Bukaryota; Metazoa; Porifera; Calcarea; Calcinea; Clathrinida;
Clathrinidae; Guancha.
NCBI_TaxID=115120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Borchiellini C., Le Parco Y.;

Sponges paraphyly and the origin of Metazoa.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, ART81295; AAR61297.1;
InterPro; IPR001023; HSP70.

PFam; PR00012; HSP70; 1.

PROSITE; PS00329; HSP70.2; 1.

PROSITE; PS00329; HSP70.2; 1.

NON_TER 467 467

SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.3%; Score 42; DB 5; Length 467;
88.9%; Pred. No. 4.8;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                Length 467
                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 467
467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;
                                                           1 1
467 467
467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                                                                                                                                             Query Match 91.3%; Score 42; DB 5; Best Local Similarity 88.9%; Pred. No. 4.8; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 AA.
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PRINTS; PR00301; HEATSHOCK70.
                       PROSITE; PS01036; HSP70_3; 1.
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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252 SLFEGIDFY 260
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SEQUENCE
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CONNUCTOR 15
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044349
AC 044349
DT 044349;
DT 01-JUN
DT 01-JUN
DE HEAT-SI
GN FUNICU
OC EUKATY
OC FUNICU
OX NCBL_TR
RN [1]
RP SEQUEN
RR SEQUEN
RL SUBMILL
RL SUBMILL
DR EMBL;
DR EMBL;
DR HERP;
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DR Pfam; PF00012; HSP70; 1.

DR PRINTS; PR00301; HEATSHOCK70.

DR PROSITE; PS00301; HEATSHOCK70.

DR PROSITE; PS00301; HSP70_2; 1.

DR PROSITE; PS00136; HSP70_2; 1.

DR PROSITE; PS00136; HSP70_2; 1.

DR PROSITE; PS00136; HSP70_2; 1.

Transparse to second to the second
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Appli Appli Appli Appli Appli

Sequence 2, Ap Sequence 2, Ap Sequence 9, Ap Sequence 9, Ap Sequence 19, Ap

19, Appl 19, Appl 7, Appli 20, Appl 55, Appl 34, Appl

Sequence

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APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 4; Length 643; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
              US-09-240-410-2

US-08-946-475-2

US-09-340-479-9

US-09-340-479-9

US-08-471-119A-2

US-08-471-119A-2

US-08-471-119A-2

US-08-471-119A-2

US-08-471-119

US-08-471-119

US-08-478-37-19

US-08-478-37-19

US-08-478-37-19

US-08-469-537A-7

US-08-469-537A-7

US-08-469-537A-7

US-08-679-006-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9901
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08797358B Patent No. 6268478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 643 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
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77.88;
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Best Local Similarity 77.5
المرابع 7; Conservative
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1 SLFEGIDIY 9
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2.487 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Al
Sequence 14, A
Sequence 5, Al
Sequence 5, Al
Sequence 61, A
Sequence 61, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 24, Seque
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Sequence 18,
Sequence 7, A
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Sequence 18,
Sequence 8, A
Sequence 8, A
                                                                                                                         ; Search time 81.43 Seconds
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2: /cgn2_6/ptcdata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/RB_COMB.pep:*
6: /cgn2_6/ptcdata/2/laa/RCTUS_COMB.pep:*
                  4.5
Compugen Ltd.
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US-08-441-139-14
US-08-209-978A-5
US-08-45-046B-61
US-08-43-83A-22
US-08-43-83A-22
US-08-455-524B-22
US-08-455-524B-22
US-08-455-524B-22
US-08-455-524B-22
US-09-198-956-6
US-08-455-524B-22
US-08-443-883A-24
US-08-443-883A-24
US-08-443-883A-24
US-08-443-883A-24
US-08-455-524B-24
US-08-455-524B-24
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US-08-455-524B-24
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US-08-455-524B-24
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US-09-347-803-14
US-08-878-989-18
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                                                                                                                                                                                                                                                                                                                           212252 seqs, 22503292 residues
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              GenCore version
Copyright (c) 1993 - 2000
                                                                                                                         6, 2001, 07:53:52
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                         December
                                                                                                                                                                                                                    Perfect score:
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                                                                                                                         Run on:
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Gaps

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Indels

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Tue Dec 11 08:46:05 2001

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STREET: 2000 Pen
CITY: Washington
STATE: DC
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ZIP: 20006-1812
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RESULT 2
US-08-441-139-14

Sequence 14, Application US/08441139
Fatent No. 5773245
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
CORRESPONDERS: 20
CORRESPONDERS: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City plaza
CITY: Garden City
STREE: NY
COUNTPY.
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER LIBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,139

FILING DATE: 15-MAY-1995

CLASSIPICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/089,997

FILING DATE: 06-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: DiGiglio, Frank S.

REGISTRATION NUMBER: 31.346

REFERENCE/DOCKET NUMBER: 8646

TELECOMMUNICATION INFORMATION:

TELECHOME: 516-742-4343

TELEFRAX: 516-742-4366

TELERAX: 516-742-4366

TELERAX: 516-742-4366

TELERAX: 516-742-4366

TELERAX: 516-742-4366
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APPLICANT: KUSTERS, YVONNE
APPLICANT: KESTER, YVONNE
APPLICANT: VISSER, JACOB
APPLICANT: VISSER, JACOB
APPLICANT: VAN OOYEN, ALBERT J.J.
APPLICANT: CALIN, CLAUS
TITLE OF INVENTION: CLONING AND EXPRESSION
TITLE OF INVENTION: EXO-POLYGALACTURONASE G
NUMBER, OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Patent No. 564834
GENERAL INFORMATION:
APPLICANT: KUSTERS-VAN SOMEREN, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 646 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
T; Conserve
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286 SLYEGIDFY 294
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US-08-290-978A-5
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CORRESPONDER DADRESSE:
STREET: 2000 PERMISSI:
CUTTY: Washington
CU
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COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.4
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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83 SYFQGIHIY 91
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Patent No. 6287835
GEBERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT PILIG DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 452;
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Sequence 22. Application US/08438753B
Sequence 22. Application US/08438753B
SENERAL INFORMATION:
APPLICANT: Inmakawa, Kazuhito
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 2;
Pred. No. 84;
                                                                                                                                                  TELECOMMUNICATION NOMBER: 4615-0044.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELERA: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
   US 08/290,978
                                                                                      NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana US-09-457-046B-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.68;
85.78;
APPLICATION NUMBER: US 0 FILING DATE: 17-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-780-869-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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165 SLFDGISAY 173
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US-09-457-0468-61
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US-08-438-753B-22
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LENGTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 1; Length 99;
Pred. No. 25;
1; Mismatches 2; Indels
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APPLICANT: Bazer, Fuller W.
APPLICANT: Dontzer, Carol H.
APPLICANT: Ott, Troy L.
APPLICANT: Van Heeke, Gino
APPLICANT: Wan Heeke, Gino
APPLICANT: Wan Heeke, Gino
APPLICANT: Imakawa, Kazuhito
APPLICANT: Imakawa, Kazuhito
APPLICANT: Interferon Tau Compositions and
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREE: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/438,753B
FILING DATE: 10-MAY-1995
                                                                                                                                                                                   FILING DATE: 10-MAY 1995
CLASSIFICATION: 435
PIOR APPLICATION 1435
PRIOR APPLICATION DATA: 435
PRIOR APPLICATION DATA: 436
PRIOR APPLICATION DATA: 436
PRIOR APPLICATION DATA: 437
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA: 436
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-0CT-1992
ATFOREY/AGENT INFORMATION: 4489
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
RECISTRATION NUMBER: 38,615
RECISTRATION NUMBER: 38,615
RECISTRATION NUMBER: 38,615
RECISTRATION NUMBER: 5600-0001.30
TELEPHONE: 415-324-0880
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LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: predicted amino acid coding sequence
US-08-631-328-22 (HuIFNtau6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.4%; Score 31; DB 2; Length 99; 66.7%; Pred. No. 25; 2; Indels:ive 1; Mismatches 2; Indels
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US-08-455-54B-22
Sequence 22, Application US/08455524B
Sequence 22, Application US/08455524B
Patent No. 594223
GENERALINFORMATION:
APPLICANT: Bazer, Fuller W. APPLICANT: Obnson, Howard M. APPLICANT: Pontzer, Carol H. APPLICANT: Ott, Troy L. APPLICANT: Ott, Troy L. APPLICANT: Ott, Troy L. APPLICANT: Ott WENTION: Interferon Tau Compositions and TITLE OF INVENTION: Methods of Use NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,524B
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
                 APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.34
TELECOMBUNICATION INFORMATION:
TELECOMBUNICATION INFORMATION:
TELEPENONE: 415-324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
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02-MAR-1989
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PRIOR APPLICATION DATA:
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Best Local Similarity 66.7
Matches 6: Conservative
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APPLICATION NUMBER: U
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APPLICATION NUMBER: 1
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| 83 SYFQGIHIY 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
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US-08-631-328-22
Sequence 22, Application US/08631328
Fatent No. 593286
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Subramaniam, Prem S.
TITLE OF INVENTION: Hybrid Interferon Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 1; Length 99;
Pred. No. 25;
1; Mismatches 2; Indels
PatentIn Release #1.0, Version #1.25
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,328
FILING DATE: 12-APR-1996
                                                                                FILING DATE:

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/139,891

FILING DATE: 19-0CT-1993

PRIOR APPLICATION DATA:

FILING DATE: 09-MR-1992

PRIOR APPLICATION NUMBER: US 07/847,741

FILING DATE: 09-MR-1992

APPLICATION NUMBER: US 07/318,050

FILING DATE: 02-MR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/969,890

FILING DATE: 30-0CT-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REFERENCE/DOCKET NUMBER: 5600-0001.30

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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STREET: 350 Cambridge Ave., Suite 250
                                                  US/08/443,883A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 66.77
Matches 6; Conservative
                      CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palo Alto
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|83 SYFQGIHIY 91
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US 07/969,890

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Gaps ; 0

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5600-0001.31
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TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 22:
REFERENCE/DOCKET NUMBER: 5600
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-324-0860
TELEFRX: 415-324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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; INDIVIDUAL ISOLATE:
US-08-455-021B-22
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
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| 83 SYFQGIHIY 91
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US-09-045-467-22
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 99
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GENERAL INFORMATION:
APPLICANT: Bazer, Fuller W.
APPLICANT: Johnson, Howard M.
APPLICANT: Ott, Troy L.
APPLICANT: Van Heeke, Gino
APPLICANT: Imakawa, Kazuhito
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 2;
Pred. No: 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS: 6 ASSOCIATES
STREET: 350 Cambridge Ave., Suite 250
                                                                               5600-0001.32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/455,021B
31-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                            NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,615
                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
                                                                                                                                          TELEFAX: 415-324-0960 INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                   67.4%;
      FILING DATE: 30-OCT-1992
                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.4
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE: INDIVIDUAL ISOLATE: FINDIVIDUAL ISOLATE: F
                                                                                                                                                                                                                                          linear
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83 SYFQGIHIY 91
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US-08-455-021B-22
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Gaps
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predicted amino acid coding sequence of SEQ ID NO:21 (HuIFNtau6).
                                                                                                                                        67.4%; Score 31; DB 2; Length 99;
66.7%; Pred. No. 25; 2; Indels
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/09045467
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
PONTZEL, Carol H.
TITLE OF INVENTION: Interferon Tau Compositions and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/045,467
FILING DATE: 20-Max-1998
CLASSIFICATION: CURRENT APPLICATION NUMBER: US/09/045,467
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: US 08/455,021
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-0CT-1993
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
APPLICATION NUMBER: US 07/949,890
FILING DATE: 02-MAR-1989
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-0CT-1992
ATTORNEY/AGNT INFORMATION:
NAME: Dehlinger: Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 28,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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us-09-673-795-1.rai

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Length 789;
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Pred. No. 2.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/08438753B
Patent No. 5705363
GENERAL INFORTION:
APPLICANT: Imakawa, Kazuhito
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF SEQUENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
          COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/727,308
FILING DATE: October 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
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PRIOR PAPLICATION DATE: 07/318,050
PRIOR APPLICATION DATE: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATE: US 07/969.80A
                                                                                                                                                                                                                               NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-727-308-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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23 SLFPGVDV 30
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                                              INDIVIDUAL ISOLATE: predicted amino acid coding sequence;
SEQUENCE DESCRIPTION: SEQ ID NO: 21 (Hulfntau6).
US-09-045-467-22
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APPLICANT: Andersen, Lene N.
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Mads E.
APPLICANT: Bornvad, Mads E.
APPLICANT: Bornvad, Mads E.
TITLE OF INVENTION: Dectin Degrading Enzymes From Bacillus
TITLE OF INVENTION: Licheniformis
TITLE OF INVENTION: Licheniformis
TITLE OF INVENTION: Licheniformis
FILE REFERENCE: 5377.200-US
CURRENT APPLICATION NUMBER: 1344/97
EARLIER FILING DATE: 1997-11-24
EARLIER PILING DATE: 1997-11-24
EARLIER FILING DATE: 1997-11-20
NUMBER: OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 415
                                                                                                                                                                                                     Score 31; DB 4; Length 99;
Pred. No. 25;
1; Mismatches 2; Indels
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57.1%; Pred. No. 1.2e+02;
ive 3; Mismatches 0;
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STREET: 805 Fifteenth Street, N.W., #700
STATE: D.C.
COUNTRY: U.S.A.
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Patent No. 6020176
GENERAL INFORMATION:
APPLICANT: VIJI KAMIYA et al.
TITLE OF INVENTION: KAURENE SYNTHASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-198-956-6
; Sequence 6, Application US/09198956
; Patent No. 6165769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bacillus licheniformis
US-09-198-956-6
                                                                                                                                                                                                   67.48;
66.78;
                                                                                                                                                                              Query Match
Best Local Similarity 66./*,
E.zhos 6; Conservative
                 TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.4
Best Local Similarity 57.1
Matches 4; Conservative
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MEDIUM TYPE: Diskett
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20005
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| 83 SYFOGIHIY 91
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INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HuIFNTau7).
US-08-438-753E-24
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Pred. No. 38;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/08443883A
Fatent No. 5738845
GENERAL INFORMATION:
APPLICANT: Bazer, Fuller W.
APPLICANT: Pontzer, Carol H.
APPLICANT: Pontzer, Carol H.
APPLICANT: Ott, Troy L.
APPLICANT: Imakawa, Kazuhito
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREE: CAPACIAGE STREET: 350 Cambridge Ave., Suite 250 CITY: Palo Alto
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APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION NUMBER: US 07/318,050
FILING DATE: 30-0CT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NC-CURRENM
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30-0CT-1992
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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| 83 SYFQGIHVY 91
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FILING DATE:
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REGISTRATION NUMBER: 33,875

REFRENCEDOMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-324-0960

INFORMATION FOR SEG ID NO: 24:

SEQUENCE CHARACTERISTICS:

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

INDIVIDUAL ISOLATE: predicted amino acid coding sequence

NOLECULE TYPE: predicted amino acid coding sequence

INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HulFNtau7).

ONE INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HulFNtau7).

OUGLY Match

Seat Local Similarity 55.6%; Pred. No. 38;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps

OY 1 SIFEGIDIY 9

| | | | | | | | |
| | Db 83 SYFQGIHVY 91

Search completed: December 6, 2001, 07:59:54
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us-09-673-795-1.rai

Tue Dec 11 08:46:05 2001

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
Littorina plena.
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090667;
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Q9u667 littorina s
Q9u669 littorina s
Q9u665 littorina p
Q9u661 littorina p
Q9u668 littorina p
Q9u668 littorina p
P81159 aplysia cal
Q90520 oncorhynchu
Q90520 oncorhynchu
Q90520 oncorhynchu
Q90520 chondrosia
Q44350 chondrosia
Q44350 chondrosia
Q44350 chondrosia
Q44354 funiculina
Q44351 eunicella c
Q4431 eunicella c
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                                                                                                        (without alignments)
7.732 Million cell updates/sec
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                                                                                       December 6, 2001, 07:56:53; Search time 170.25 Seconds
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                                                                                                                                                                                                                                                                                           473505
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Q9NJ92
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sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
sp_fungi:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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09c7x7 arabidopsis 993147 botryllus s 015766 dictyostell 09800 fugu rubrip 091869 oryzias lat 093201 caenorhabdi 093320 paralichthy 063256 rattus norv 096451 setaria dig 09njb7 wuchereria 096541 setaria dig 09njb7 wuchereria 091655 schizosach 041027 pisum sativ 09177 stylophora 092555 arabidopsis 09188 arabidopsis 09188 arabidopsis 09252 crassostrea 024952 geodia cydo 044346 asbestoplum 044346 asbestoplum 044347 petrosia fi	dae; Phycodnavirus. an Etten J.L.; 30-kb genome: map C64; ngth 289; Indels 0; Gaps 0;	
Q9C7X7 Q93147 Q93146 Q15746 Q15746 Q98900 Q918F9 Q93240 Q93240 Q93250 Q9000 Q9000 Q41027 Q910	IGNMENTS  ; 289 AA. ed) sequence update) annotation update) us 1 (PBCV-1). age; Phycodnavirida A., Rock D.L., Van la virus PBCV-1 330 BF7AF4A9E857F1 CRC6 BF7AF4A9E857F1 CRC6 BF7AF4A9E857F1 CRC6 ismatches 1; In In	
617 10 628 5 628 5 632 6 632 6 632 6 632 6 632 6 632 6 644 0 644 0 644 1 644 1 644 1 645 1 645 1 645 1 655 1	(Tremblrel. 02, Cr. (Tremblrel. 02, La. (Tremblrel. 03, La. (Tremblrel. 03, La. Ind. SEQUENCE. 03, La. Ind. SEQUENCE. 0506; M.A. 050	9 258
20 21 22 23 23 24 25 25 26 27 27 28 29 20 20 21 22 23 24 25 26 27 28 39 81 81 31 32 33 34 81 35 81 81 81 81 81 81 81 81 81 81	1 98505 98505; 1-FEB-1997 1-NEW-1998 ENOME, PART ATAMES, GSD 1140895; GSD 1141895; GSD ENLINE=9640 ENLISH G.F., ANALCH TORY 223 4BL; U42580 EQUENCE E	1 SLFEGIDGY      :    250 SLFEGLQGY
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PRT; 146 AA.

PRELIMINARY;

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Neotaenioglossa; Littorinoidea; Littoriniae; Littorina.
NCBI_raxID=31219;
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Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; P191180; AAF12789.1; -.
HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                                                      Length 155
                                                                                                    Hoheniohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Bubmitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191826; AAF12785.1; -.
HSSP; P19120; IPAL.
InterPro; IPR001023; HSP70.
PROSITE; PS01036; HSP70._3; 1.
Neotalenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31221;
                                                                                                                                                                                                                                                                                 157 AA; 17834 MW; E8F743382B285EB2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUNS-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090665 PRELIMINARY; PRT; 157 AA.
090665;
01-MAY-2000 (TYEMBLYEL 13, Created)
01-MAY-2001 (TYEMBLYEL 13, Last sequence update)
01-JUN-2001 (TYEMBLYEL 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 5;
Pred. No. 7.6;
0; Mismatches
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        81.2%;
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Best Local Similarity 88.3
استرت 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                SEQUENCE FROM N.A.
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82 SLFEGIDFY 90
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NON_TER
SEQUENCE
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Neotaenioglossa, Littorinoidea, Littorinidae, Littorina.
NCBI_TaxID=31221;
          Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.2%; Score 39; DB 5; Length 153; Best Local Similarity 88.9%; Pred. No. 7.5; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hohen the P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (Oct-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAF12784.1; ...
EMBL; AF191825; AAF12784.1; ...
InterPro; IPROJ001033; HSP70.
PROSITE; PS01036; HSP70.3; 1.
NON_TER 153 153
SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 5; Length 146;
Pred. No. 7.1;
0; Mismatches 1; Indels
                                                                                                                                   Medical Parts in the heat-stressed genus Littorina."; Heat-shock genes in the heat-stressed genus Littorina."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191828; AAF12787.1; -... HSSP: P19120; 1BA1. Interpro; IPR001023; HSP70. Interpro; IPR001023; HSP70. Interpre; PS01036; HSP70. In TER Interprese (IPR05112) in 
                                                                                                                                                                                                                                                                                                                                             146 146
146 AA; 16607 MW; C3F3556AlAF438BB CRC64;
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01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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79 SLFEGIDFY 87
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NON_TER
SEQUENCE
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Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysiidae; Aplysia.
NCBI_TaxID=6500;
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     Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                               Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
"Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191829; AAF12788.1; -.
HSSP; P19120; 1BA1.
InterPro; IPR010033; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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88.9%; Pred. No. 11;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                81.2%; Score 39; DB 5; Length 158;
88.9%; Pred. No. 7.7;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                              158 AA; 17891 MW; B41E5356BCECAD2F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
HSC70.
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01-JUN-1998 (TrEMBLrel. 06, Created)
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NON_TER 1 1

NON_TER 220 220

SEQUENCE 220 AA; 24684 MW;
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Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                       SEQUENCE FROM N.A.
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85 SLFEGIDFY 93
                            NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                   1 SLFEGIDGY 9
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SEQUENCE
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Neotaenioglossa; Littorinoidea; Littorinidae, Littorina.
NCBL_TaxID=31219;
                                                   Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191824; AAF12783.1; -.
HSSP; P19120; IBA1.
InterPro; PR001013; HSP70.
PROSITE; PS01036; HSP70_3; 1.
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                                                                                                                                                                                                                                               1; Indels
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID-31221;
                                                                                                                                                                                 SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 AA; 17868 MW; D2ECE71042EC44CB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 5;
Pred. No. 7.7;
0; Mismatches
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Pred. No. 7.7;
0; Mismatches
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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88.9%;
                                                                                                                                                                                                                    Query Match 81.2
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
                                          SEQUENCE FROM N.A.
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063718;
01-NOV-1996 (TEMBLEEL. 01, Created)
01-NOV-1996 (TEMBLEEL. 01, Last sequence update)
01-JUN-2001 (TEMBLEEL. 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
Rattus norvegicus (Rat).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Euteleostei; Neofeleostei;
Acathomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H., D'Ambrosio E.;
Submitted (Nov-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, 227118; CAA81642.1; -.
HSSP; P08107; 1HJO.
InterPro; IPR001023; HSP70.
Pfam: PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PRINTS; PR00301; HSP70_2; 1.
                                       Score 39; DB 13; Length 278; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 367; 21;
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EMBL, Y08578; CAA69892.1; -.
HSSP: P19120; 3HSC.
InterPro; IRR001023; HSP70.
Pfam; |PF00012; HSP70; 1.
PRINTS; PR00301; HBATSHOCK70.
PROSTITE; PS010395; HSP70_1; 1.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              367 AA
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                                                                                                    Mismatches
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88.9%; Pred. No.
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01-JUN-2001 (TrEMBLREL 17, Last anno
70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                       81.2%;
88.9%;
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Matches | 8; Conserv
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Matches 8; Conserv
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SEQUENCE FROM N.A.
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                                          Query Match
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Q98899;
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A Kuhl D., Kennedy T., Barzilai A., Kandel E.;
A Kuhl D., Kennedy T., Barzilai A., Kandel E.;
Long-term sensitization training in Aplysia leads to an increase in the expression of BlP, the major protein chaperon of the ER.";
L J. Cell Biol. 119:1069-1076(1992).
C -i - SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
R EMBL; 215037; CAA76755.1;
R InterPro: IPR001023; HSP70.
R PRINTS; PR00312; HSP70.
R PRINTS; PR00312; HSP70.2;
R PROSITE; PS00329; HSP70.2;
R PROSITE; PS01036; HSP70.2;
W Heat shock; Miltigene family.
                                                                                                                                                                                       Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysiidae; Aplysia.
NCBL_TaxID=6500;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
OGCOLNYNCHUS MÇKISS (RAINDOW LTOUT) (Salmo gairdneri).
RAINDOW TROUT 70 KDA HEAT SHOCK PROTEIN (PRAGMENT).
Actinopterygli; Neopterygli; Teleostel; Buteleostel;
Protacanthopterygli; Salmoniformes; Salmonidae; Oncorhynchus.
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"70-Kilodalton heat shock polypeptides from rainbow trout:
"Totaracterization of cDNA sequences.";
Mol. Cell. Biol. 4:1785-1791(1984).
EMBL; K02549; AAA49562.1; -
HSSP; P08109; ICKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.2%; Score 39; DB 5; Length 221; 88.9%; Pred. No. 11;
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P81157 PRELIMINARY; PRT; 221 AA.
P81157; COU-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).
HSP70A.
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PROSITE; PS01035; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
NON_TER 1 1
NON_TER 278
SEQUENCE 278 AA; 30327 MW;
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Pfam; PF00012; HSP70; 1.
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InterPro; IPR001023; HSP70.
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Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
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Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Chondrosida; Chondrillidae; Chondrosia.
NCBI_TaxID=68574;
                                                                                       Query Match 81.2%; Score 39; DB 11; Length 455; Best Local Similarity 88.9%; Pred. No. 27; Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Bubmitted (SRP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AROJ6217; AAC05362.1; -.
HSSP; P08109; 1CKR.
InterPro: IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HRATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borchiellini C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026520; AAC05364.1; -.
HSSP; P08109; 1CKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 AA; 51707 MW; ODBE6920F2E6EA96 CRC64;
            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
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PROSITE; PS01036; HSP70_3; 1
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Best Local Similarity 88.9
Matches 8; Conservative
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254 SLFEGIDFY 262
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NCBI_TaxID=68578;
                                                                                                                                             1 SLFEGIDGY 9
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DR InterPro; IPRO1012; HSP70.

DR Pfam; PF001012; HSP70: 1.

DR PRINTS; PR00301; HEATSHOCK70.

DR PROSTE; PS01036; HSP70.3; 1.

FT NON_TER 467 467

SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match 81.2%; Score 39; DB 5; Length 467;

Best Local Similarity 88.9%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1 SLFEGIDEY 9

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Db 252 SLFEGIDEY 260

Search completed: December 6, 2001, 07:56:53

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                                                                                                                       December 6, 2001, 07:59:54; search time 81.43 Seconds (without alignments) 2.487 Million cell updates/sec
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Sequence 2
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-457-0468-61
US-08-946-475-2
US-08-340-475-2
US-08-346-475-9
US-08-946-475-9
US-08-617-811-55
US-08-679-006-34
US-08-239-823-1
US-08-209-508-3
US-08-209-508-3
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US-09-347-803-10
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                                                                                                                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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ö Gaps TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN NUMBER OF SEQUENCES: 9 ö Length 643; Indels CITY: San Diego
STATE: California
COUNTRY: United States
2 IP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700 Score 41; DB 4; Pred. No. 1.7; 1; Mismatches NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPA: (619) 535-9049
INFORMATION FOR SEQ ID NO: 3: APPLICATION NUMBER: US/08/797,358B FILING DATE: 11-Feb-1997 CLASSIFICATION: CLASSIFICATION SATE: CLASSIFICATION OWBER: US 60/011,491 FILING DATE: 12-FEB-1996 ATTONNEY/AGENT INFORMATION: ALIGNMENTS Sequence 3, Application US/08797358B Patent No. 6268478 GENERAL INFORMATION: APPLICANT: Adams, John MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID US-08-797-358B-3 LENGTH: 643 amino acids STRANDEDNESS: unknown SEQUENCE CHARACTERISTICS 89.1%; 77.8%; TOPOLOGY: unknown Query Match
Best Local Similarity 77.8° TYPE: amino acid

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Gaps
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US-09-347-803-14
Sequence 14, Application US/09347803
Sequence 14, Application US/09347803
Sequence 14, Application US/09347803
GENERAL INFORMATION:
APPLICANT: Famedu, Layo O.
APPLICANT: Kinney, Tony
APPLICANT: Kinney, Tony
TITLE OF INVENTION: Plant Scrbitol Biosynthetic Enzymes
FILE REFERENCE: BB-117
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
SEALIER PILLICATION NUMBER: 60/092,952
SEALIER PILLING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
SOFTWARE: MICROSOft Office 97
SEQ ID NO 14
SEQ ID NO 14
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 3; Length 161;
Pred. No. 24;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%; Pred. No. 43;
Matches | 5; Conservative 2; Mismatches 0; Indels
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: 1344/97
EARLIER FILING DATE: 1997-11-24
EARLIER FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Synferon
FILE REFERENCE: PF404
CURRENT APPLICATION NUMBER: US/09/205,264
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/067,746
EARLIER FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-205-264-2
Sequence 2, Application US/09205264
Patent No. 6114145
GENERAL INFORMATION:
                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Bacillus licheniformis
US-09-198-956-6
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-205-264-2
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118 FEGVELY 124
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LENGTH: 161
                                                                                                                                                                               LENGTH: 415
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; Patent No. 6165769
; GENERAL INCORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schulein, Martin
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schoor, Kirk
; APPLICANT: Schoor, Kirk
; TITLE OF INVENTION: Licheniformis
; TITLE OF INVENTION: Licheniformis
; FILE REFERENCE: 5377.200-US
; CURRENT APPLICATION NUMBER: US/09/198,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 646;
Pred. No. 4.3;
                                                                                                                                                                                                 APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CAURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-MAY-1995
CLASSTRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-UL1-199
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,3446
                                                                                                                                    Sequence 14, Application US/08441139
Patent No. 5773245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEFHONE: 516-742-4343
TELEFAX: 536-901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.8%;
77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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STATE: NY
COUNTRY:
                                                                                                                       JS-08-441-139-14
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US-09-198-956-6
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GWYNN, Michael
APPLICANT: GWYNN, Michael
APPLICANT: Balmer, Leslie
TITLE OF INVENTION: TOPOISOMERASE I
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Frussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARRE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/946,475
FILING DATE: 08-CCT-1997
APPLICATION NUMBER: 60/027,973
FILING DATE: 08-CCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimml, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50560
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-340-479-2
Sequence 2, Application US/09340479
; Patent No. 6274139
  REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPAN: 610-270-4478
TELEPAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 691 amino acids
TYPE: amino acid
STRANDEDNESS: single
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LENGTH: 691 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 85.7
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-946-475-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-340-479-2
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283 LYEGIDL 289
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                                                                                                                                                                                                                                                                                                            Sequence 61, Application US/09457046B
Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 15879
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 61
LENGTH: 458
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                                                                                 Score 32; DB 4; Length 309;
Pred. No. 49;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUMTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASIESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,475
FILING DATE: 08-OCT-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/027,973
FILING DATE: 08-OCT-1996
ATTORNEY ADELICATION SOWARTION:
NAME: GIMMI, EGWARTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08946475
; Sequence 2, Application US/08946475
; Patent No. 6013505
; GENERAL INFORMATION:
APPLICANT: GENTON, Michael
APPLICANT: Kallender, Howard
APPLICANT: Rallender, Leslie
TITLE OF INVENTION: TOPOISOMERASE I
COURSEPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corpor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Arabidopsis thaliana US-09-457-046B-61
                                                                                   69.68;
66.78;
                                                           Query Match
Best Local Similarity 66./°,
Fina 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 69.6
Best Local Similarity 66.7
Matches 6; Conservative
; ORGANISM: Glycine max US-09-347-803-14
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US-09-457-046B-61
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Gaps ö 69.6%; Score 32; DB 3; Length 691; 85.7%; Pred. No. 1.2e+02; 0; Indels 1; Mismatches

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303 LYEGIDE 309
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0
  69.6%; Score 32; DB 4; Length 691; 85.7%; Pred. No. 1.2e+02; Live 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPURE: FA
COMPURE: FA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEN DOS
SOFTWARE: FASTSEN FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,475
FILING DATE: 08-0CT-1997
FILING DATE: 08-0CT-1997
FILING DATE: 08-0CT-1997
ATORNEY APPLICATION NUMBER: 60/027,973
ATORNEY AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                             APPLICANT: Gwynn, Michael
APPLICANT: Kallender, Howard
APPLICANT: Palmer, Leslie
TITLE OF INVENTION: TOPOISOMERASE I
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-340-479-9
Sequence 9, Application US/09340479
Fatent No. 627439
GENERAL INFORMATION:
APPLICANT: Gwynn, Michael
APPLICANT: Rallender, Howard
APPLICANT: Palmer, Leslie
                                                                                                                                                                                                            US-08-946-475-9; Sequence 9, Application US/08946475; Patent No. 6013505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85./*,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 711 amino acids
TYPE: amino acid
STRANDEDNESS: single
Query Match 69.6
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                         1:1111
283 LYEGIDL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1:|||||
303 LYEGIDL 309
                                                                                     2 LFEGIDL 8
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Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application US/08817811
Fatent No. 6174528
GENERAL INFORMATION:
APPLICANT: Good, Michael F.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
ITLE OF INVENTION: COMPRESING SAME
NUMBER OF ENCENTION: COMPRESING SAME
NUMBER OF SOUTHORES:
ADDRESSEE: Arnold, White & Durkee
STREET: Po. Box 4433
CITY: Houston
STAFET: Texas
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 4; Le
Pred. No. 1.2e+02;
1; Mismatches 0;
                                                                                                                                                                                                  SOFTWARE: FASESEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,479
FILING DATE:
CLASSIFICATION:
PRIOR; APPLICATION:
                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/946,475
FILING DATE: 08-OCT-1997
APPLICATION NUMBER: 60/027,973
FILING DATE: 08-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50560
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: TOPOISOMERASE I NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 711 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-340-479-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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APPLICANT: PAYNE, MARK S.
APPLICANT: ANTON, DAVID L.
APPLICANT: BICOSIMO, ROBERT
APPLICANT: BOYAGAN, JOHN E.
TITLE OF INVENTION: production of glycolate oxidase
TITLE OF INVENTION: in methylotrophic yeast
NUMBER OF SEQUENCES:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                               GLYCOLATE OXIDASE PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORPUTER, INTERCOSOFT WINDOWS V3.0
SOFTWARE: MICROSOFT WORD V2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,823
PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: 08/085,488
FILING DATE: JULY 1, 1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH 1.0 MB
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH SYSTEM, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-290-508-3
; Sequence 3, Application US/08290508
; Patent No. 5693490
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08253823
Patent No. 5541094
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1007 MARKET STREET
                                             67.48;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GLYCOLA NUMBER OF SEQUENCES: 1 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity ?
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||||
183 FEGIDL 188
                                                                                                                                                                                46 LFEGFDL 52
                                                                                                                                       2 LFEGIDL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 FEGIDL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
CITY: WI
                                                                                                                                                                                                                                                       RESULT 13
US-08-253-823-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-253-823-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Salerno, John C.
TITLE OF INVENTION: APPLICATIONS FOR REGULATORY REGION OF
TITLE OF INVENTION: NOS ISOFORMS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 4; Length 81;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/679,006
FILING DATE: 12-JUL-1996
CLASSIFICATION: 514
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
           CURRENT AGENCIALIN RELEASE FLOO, VET
CURRENT APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 96/11944
FILING DATE: 25-APR-1996
ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 97,642
REGISTRATION NUMBER: FERC:005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JCS96-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/08679006
Patent No. 6150500
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: JCS96
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 861-6240
TELEFRAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.v.
--heq 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-679-006-34
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 81 amino
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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20 SILEGLNLY 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-08-817-811-55.
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-679-006-34
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                           Gaps
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Score 31; DB 4; Length 120;
Pred. No. 27;
0; Mismatches 1; Indels
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Gaps ö Length 369; 0; Indels 67.4%; Score 31; DB 1; 100.0%; Pred. No. 95; iive 0; Mismatches

pepl-mod81.rai

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3 FEGIDL 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.4%; Score 31; DB 1; Length 369; 100.0%; Pred. No. 95; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DAVID LEROY ANTON
APPLICANT: DAVID LEROY ANTON
APPLICANT: ROBERT DICOSIMO
TITLE OF INVENTION: OXIDATION OF GIYCOLIC ACID TITLE OF INVENTION: GLYOXYLIC ACID USING A
TITLE OF INVENTION: MICROBIAL CELL TRANSFORMANT
TITLE OF INVENTION: AS CATALYST
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.JI.JDUJPONTJDEJNEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: MILMINGTON
STREET: DELAMARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH 2.0 MB COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS, 3.1 SOFTWARE: MICROSOFT WORD VERSION 6.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/606,144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/817,165
FILING DATE: JANUARY 6, 1992
ATTORNEY, AGENT INFORMATION:
NAME: GREGORY, THEODORE C.
REGISTRATION NUMBER: 25,243
REFERENCE,/DOCKET NUMBER: CH-2087-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
               PAPPLICATION NUMBER: US/08/290,508
FILING DATE: 15-AUG-1994
CLASSIFICATION NUMBER: US/08/290,508
FILING DATE: 15-AUG-1994
FILING DATE: 03-MAR-1993
APPLICATION NUMBER: 08/025,495
FILING DATE: 03-MAR-1993
ATTORNEY/AGNT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9271
TELECOMMUNICATION INFORMATION:
TELEFAN: 302-892-7342
TELEFAN: 302-892-7342
TELEFAN: 302-892-7949
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08606144; Patent No. 5834262; GENERAL INFORMATION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.4
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        S: unknown
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-290-508-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: DELAWARE
COUNTRY: U.S A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 FEGIDL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 FEGIDL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-606-144-1
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; SEQUENCE CHARACTERISTICS:
; TYPE: amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: protein
US-08-606-144-1

Query Match
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 3 FEGIDL 8
[1|1|1]
Db 183 FEGIDL 188

Search completed: December 6, 2001, 07:59:54
Job time: 362 sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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model
3
using
search,
protein
1
protein
Θ

Run on: December 6, 2001, 07:58:26; Search time 88.19 Seconds (without alignments)
7.774 Million cell updates/sec
Title: PEPI-MODBL
Perfect score: 46

Perfect score: 46
Sequence: 1 SLFEGIDLY 9

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_68:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

4: pir4:\*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Length	图 :	QI	Description
-	42	91.3	208	7	B44261	dnaK-type molecula
7	42	91.3	278	~	151344	dnaK-type molecula
m	42	91.3	420	~	A26283	dnaK-type molecula
4	42	91.3	467	7	T45477	heat-shock protein
Ŋ	42	91.3	467	7	T45479	heat-shock protein
9	42	91.3	468	7	T45476	heat-shock protein
7	42	91.3	469	~	T45478	heat-shock protein
80	42	91.3	617	7	н96605	2
6	42	91.3	632	7	T45471	dnaK-type molecula
10	42	91.3	634	~	A25646	
11	42	91.3	636	~	A48872	
12	42	91.3	638	7	S31766	
13	42	91.3	639	7	JC1391	dnaK-type molecula
14	42	91.3	639	7	S20139	
15	42	91.3	640	7	HHKW7A	dnaK-type molecula
16	42	91.3	640	7	A29160	
17	42	91.3	640	~	S37394	dnaK-type molecula
18	42	91.3	640	7	T21394	hypothetical prote
19	42	91.3	640	7	T43724	_
20	42	91.3	641	7	S53357	dnaK-type molecula
21	42	91.3	641	~	S35718	
22	43	•	641	~	I54542	dnaK-type molecula
23	42	91.3	641	7	A45871	dnaK-type molecula
24	42	91.3	642	-	HHBYA1	
25	42	٠	642	7	JH0095	
26	42	•	642	7	B36590	dnaK-type molecula
27	42	91.3	644	7	A45635	dnaK-type molecula
28	42	91.3	645	7	11	dnaK-type molecula
29	42	91.3	646	~	T46650	heat shock protein

draK-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)
N.Alternate names: 70K heat shock protein
C.Species: Oncorhynchus myKiss (rainbow trout)
C.Species: Oncorhynchus myKiss (rainbow trout)
C.Sacession: I51344
R.Kochary, R.K.; Jones, D.; Candido, E.P.M.
MOI. Cell. Biol. 4, 1785-1791, 1984
A.Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o
A;Reference number: 151344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-278 <KOT>
A;Residues: 1-278 <KOT>
A;Residues: 1-278 <KOT>
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70

dnaK-type molecula dnaK-type molecula	heat shock protein heat shock protein	dnak-type molecula dnak-type molecula dnak-type molecula	dnak-type molecula heat-shock protein	heat-shock protein dnaK-type molecula	heat shock protein dnaK-type molecula	dnaK-type molecula heat shock protein	heat shock protein
HHXL70 S44168	T41121 JC7088	A03309 PO0138	146588 T45473	T45474 JN0668	PC7036 S25585	S09036 T45517	JC7132
7	900	9 77 79	00	77	77	77	7
647 647	650	214	379	467 641	641 643	643 651	651
91.3 91.3	91.3	89.1 89.1	89.1 89.1	89.1 89.1	89.1 89.1	89.1 89.1	89.1
42	244	4 4 4	4 4	41	417	4 4	41
30 31	332	322 302	37 38	39 40	<b>4</b> 1	4 4 4 4	45

## ALIGNMENT

K-type molecular chaperone HSC70 - California sea hare (fragment) their and a shock protein 70 homolog HSC70 (becies: Aplysia californica (California sea hare) acts (California acaiifornia acaiifornia acaiifornia acaiifornia acaiifornia acaiifornia acaiifornia acaiifornia sea hare) acts (04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-ha (Cassion: B44261; MODS) 1076, 1992 (Cali Biol. 119, 1069-1076, 1992) (Cali Biol. 119, 1069-1076, 1992) (Cali Biol. 19, 1069-1076) (Cali Biol. 1908 (Cali Biol. 1908) (Ca	
C; Species: Aplysia californica (California sea ĥare) C; Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-C; Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-C: Accession: B44261 R; Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R. A. Cell Biol. 119, 1069-1076, 1992 A; Cell Biol. 119, 1069-1076, 1992 A; Reference number: A44261; MUID: 93077669 A; Reference number: A44261; MUID: 93077669 A; Actus: preliminary; not compared with conceptual translation A; Residues: 1-208 «KUH> A; Residues: 1-208 (KUH) C; Respection: A; Genetics: A; Gene	lar chaperone HSC70 - California sea hare (fragment) s: heat shock protein 70 homolog HSC70
C; Accession: B44261  F; Kikuli, D; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.  J. Call Biol. 119, 1069-1076, 1992  A; Title: Long-term sensitization training in Aplysia leads to an increa A; Reference number: A44261; MUID:93077669  A; Reference number: A44261; MUID:93077669  A; Reference number: A44261; MUID:93077669  A; Rederics: preliminary; not compared with conceptual translation  A; Rederics: nucleic acid  A; Rederics: nucleic acid  A; Rederics: RGT0  C; Genetics: A; RGT0  C; Genetics: RGT0  C; Reywords: ATP; molecular chaperone  Q; Reywords: ATP; molecular chaperone  Q; Reywords: ATP; molecular chaperone  Q; Reywords: ATP; MGT0  C;	la californica (California sea hare) 998 #sequence revision 04-Sep-1998 #text_change 13-Aug-1999
R; Kuhi, D; Kennedy, T.E.; Barzilai, A.; Kandel, E.R. A; Title: Long-term sensitization training in Aplysia leads to an increa A; Reference number: A44261; MUID:93077669 A; Retaus: preliminary; not compared with conceptual translation A; Molecule type: nucleic acid A; Relatus: preliminary; not compared with conceptual translation A; Relatus: preliminary; not compared from NCBI backbone (NCBIP:118950) C; Genetics: A; Resultes: 1-208 - KNUH> A; Cenetics: C; Genetics: A; Genetics: C; Function: C; F	261
A;Tifle: Long-term sensitization training in Aplysia leads to an increa A;Reference number: A44261; MUID:93077669 A;Accession: B44261 A;Accession: B44261 A;Accession: B44261 A;Accession: B44261 A;Releant type: nucleic acid A;Releant type: nucleic from NCBI backbone (NCBIP:118950) C;Genetics: A;Releant type: nucleic acid A;Releant type: nucleic type: nucl	edy, T.E.; Barzilai, A.; Kandel, E.R.
A; Reference number: A44261; MUID:93077669 A; Accession: B44261 A; Status: preliminary; not compared with conceptual translation A; Molecule type: nucleic acid A; Relatus: preliminary; not compared with conceptual translation A; Molecule type: nucleic acid A; Relatus: 1-208 - KKUH> A; Residues: 1-208 - KKUH> A; Residues: 1-208 - KKUH> A; Genetics: C; Genetics: A; Genetics: C; Function: C; Fun	rm sensitization training in Aplysia leads to an increase in the exp
As Actacus: preliminary; not compared with conceptual translation As Astatus: preliminary; not compared with conceptual translation As Residues: 1-208 «KUH> As Residues: 1-208 «KUH> As Note: sequence extracted from NCBI backbone (NCBIP:118950) Csenetics: As Gene: HSC70 Cs. Function: As Gene: HSC70 C; Function: Involved in protein folding and assembling/disassembling C; Superfamily: heat shock protein 70 C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone Query Match Best Local Similarity 88.9%; Pred. No. 0.39; Matches 8; Conservative 0; Mismatches 1; Indels 0; Ga () 1 SLFEGIDLY 9 () 1 SLFEGIDLY 9	er: A44261; MUID:93077669
A; Molecule type: nucleic acid minimus of the configuration of the confi	261 inary: not compared with conceptual translation
A; Residues: 1-208 <pre>A; Residues: 1-208 <pre>A; Rote: sequence extracted from NCBI backbone (NCBIP:118950)</pre> A; Note: sequence extracted from NCBI backbone (NCBIP:118950) C; Genetics: A; Gene: HSC70 C; Fuction: involved in protein folding and assembling/disassembling C; Superfamily: heat shock protein 70 C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone Query Match Best Local Similarity 88.9%; Pred. No. 0.39; Best Local Similarity 88.9%; Pred. No. 0.39; Matches 8; Conservative 0; Mismatches 1; Indels 0; Ga () ISLFEGIDLY 9 () ISLFEGIDLY 9</pre>	nucleic acid
A;Note: sequence extracted from NCBI backbone (NCBIP:118950) C;Genetics: A;Gene: HSC70 C;Function: A;Description: involved in protein folding and assembling/disassembling C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone Query Match Best Local Similarity 88.98; Pred. No. 0.39; Matches 8; Conservative 0; Mismatches 1; Indels 0; Ga Qy 1 SLFEGIDLY 9	8 <kuh></kuh>
C; Genetics: A; Gene: HSC70 C; Function: A; Description: involved in protein folding and assembling/disassembling C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone Query Match Best Local Similarity 88:3%; Pred. No. 0.39; Matches 8; Conservative 0; Mismatches 1; Indels 0; Ga Qy 1 SLFEGIDLY 9	extracted from NCBI backbone (NCBIP:118950)
A; Gene: HSC70 C; Function: A; Description: involved in protein folding and assembling/disassembling C; Superfamily: heat shock protein 70 C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone Query Match Best Local Similarity 88.9%; Pred. No. 0.39; Matches 8; Conservative 0; Mismatches 1; Indels 0; Ga Qy 1 SLFEGIDLY 9	
C; Function: A; Description: involved in protein folding and assembling/disassembling C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone C; Keywords: ATP; molecular chaperone Query Match Best Local Similarity 88.9%; Pred. No. 0.39; Matches 8; Conservative 0; Mismatches 1; Indels 0; Ga Qy 1 SLFEGIDLY 9	
A; Description: involved in protein folding and assembling/disassembling (S; Superfamily: heat shock protein 70 C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone Query Match 91.3%; Score 42; DB 2; Length 208; Best Local Similarity 88.9%; Pred. No. 0.39; Matches 8; Conservative 0; Mismatches 1; Indels 0; Ga Qy 1 SLFEGIDLY 9	
uperfamily; heat shock protein 70 (eywords: ATP; molecular chaperone  uery Match  91.3%; Score 42; DB 2; Length 208;  est Local Similarity 88.9%; Pred. No. 0.39;  fatches 8; Conservative 0; Mismatches 1; Indels 0;    SEFEGIDLY 9	nvolved in protein folding and assembling/disassembling of protein o
vuery Match       91.3%; Score 42; DB 2; Length 208;         dest Local Similarity 88.9%; Pred. No. 0.39;         fatches 8; Conservative 0; Mismatches 1; Indels 0;         1 SLFEGIDLY 9	aat shock protein 70 molecular chaperone
datches 8; Conservative 0; Mismatches 1; Indels 0; 1 SLFEGIDLY 9	38; Score 42; DB 2;
	9%; Fred. No. 0.39; 0; Mismatches 1; Indels
	DLY 9
Db 132 SLFEGIDFY 140	DFY 140

C;Keywords: ATP; molecular chaperone

91.3%; 88.9%;

Query Match 91.3 Best Local Similarity 88.9 Matches 8; Conservative

1 SLFEGIDLY 9

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C;Species: Eunicella cavolini
C;Accession: T45479
R;Borchiellini, C.; Le Parco, Y.
Submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
A;Reference number: 222983
A;Reference number: 222983
A;Reference number: Preliminary; translated from GB/EMBL/DDBJ
A;Reference selection: T45479
A;Reference number: EMBL:AF02520; PIDN:AAC05364.1
C;Genetics: A;Genetics: A;Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment) C; Species: Funiculina quadrangularis C; Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000 C; Accession: T45476 R; Borchiellini, C; Le Parco, Y. Submitted to the EMBL Data Library, September 1997 A; Reference number: 222983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
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heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 467;
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A) Cross-references: EMBL:AF026516; PIDN:AAC05361.1 C) Genetics: A; Genetics: A; Genetics: C) Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2;
Pred. No. 0.96;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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A:Residues: 1-469 <BOR>
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1
A:Gene: Hsp70
C;Superfamily: heat shock protein 70
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Sibarchiallini, C; Le Parco, X.
Submitted to the EMBL Data Library, September 1997
A; Reference number: Z22983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  daak-type molecular chaperone - mouse (fragment)
N.Alternate names: heat shock protein 68
S.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C.Accession: A26283
R.Lowe, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A.Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
A.Reference number: A26283; MUID:86111900
A.Recession: A26283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208
A;Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                     ;
0
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C;Species: Chondrosia reniformis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45477
R;Borchiellini, C.; Le Parco, Y.
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                        Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 2; Length 420;
Pred. No. 0.85;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 2; Length 467;
Pred. No. 0.96;
0; Mismatches 1; Indels
                                                                                                                                                                         1; Indels
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                                                                                            Score 42; DB 2;
Pred. No. 0.54;
0; Mismatches
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A;Cross-references: EMBL:AF026517; PIDN:AAC05362.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "...ourcniellini, C.; Le Parco, Y. submitted to the EMBL Data Library, September 1997 A.Reference number: 222983 A.Accession: T45477 A.Statine...
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Query Match 91.3%; Best Local Similarity 88.9%; Matches 8; Conservative

SLFEGIDEY 73 1 SLFEGIDLY 9

65

ŏ g RESULT

A; Molecule type: mRNA A; Residues: 1-420 <LOW>

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A;Gene: Hsp70 C;Superfamily: heat shock protein 70

C; Genetics

91.3%;

Query Match
Best Local Similarity 88.9
Matches 8; Conservative

|||||||| | 252 SLFEGIDFY 260

RESULT T45479

1 SLFEGIDLY 9

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Matches

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dnak-type molecular chaperone - chicken
NiAlternate names: heat shock protein 70
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
Sincindoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 12659-12699, 1986
A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 ge
A;Accession: A25646
A;Molecule type: DNA
A;Rocasion: A25646
A;Molecule type: DNA
A;Rocasion: A25646
A;Molecule type: DNA
A;Rosidues: 1-634 <AMOR>
A;Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A;Note: the authors translated the codon TCG for residue 583 as Trp
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diak-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)
N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein
C;Specias: Dictyostelium discoideum
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C;Accession: A48872
R;Eddy, R.J.; Sauterer, R.A.; Condeells, J.S.
J. Biol. Chem. 268, 23267-23274, 1997
A;Title: Aqinactin, an agonist-regulated F-actin capping activity is associated with
A;Reference number: A48872; MUID:94043116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A48872
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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S31766
dnaK-type molecular chaperone hsp70 - green monkey
dnaK-type molecular shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
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Pred. No. 1.3;
0; Mismatches 1; Indels
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Matches 8; Conservative
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285 SLFEGIDEY 293
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280 SLFEGIDFY 288
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289 SLFEGIDFY 297
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                                                                                                                                                                                                                                                                                                               probable heat shock protein [imported] - Arabidopsis thaliana probable heat shock protein [imported] - Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chi, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 200

A;Authors: Hunter, J.L.; Jankins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of Chromosome I of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)
N;Alternate names: heat shock cognate protein 70
C;Species: Dictyostelium discoideum
C;Date: 31-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
C;Accession: 745471
R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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A;Molecule type: DNA
A;Residues: 1-617 <STO>
A;Cross-references: GB:AE005173; NID:g11024845; PIDN:AAG26930.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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         Length 469;
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   DB 2;
0.96;
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A; Accession: T45471
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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A;Cross-references: EMBL:AF025951; PIDN:AAB81865.1
A;Experimental source: strain AX3
C;Genetics:
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Pred. No. 1.3;
0; Mismatches
Score 42; DB 2
Pred. No. 0.96;
0; Mismatches
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C; Superfamily: heat shock protein 70
   91.3%;
88.9%;
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88.9%;
                                                               8; Conservative
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Best Local Similarity
Matches 8; Conser
                                 Best Local Similarity
                                                                                                                                                       111111 | 254 SLFEGIDFY 262
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                                                                                                                      1 SLFEGIDLY 9
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A;Note: locali;
C;Superfamily:
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A; Residues: 1-639 <SLA>
A; Reference number: S64761
A; Reference number: S64772
A; Molecule type: DNA
A; Residues: 1-639 <GOP>
A; Molecule type: DNA
A; Residues: 1-639 <GOP>
A; Robertinger a; RMBL:273129; NID:91360201; PIDN:CAA97472.1; PID:91360202; MIPS:YL
A; Ribusteringer b; Ribuster b; Ribusteringer b; Ribuster b; Ribuster b; Ribuster b; Ribuster b; Ribuster b; Ribuster Ribuster b; Ribuster b; Ribuster Ribuster B; Ribuster Ribuster B; Ribuster Ribuster Ribuster B; Ribuster Ribuster Ribuster Ri
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A; Residues; 1-640 <SNU>
A; Residues; 1-640 <SNU>
A; Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352
A; Note: genomic clones representing six distinct members of the hsp70 gone family wer
A; Note: transcripts of hsp70A are abundant in control worms and also increase two- to
A; Note: one, of the three introns in hsp70A is in a position similar to an intron in D
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Gene 64, 241-255, 1988
A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri
A;Reference number: JT0285; MUID:88297155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. Experimental source: strain 5288C
R. Purnelle; B.; Goffeau, A.
submitted to the EMBL Data Library, April 1996
A. Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals mily and a new ABC transporter homologous to the human multidrug resistance protein.
A. Reference number: $69380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues; 1-639 <PUR>
A; Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007
                                                     20-Jun-2000
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                                       C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-C;Accession: $20139; $64772; $64775; $69383 $R;Slater, M.R.; Craig, E.A. Nucleic Acids Res. 17, 805-806, 1989 AjTitle: The $SAl and $SA2 genes of the yeast Saccharomyces cerevisiae. A;Reference number: $20139; MUD:89128457 Ascession: $20139
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Pred. No.
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88.9%;
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Matches 8; Conserv
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C; Accession: S31766; 136927

R; Sainls, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.

submitted to the EMBL Data Library, January 1993

A; Description: Nucleotide sequence of the CDNA encoding a monkey 70kd heat shock protein

A; Reference number: S31766

A; Accession: S3176

A; Accession: S3176

A; Molecule type: mRNA

A; Residues: 1-638 <AI>
Fisainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.

Fisainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.

Fisainis: The hsc70 gene which is slightly induced by heat is the main virus inducible me

A; Reference number: 136927; MUID:95080396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Wolecule type: DNA
A; Residues: 1-639 <SCO>
A; Residues: 1-639 <SCO>
C; Gonesics: references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917
C; Genetics:
A; Gene: hsp701V
A; Of the control o
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MyAlternate names: heat shock protein 70IV; hsp70IV protein

C;Species: Paracentrotus lividus (common urchin)

C;Date: 10-Jun-1991 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999

C;Accession: JOISI

R;Sconzo, G.; Scardina, G.; Ferraro, M.G.

R;Sconzo, G.; Scardina, G.; Ferraro, M.G.

A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70

A;Accession: JOI391; MUID:93077053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: involved in protein folding and assembling/disassembling of C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dnaK-type molecular chaperone SSA2 – yeast (Saccharomyces cerevisiae)
N;Alternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-638 <RES>
A; Residues: EMBL:X70684; NID:922781; PIDN:CAA50019.1; PID:922782
A; Experimental source: kidney; cell line COS-1
C; Genetics:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 1.4;
0; Mismatches
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); Mismatches
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284 SLFEGIDFY 292
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286 SLFEGIDFY 294
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Best Local Si
Matches 8;
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C;Genetics:
A;Gene: hsp70A
A;Map position: IV
A;Introns: 69/1; 331/3; 558/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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ö 0; Gaps Query Match

91.3%; Score 42; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels

1 SLFEGIDLY 9 ||||||| | 287 SLFEGIDFY 295

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Search completed: December 6, 2001, 07:58:26 Job time: 274 sec

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pepl-mod81.rsp

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 6, 2001, 08:00:50 ; Search time 50.21 Seconds (without alignments) 6.572 Million cell updates/sec Run on:

1 SLFEGIDLY 9 PEP1-MODBL Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P91902 ceratitis c	P11503 onchocerca	_		_	Q28222 cercopithec	P10592 saccharomyc	Q06248 paracentrot		P36415 dictyosteli	Q27975 bos taurus		P17879 mus musculu	P34930 sus scrofa	Q07439 rattus norv	P10591 saccharomyc	Q27965 bos taurus		P27541 brugia mala		Q91291 pleurodeles	Q01233 neurospora		P48720 blastocladi	_	P02826 drosophila	P22623 paracentrot	P34934 sus scrofa	P29843 drosophila	P17066 homo sapien	Q04967 sus scrofa	Q01877 puccinia gr	P55063 rattus norv
SUMMARIES	a	HS70_CERCA	HS70_ONCVO	HS73_MOUSE	HS70_PENCI	HS70_CHICK	HS71_CERAE	HS72_YEAST	HS74_PARLI	HS7A_CAEEL	HS7C_DICDI	HS71_BOVIN	HS71_HUMAN	HS71_MOUSE	HS71_PIG	HS71_RAT	HS71_YEAST	HS72_BOVIN	HS74_YEAST	HS70_BRUMA	HS70_ONCTS	HS70_PLEWA	HS70_NEUCR	HS70_XENLA	HS70_BLAEM	HS7D_MANSE	HS7A_DROSI	HS72_PARLI	HS7X_PIG	HS7A_DROME	HS76_HUMAN	HS76_PIG	HS71_PUCGR	HS73_RAT
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P34931 homo sapien P16627 mus musculu P53623 pichia angu Q10265 schiztosacch P53421 pichia angu P27322 lycopersico P6413 glycine max P19378 cricetulus P11142 homo sapien P08109 mus musculu P87047 paracoccidi O65719 arabidopsis	ALIGNMENTS  BESULT 1  1870_CERCA D 1870_CERCA STANDARD; PRT; 638 AA. D 1870_CERCA STANDARD; PRT; 638 AA. D 1870_CERCA T15-JUL-1998 (Rel. 36, Last aequence update) T15-JUL-1998 (Rel. 36, Last annotation update) T25-JUL-1998 (Rel. 36, Last annotation update) T27-JUL-1998 (Rel. 36, Last annotation update) T28-Rel. 1998 (Rel. 36, Last annotation update) T27-JUL-1998 (Rel. 36, Last annotation update) T28-Rel. 1998 (Rel. 1998 (	93.5%; Score 43; DB 1; Length 638; 88.9%; Pred. No. 0.5; Cive 1; Mismatches 0; Indels 0; Gaps 0; Live 1; Mismatches 0; Indels 0; Caps 0; Created)  Created)  Created)  Last sequence update)  Last annotation update)  Last annotation update)
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	RESULT 1  HS70_CERCA STA AC P91902. DT 15-JUL-1998 (Rel.) DT 15-JUL-1998 (Rel.) DT 15-JUL-1998 (Rel.) DF HEAT SHOCK PROPEINO CCATALLIS GEATCADA OC PLENYOCES, NeOPIER NOBL_TAXALD=7213; RN [1] TAXALD=7213; RN [1] TAXALD=7213; RN SEQUENCE FROM N.A. RA MINIZAS A.C.; CC This SWISS-PROT en CC The European Bloin CC The European Bloin CC This SWISS-PROT en CC The European Bloin CC This SWISS-PROT en CC This SWISS-PROTO! CC THIS SWISS-PROT	Query Match Best Local Similarity Matches 8; Conservat My 1 SLFEGIDLY 9 :
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EMBL; U64207; AAB06397.1; -.
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Q92260;
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                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMHL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license alreament (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementary to three mouse
                                                            Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
          Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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                                                                                                                                                                                                                                                                                                                                                                          91.3%; Score 42; DB 1; Length 322; 88.9%; Pred. No. 0.38;
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                                                                                                                                                                                                                                                                                                                                            35614 MW; 2BA3A2E8155A7180 CRC64;
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Q61696; Q61697; G61697;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 NDA PROTEIN 3 (HSP70.3) (FRAGMENT).
HSP70-3 OR HSP70A1.
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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SEQUENCE FROM N.A.
MEDLINE-86111900; PubMed-2868009;
LOWE D.G., MOTAN L.A.;
"Molecular cloning and analysis of DNA c
Mr = 68,000 heat shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
                                                                                                                                                                                                                                                                    Pfam; PF00012; HSP70; 1.
PROSITE; PS00297; HSP70_1; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 155-420 FROM N.A. MEDLINE=94357449; Pubmed=8076831;
                                                                                                                                                                                                                                       EMBL; J04006; AAA29417.1; -. HSSP; P19120; 1ATR.
                                                                                                                                                                                                                                                            InterPro; IPR001023; HSP70.
                      Onchocercidae; Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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322 AA;
  Onchocerca volvulus.
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Best Local Similarity
Matches 8; Conserv
                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
                                                                                                                                                                               HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
--- INDUCTION: BY HEAT SHOCK.
--- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium
                                                                                                                  THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.

"Molecular Doning and expression of a Penicillium citrinum allergen with sequence homology and antigenic cross-reactivity to a hsp?"O human heat shock protein.", submitted (Jul.-1996) to the EMBL/Genbank/DDBJ databases.

-I. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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Pred. No. 0.51;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AuG-2001 (Rel. 40, Created)
20-AuG-2001 (Rel. 40, Last sequence update)
20-AuG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V -> G. 5DA1C6155C7B16B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Chaperone; Heat shock; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS0012; HSP70; 1.
PROSITE; PS00297; HSP70_1; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 AA; 46292 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M12571; AAA57234.1; -. EMBL; M12572; AAA57235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P19120; IATR.
MGD; MGI:96244; Hsp70-3.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penicillium citrinum.
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PRT;
                                                                                                                                                                                                                            TISSUE=Kidney;
MEDLINE=95080396; PubMed=7988690;
                                                                                                                                                                  Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00297; HSP70_1; 1. PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00301; HEATSHOCK70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X70684; CAA50019.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SLFEGIDLY 9
                                                                                                                                                                                 NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS72_YEAST
P10592;
                 HS71_CERAE
Q28222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       HEAT SHOCK 70 KDA PROTEIN (HSP70).
Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-86304452; PubMed-3017985;
Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
"Organization, nucleotide sequence, and transcription of the chicken J. BSP70 gene.";
J. Biol. Chem. 261:12692-12699(1986).
-: SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                  Length 503;
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                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat shock; Multigene family.
34 AA; 69750 MW; 4270F7F08D365AEB CRC64;
                                                                                                                     SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 1;
Pred. No. 0.79;
0; Mismatches 1
                                                                                                                                                                Score 42; DB 1;
Pred. No. 0.62;
HSSP; P19120; 3HSC.
InterPro; IPRO1023; HSP70.
InterPro; IPRO1012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS010329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                              08, Last sequence update)
28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 634 AA
                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             08, Created)
08, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P19120; 1ATR.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS0139; HSP70_2; 1.
                                                                                                                                                                  91.3%;
88.9%;
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88.9%;
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PIR; A25646; A25646.
                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.3
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           634 AA;
                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                   154 SLFEGIDFY 162
                                                                                                                                                                                                                                                                                                                                               PO8106;
01-AUG-1988 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111111 |
289 SLFEGIDFY 297
                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel. 01-FEB-1994 (Rel.
                                                                                                                                                                                                                          1 SLFEGIDLY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLFEGIDLY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding;
                                                                                                                                                                                                                                                                                                                               HS70_CHICK
P08106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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RESULT 5
H870\_CHICK
H870\_CHICK
DT 01-AUG
DT 01

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                    Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Chaperone; Heat shock; Multigene family; MHC III.
638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.3%; Score 42; DB 1; Length 638; 88.9%; Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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01-CT-1994 (Rel. 30, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSA2.
SSA2 OR YLL024C OR L0931.
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       638 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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PRINTS, PR00301; HEATSHOCK70. PROSITE, PS000297; HSP70\_1; 1. PR0SITE; PS00129; HSP70\_2; 1. PROSITE; PS01036; HSP70\_3; 1.

Pfam; PF00012; HSP70;

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                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93077053; PubMed=1339375; MEDLINE=93077053; PubMed=1339375; MeDLINE=93077053; PubMed=1339375; Mediacterization G, Ferraro M.G.; Characterization of a new member of the sea urchin Paracentrotus 11vidus hap70 gene family and its expression."; Gene 121:353-358(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
Paracentrotus.
                                                                                                                                                                                         Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: X01379; CAA40653.1; -. PTR; J01391; J01391. J013
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                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Heat shock; ATP-binding; Multigene family; Acetylation;
                                                                                ACETYLATION.
23BDDD120C194912 CRC64;
                                                                                                                                                                                      Score 42; DB 1;
Pred. No. 0.8;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.3%; Score 42; DB 1; 88.9%; Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                         69338 MW;
                                                                                                                                                                                      91.3%;
88.9%;
                                                                                                                                                                                 Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                      638 AA;
                                                                                                                                                                                                                                                                                                                          1111111 1
282 SLFEGIDEY 290
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 SLFEGIDFY 294
                      Phosphorylation.
INIT_MET 0
MOD_RES 1
                                                                                                                                                                                                                                                                                                1 SLFEGIDLY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HS74_PARLI
Q06248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS7A_CAEEL
P09446;
                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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HS7A_CAEEL,
ID HS7A_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS74_PARLI
  N N L L S
                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                    qq
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CONFLICT
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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H971_BOVIN
1D H871_BOVIN
DT 01-NOV
DT 01-NOV
DT 15-JUL
DE HEAT SI
GN HSPPT SI
GN HSPPT SI
CO EURATY
CO MAMMMA II
CO EDVIDATE
NO NCBI_TE
RN II]
RN II]
RP TISSUEN
RC TISSUEN
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        RRARAR RR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88297155; PubMed-2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F., Mogela A.A., Schlaicher M.; "The heat shock cognate protein from Dictyostelium affects actin polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
STRAIN-AX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 64:241-255(1988).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length. 640;
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Pfam; PF00012; HSP70; 1.

PRINTS; PR001301; HBATSHCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS01039; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

***no-hinding; Heat shock; Multigene family.

f9823 MW; ED15409D06C500C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1;
Pred. No. 0.8;
); Mismatches
(Rel. 10, Created)
(Rel. 10, Last sequence update)
(Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UN-1994 (Rel. 29, Last sequence update)
OV-1997 (Rel. 35, Last annotation update)
SHOCK COGNATE PROTEIN (AGINACTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640 AA
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01-JUN-1994 (Rel. 29, Last seq
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.3%;
88.9%;
                                                                             01-FEB-1994 (Rel. 28, Last a
HEAT SHOCK 70 KDA PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M18540; AAA28078.1; -. PIR; JT0285; HHKW7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P19120; 1NGI.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 12:3763-3771(1993).
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                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 SLFEGIDFY 295
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SLFEGIDLY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterization
                                                                                                                                                           HSP70A.
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01-MAR-1989 (
01-MAR-1989 (
01-FEB-1994 (
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P36415;
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ID HS7C_DICDI

DT 01-JJJ

DT 01-JJJ

DT 01-JJJ

DT 01-JJJ

DE 01-JJJ

DE WENTON

CC EURATY

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RN [1]

RN [1]

RN REDLII

RN MEDLII

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DDARRAY BRANK OCCOOR OC
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                  Eddy R.J., Sauterer R.A., Condeelis J.S.;
"Aginactin, an agonist-regulated F-actin capping activity is associated with an HSC70 in Dictyostelium.";
J. Biol. Chem. 268:23267-23274(1993).
-!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROPEIN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REPOLING OF DENATURATED CAP32 AND CAP34.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                       OF THE CELL CORTEX AND CELL PROTRUSIONS.
-!- DEVELOPMENTAL STAGE: HEAT SHOOK COGNITY PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSSIGIDLGTTYSCVGVWQNDRVEIIAND -> IHHHINGNATWVVESGPVSEVLSFN (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2E6BDC2DB96A9F5D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94043116; PubMed-8226849;
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PROSITE; PS000297; HSP70_1; 1.
PROSITE; PS00129; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X75263; CAA53039.1; -. EMBL; L27736; AAA33219.1; -. PIR; 837394; S37394. HSSP; P19120; HNGJ. SWISS-2DPAGE; P36415; DICTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.3%;
88.9%;
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Pfam; PF00012; HSP70; 1.
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64
180
237
240
341
352
70499 M
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Best Local Similarity 88.9
Matches 8; Conservative
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SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DictyDb; DD01078; hspB.
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240
341
352
640 AA;
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MEDLINE-91055806; PubMed=1700760;
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                                                                                                                                                        (HSP70-1) locus.";
Anim. Genet. 25:196-196(1994).
PREEXISTENT COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
-!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
-!- FUNCTION: TARNILLERED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
OF NEWLY TRANSLAFED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CONFORMATIONS OF OTHER PROTIENS. THEY BIND EXTENDED PEPTIDE
SECMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
DURING TRANSLAFORD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
             Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                            Grosz M.D., Skow L.C., Stone R.T.;
"An AluI polymorphism at the bovine 70 kD heat-shock protein-1
                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%; Score 42; DB 1; Length 641; 88.9%; Pred. No. 0.8; 1; Indels iive 0; Mismatches 1; Indels
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P08107; P19790; O9UGMD; Q9UGL9;
01-AGG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
(HSPAIA OR HSPAI) AND HSPAIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00012; HSF/U; 1.
PRINTS; PR00301; HEATSHCK70.
PROSITE; PS00029; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
ATP-binding; Chaperone; Heat shock; Multigene family.
                                                                                                               MEDLINE=95030563; PubMed=7943958;
    MEDLINE-95126904; PubMed=7826329;
                                                                                                                                                                                                                                                                                                                                     STRESS-INDUCED DAMAGE.
INDUCTION: BY HEAT SHOCK.
                                                                                     SEQUENCE OF 212-641 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U09861; AAA73914.1; -. EMBL; U02891; AAA03450.1; -. HSSP; P19120; 1NGC.
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Matches 8; Conservative
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                                                                                                     STRAIN-ANGUS;
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HS71_HUMAN
LD HS71_HU
AC P0810_T
DT 01-AUG
DT 20-AUG
DE HEAT SI
GN (HSPA1)
GN HORDAI
OC BURATYI
OC MARMMAI
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RP SEQUEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dabent B., Genthe A., Benecke B.-J.;
"In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";
Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                      SEQUENCE FROM N.A.
MEDLINE-86016721; PubMed-3931075;
Hunt C., Morimoto R.I.;
"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).
Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89184548; PubMed-2538825; Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.; Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";
Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989)
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EMBL; M24743; AAA59844.1; --
EMBL; M24744; AAA59845.1; --
EMBL; X04676; CAA28381.1; --
EMBL; X04677; CAA28382.1; --
PIR; A45871; A45871.
PIR; A45871; A45871.
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PIR; S35718; S35718.
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MEDLINE-92175874; Pubmed-1339404;
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
                                                                                                                                                                                                                                          91.3%;
88.9%;
                        EMBL; M35021; AAA37864.1; -. EMBL; M76613; AAA57233.1; -.
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HSSP; P19120; 1NGC.
InterPro; IPR001023; HSP70.
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                     641 AA;
                                                                                                                                                                                                                                                                                                           1 SLFEGIDLY 9
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HS71_PIG
ID HS71_PIG
AC P34930;
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-I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREZISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYFEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATURE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES SEGNENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDICED DAMAGE.
                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE-94357449; PubMed-8076831;
Perry M.D., Aujame L., Shtang S., Moran L.A.;
"Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                    PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS003329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=90236310; PubMed=2332169;
Hunt C., Calderwood S.;
"Characterization and sequence of a mouse hsp70 gene and its expression in mouse cell lines.";
Gene 87:199-204(1990).
                                                                                                                                                I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
W; 78F513118C96DE66 CRC64;
                                                                                                                                                                                                                                                     Score 42; DB 1; Length 641;
Pred. No. 0.8;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                             HS71_MOUSE STANDARD; PRT; 641 AA. P17879; 061689; 01-40G-1990 (Rel. 15, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2). HSPAI OR HSP70-1 OR HCP70.1.
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                                               InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                     91.3%;
88.9%;
         SWISS-2DPAGE; P08107; HUMAN.
MIM; 140550; -.
MIM; 603012; -.
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Best Local Similarity 88.70.
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PDB; 1HJO; 21-OCT-98
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                                                                                                                                        3D-structure.
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Pegelman L.J., de Weden A.B., Coppieters W.R., van Zeveren A.J.,
Bouquet Y.H.;
"Complete nucleotide sequence of a porcine HSP70 gene.";
"Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-289(1992).
-I-FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISPERT PROTEINS TAGENEGATION AND MEDIATE THE POLLING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
OR NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
THROUGH THEIR ABILLITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
ORTHER PROTEINS. THEY BIND EXTENDED DEPTIDES EGGMENTS WITH A NET
HYDROPHOBIC CHARACTER EXPOSED BY POLLOWING STRESS-INDUCED DAMAGE.
-I-SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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HSSP; JH0095; JH0095.
HSSP; P19120; 1NGC.
HGC, MGI:99517; HSP70-1.
InterPro; IPR00102; HSP70-1.
PRINTS: PR00301; HSP700; 1.
PROSITE; PS00309; HSP70_2; 1.
PROSITE; PS00309; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
CONFLICT 342
CONFLICT 627
CONFLICT 627
P -> PP (IN REF. 1).
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Pred. No. 0.8;
0; Mismatches 1; Indels
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P -> PP (IN REF. 1).
41475360F6749F2F CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
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11 FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISEPRENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DORING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN=LEW.IN/GUN;
MEDILINE—9501243: PubMed=7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-
linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
"cDNA cloning and expression of stress-inducible rat hsp70 in normal
and injured rat brain.";
J. Neurosci. Res. 36:325-335(1993).
                                                                                                                                                                     Gaps
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                                                                                                                            Score 42; DB 1; Length 641;
Pred. No. 0.8;
                                                                                                                                                                     1; Indels
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                       HS71_RAT STANDARD; PRT; 641 AA. Q07439; P42853; 01-FEB-1995 (Rel. 31, Created) 1-FEB-1995 (Rel. 31, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) HEAT SHOCK 70 KDA PROFEIN 1/2 (HSP70.1/2).
                                                                                                                                                                     0; Mismatches
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MEDLINE-94368874; PubMed-8086479;
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MEDLINE=94096443; Pubmed=8271311;
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                                                                                                                            91.3%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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286 SLFEGIDFY 294
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Pred. No. 0.8;
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Best Local Similarity 88.9
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090689 littorina p
091969 fugu rubrip
0463718 rattus norv
044350 chondrosia
09099 guancha lac
044351 eunicalina
044495 funiculina
044495 funiculina
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q9C7x7 arabidopsis Q93147 botryllus s Q93146 botryllus s O15766 dictyosteli		Q03230 rattus norv Q9qwj5 mus musculu O96541 setaria dig Q9njb7 wuchereria Q9ngk9 wuchereria	048563 brassica na 059855 schizosacch 041027 pisum aativ Q9u777 stylophora Q9zs55 arabidopsis 09lha8 arabidoosis	TO F 6 6 77
Q9C7X7 Q93147 Q93146 O15766	Q98900 Q918F9 Q93601 O93240	Q63256 Q9QWJ5 O96541 Q9NJB7 Q9NGK9	048563 059855 Q41027 Q9U777 Q92S55	P93937 094805 09XZJ2 09U9B4 P81157 044346
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## ALIGNMENTS

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Pneumocystis carinii f. sp. carinii.
Bukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystis.
NCBI_TaxID=38081;
                                                                                                                                                                                                                                                                          MEDLINE—97045128; PubMed=8890193;
MEDLINE—97045128; PubMed=8890193;
Stedman T.T., Buck G.A.;
Identification, characterization, and expression of the BiP
endoplasmic reticulum resident chaperonins in Pneumocystis carinil.";
Infect. Immuu. 64:4463.4471(1996).
EMBL: U80967; AAD00455.1;
InterPro; IPR001023; HSP70.
InterPro; IPR001023; Thiolprot_act_site.
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70884 MW; 6D8CF90433BB163F CRC64;
                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; UNKNOWN_1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
645 AA
PRT;
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PRELIMINARY;
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Best Local Similarity
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Littorina scutulata.
Eukaryota, Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
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                                                                                                                                                                                                                                                                                       Eukarjota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaénioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFF191826; AAF12785.1; --
HSSP; P19120; LBAL.
Interpro; IPR001023; HSP70.
PROSITE; PS01036; HSP70._3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 153;
                                                                                                                                                                                                                                                                                                                                                                                   Hohenlohe P.A.; Hard-shook genes in the heat-stressed genus Littorina."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191825; AAF12784.1; -.. EMBL; AF191805; AAF12784.1; -.. EMBL; AF19180; IBAP70.18A1.
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Indels
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155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;
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153 AA; 17352 MW; E29EE20C4CAF934D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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Pred. No. 1.1;
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Matches 8; Conserv
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                                                                                                                                                                                            Pneumocystis carinii.
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
Pneumocystis.
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Paul S.P., Graves D.C.;
Paul S.P., Graves D.C.;
"Phylogeny and sequence analysis of Pneumocystis carinii HSP70.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U71151; AAD09565.1;
HSSP; P19120; 3HSC.
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 146;
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"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191828; AAF12787.1; --
HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.5%; Score 43; DB 3; Length 647; 88.9%; Pred. No. 3.8;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROPEIN (FRAGMENT).
                                                                                                             01-WAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001023; HSP70.
InterPro; IPR001029; Thiolprot_act_site.
InterPro; IPR0010169; Thiolprot_act_site.
Pfam; PR00121; HSP70; 1.
PROSITE; PS00297; HSP70,1; UNKNOWN_1.
PROSITE; PS00329; HSP70_1; UNKNOWN_1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS00639; THIOL_PROFEASE_HIS; UNKNOWN_1.
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Pred. No. 1;
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SEQUENCE 146 AA; 16607 MW;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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SEQUENCE FROM N.A.
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288 SLYEGIDLY 296
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SEQUENCE 6
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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
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Neotaenioglossa, Littorinoidea, Littorinidae, Littorina.
                                                                                                                                                                                                                                                                                                                                   Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
"Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191827; AAF12786.1; -.
HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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Pred. No. 1.1;
0; Mismatches 1; Indels
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"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191829; AAF12788.1; -.
HSSP; P19120; IBAl.
THGFPO: PPR01013; HSP70.
PRINTS; PR00101; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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158 AA; 17891 MW; B41E5356BCECAD2F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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U-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

HEAT-SHOCK PROTEIN (FRAGMENT).
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Best Local Similarity 88.9%;
Matches 8; Conservative
8; Conservative
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Neotaenioglossa, Littorinoidea, Littorinidae, Littorina.
NCBL_TaxID=31219;
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Sukaryota: Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglosas: Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID-31221;
                                                                                                                                                                                                                                                                                                                      Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191830; AAF12789.1; -.
HSSP; P19120; LBAL.
InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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Pred. No. 1.1;
0; Mismatches 1; Indels
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Pred. No. 1.1;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
                              82 SLFEGIDFY 90
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                                                                                                                                                                                                                              Littorina plena.
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063718;
063718;
01.NOV-1996 (TERBILE) 01, Created)
01.NOV-1996 (TERBILE) 01, Last sequence update)
01.NOV-1996 (TERBILE) 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
HATUS NOTESTORY (FORGATA; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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Pred. No. 3.1;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                        Score 42; DB 13; Length 278;
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lill a.i. (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X08578; CAA69892.1; -
HSSP; P19120; 3HSC.
InterPro; IFRO01023; HSP70.
Pfam; PF00012; HSP70; 1.
PRONSITE; PR003027; HBR70_1; 1.
PROSITE; PS010397; HSP70_1; 1.
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                                                                                                                                                                                               278 AA; 30327 MW; E4C745DE5484C17A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 AA
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                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                           PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
NON_TER
                                                                                                                                                                                                                                                            91.3%;
88.9%;
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88.9%;
HSSP; P08109; 1CKR.
Interpro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
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Best Local Similarity 88.9
Matches , 8; Conservative
                                                                                                                                                                                                                                                               Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
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367 AA;
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                                                                                                                                                                                                                                                                                                                                                                                            156 SLFEGIDFY 164
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A Kuhl D., Kennedy T., Barzilai A., Kandel E.;

T. Long-term sensitization training in Aplysia leads to an increase in the expression of BiP, the major protein chaperon of the ER.";

J. Cell Biol. 119:1069-1076(1992).

C. -I. INDOCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.

C. -I. SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

EMBL: Z15039; CAA78757.1; -..

RR HSSP: P19120; 1BA1.

InterPro: IPR001023; HSP70.

R PRINTS: PR00301; HSP70.1.

R PRINTS: P800312; HSP70.2; 1.

R PROSITE; PS00329; HSP70.2; 1.

R PROSITE; PS00329; HSP70.2; 1.
                                                                                                                                                                                                                                                                                                                                                                     Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysiidae; Aplysia.
NCBI_TaxID=6500;
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                           Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
0ncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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MEDLINE-88036330; PubMed-6092938;
Kothary R.K., Jones D., Candido E.P.M.;
"70-Kilodalton heat shock polypeptides from rainbow trout: characterization of cDNA sequences.";
Mol. Cell. Biol. 4:1785-1791(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.3%; Score 42; DB 5; Length 220; 88.9%; Pred. No. 1.7; Live 0; Mismatches 1; Indels
                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24684 MW; FA8557F2BB85C37A CRC64;
                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK COGNATE 71 KDA PROFEIN (FRAGMENT).
HSC70.
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         Pred. No. 1.1;
                           Mismatches
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      88.98;
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         Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                 1 SLFEGIDLY 9
                                                                        1 SLFEGIDLY 9
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P81159;
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090520
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P81159
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Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
Petrobiona.
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BOCCHALLINI C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026520; AAC05364.1; -.
HSSP; P08109; ICKR.
InterPro; IPR00102; HSP70.
InterPro; PR00012; HSP70; 1.
PRINTS; PR00011; HEATSHOCK70.
PROSTIE: PS01036; HSP70.3; 1.
NON_TER 467 467
SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;
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Pred. No. 4.1;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 91.3%;
Best Local Similarity 88.9%;
Matches 8; Conservative
                            Petrobiona massiliana
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252 SLFEGIDFY 260
                                                                                                NCBI_TaxID=68578;
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                                            Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H., D'Ambrosio E.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, 227118. CAA81642.1; -
HSSP: P08107; HNO.
InterPro; IPR001023; HSP70.
Pfam; PR00012, HSP70.
PRINTS; PR00321; HSP70.2; 1.
PROSITE; PS00329; HSP70.2; 1.
PROSITE; PS01036; HSP70.3; 1.
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Eukaryota, Metazoa; Porifera; Demospongiae; Tetractinomorpha; Chondrosida; Chondrillidae; Chondrosia.
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BEQUENCE FROM N.A.

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L SUDMitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

BEMBL, AF026517; AAC05362.1;

R HSSP; P08109; 1CKR.

R HSSP; P08109; 1CKR.

R INTERPROJ 1PR001023; HSP70.

DR PFAM; PR00312; HSP70.

DR PRINTS; PR00329; HSP70.

DR PROSITE; PS01329; HSP70.2; 1.

PROSITE; PS01339; HSP70.2; 1.

DR PROSITE; PS01036; HSP70.3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 91.3%; Score 42; DB 11; Length 455; Best Local Similarity 88.9%; Pred. No. 3.9; Matches 8; Conservative 0; Mismatches 1; Indels
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Pred. No. 4.1;
0; Mismatches 1; Indels
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455 455
455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;
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51707 MW; ODBE6920F2E6EA96 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 AA
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88.9%;
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در 8; Conservative
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254 SLFEGIDEY 262
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SEQUENCE FROM N.A.
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044352
ID 044352
AC 044352,
DT 01-JUN-1
DT 01-JUN-1
DT 01-JUN-1
DT HEAT-SHC
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044350
DC 044350
DT 044350
DT 01-JUN-
DT 01-JUN-
DE HEAT-Si
GN HSP70.
GN Chondro
OC Chondro
OX CLONDE
RR SEQUEN
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22, Appl 22, Appl 7, Appli 20, Appli 3, Appli 32, Appli 32, Appli 32, Appli 32, Appli

Sequence

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APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
AEDPONDESSER: ADDRESSER:
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Sallfornia

CONTRRY: United States

LIP: 9212

IP: 9212

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

CORPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/797,358B

FILING DATE: 11-Feb-1997

CLASSIFICATION NUMBER: US 60/011,491

FILING DATE: 12-FEB-1996

ATTORNEY/ACENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: 31,815

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-901

TELEPHONE: (619) 535-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 4; Length 643;
Pred. No. 3.1;
1; Mismatches 1; Indels
        US-09-083-711-2
US-09-083-711-2
US-08-453-2748-22
US-08-453-695A-22
US-08-161A-22
US-09-099-639-22
PCT-US95-08071-22
PCT-US95-08071-22
US-08-469-537A-7
US-08-469-537A-7
US-08-469-537A-7
US-08-646-5908-32
US-08-646-5908-32
US-08-646-5908-32
US-08-646-5908-32
US-08-646-5908-32
US-08-646-5908-32
US-08-646-5908-32
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                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: UNKNOWN

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08797358B Patent No. 6268478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 643 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
1 SLFEGIDVY 9
                                                                                                                                                                                                                                                                                                                        US-08-797-358B-3
  0
  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
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Sequence 14, Appli
Sequence 1, Appli
Sequence 24, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
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Appl
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                                                                                         ; Search time 81.43 Seconds
(without alignments)
2.487 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 22, 8 Sequence 22, 8 Sequence 22, 8 Sequence 22, 8 Sequence 1, 8 Sequence 7, 8 Sequence 7, 8 Sequence 18, 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Al Sequence 2, Al Sequence 2, Al Sequence 22, Al Sequence 22, Al Sequence 22, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                   1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/fB_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-797-358B-3
US-08-441-139-14
US-08-447-7046B-11
US-08-727-308-1
US-08-443-883A-24
US-08-631-328-24
US-08-631-328-24
US-08-631-328-24
US-08-631-328-24
US-08-455-021B-24
US-08-2978A-5
US-09-24-410-2
US-09-24-410-2
US-08-443-883A-22
US-08-455-524B-22
US-08-455-524B-22
US-08-455-621B-22
US-08-455-621B-22
US-08-455-621B-22
US-08-455-63-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-860-150-7
US-09-338-132-7
US-09-272-796-18
US-08-560-916-8
US-08-676-841-8
                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                          6, 2001, 07:59:54
                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
                                                                                                                                                                        1 SLFEGIDVY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
                                                                                                                                               PEP1-MOD8V
                                                                                            December
                                                                                                                                                          Perfect score:
                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein
                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                         Database
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                                                                                                                                               Title:
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Gaps

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RESULT 5
US-08-438-753B-24
Sequence 24, Application US/08438753B
Patent No. 5705363
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  RESULT 4
US-08727-308-1
'S-quence 1, Application US/08727308
'Patent No. 6020176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.6%;
                                                                                              71.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.6
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                Query Match 71.7
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Oct CLASSIFICATION:
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|165 SLFDGISAY 173
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23 SLFPGVDV 30
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Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT APPLICATION NUMBER: US/09/457,046B
NUMBER OF SEQ ID NOS: 74
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 61
**LENGTH: 458
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                                                                                                    US-08-441-139-14

Sequence 14, Application US/08441139

Fatent No. 577345

GENERAL INFORMATION:

APPLICANT: Wittrup, Dr. Karl D.

APPLICANT: Wittrup, Dr. Karl D.

TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 646;
Pred. No. 7.8;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASALLCATION: 43.2

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-UU-1993
ATORNEY/AGENT INFORMATION:
NAME: D1619110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELEFROMENICATION INFORMATION:
TELEFROME 516-742-433
TELEFROME 516-742-433
TELEFROME 516-742-436
TELERY 230 901 SANS UR
INFORMATION FOR SED 1D NO: 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 646 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: protein US-08-441-139-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1|:|||| |
286 SLYEGIDFY 294
        ||||||:| |
288 SLFEGVDFY 296
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US-09-457-046B-61
                                                                                                                                                                                                                                                                                                                                                      CITY: G
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                                     Gaps
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Pred. No. 1.5e+02;
1; Mismatches 1; Indels
Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: ISM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,308
Score 33; DB 4;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                       Mismatches
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Yuji KAMIYA et al.
TITLE OF INVENTION: KAURENE SYNTHASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                   Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                October 8, 1996
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predicted amino acid coding sequence of SEQ ID NO:23 (HuIFNtau7).
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Patent No. 5939286
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Subramaniam, Prem S.
TITLE OF INVENTION: Hybrid Interferon Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.4%; Score 31; DB 1; Length 95; 66.7%; Pred. No. 24; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 5600-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
                                  SSEE: Dehlinger & Associates
F: 350 Cambridge Ave., Suite 250
Palo Alto
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 40
PRIOR APPLICATION NUMBER: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-199
PRIOR APPLICATION NUMBER: US 07/318,050
FILING DATE: 30-0CT-1992
FILING DATE: 30-0CT-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/443,883A
                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.4
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-443-883A-24
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |:|| ||
83 SYFQGIHVY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLFEGIDVY 9
                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                    94306
                                              ADDRESSEE:
                                                                                   CITY: Pal
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-631-328-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.4%; Score 31; DB 1; Length 95; 66.7%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                    OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/438,753B
FILING DATE: US/08/438,753B
FLING APPLICATION DATA:
APPLICATION NUMBER: US/08/438,753B
FLING APPLICATION TAX:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATPONEY/AGENT INFORMATION:
NAME: ADAILY CHARTICEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ott, Troy L.
Van Heeke, Gino
Imakawa, Kazuhito
KENTION: Interferon Tau Compositions and
VENTION: Methods of Use
                  TITLE OF INVENTION: Interferon Tau Compositions and TITLE OF INVENTION: Methods of Use WUMBER OF SQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.30
TELECOMMUICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 24:
                                                                                                        ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/08443883A
Patent No. 5738845
GENERAL INFORMATION:
APPLICANT: Bazer, Fuller W.
APPLICANT: Johnson, Howard M.
APPLICANT: Ort, Troy L.
APPLICANT: Van Heeke, Gino
APPLICANT: Imakawa, Kazuhito
                                                                                                                                                                                           COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Imakawa, Kazuhito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
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83 SYFQGIHVY 91
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US-08-443-883A-24
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APPLICANT:
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Gaps

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; INDIVIDUAL ISOLATE: predicted amino acid coding sequence; INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HuIFNtau7).
US-08-455-5248-24
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bazer, Fuller W.
APPLICANT: Johnson, Howard M.
APPLICANT: Johnson, Howard M.
APPLICANT: Ott, Troy L.
APPLICANT: Van Heeke, Gino
APPLICANT: Imakawa, Kazuhito
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/455,021B
FILING DATE: 31-MAY-1995
FILING DATE: 10-MAY-1995
PRIOR APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER: US 08/139,891
FILING DATE: 09-OCT-1993
PRIOR APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/ACBNT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATTON NUMBER: 5600-0001.32
TELEPRONE: 415-324-0860
TELEPRAKE: 415-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Dehlinger & Associates
F: 350 Cambridge Ave., Suite 250
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-455-021B-24; Sequence 24, Application US/08455021B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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83 SYFQGIHVY 91
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Pred. No. 24;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/08455524B
Patent No. 594223
GENERAL INFORMATION:
APPLICANT: Baser, Fuller W.
APPLICANT: Ott, Troy L.
APPLICANT: Ott, Troy L.
APPLICANT: Van Heeke, Gino
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
                                                                                                                                OVETRALE: PATENTIN STATEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/631,328

FILING DATE: 12-APR-1996

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US/08/438,753

FILING DATE: 10-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 5600-0001.34

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFERX: 415-324-0860

TELEFERX: 415-324-0860
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARR: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/455,524B
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
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                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
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66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-631-328-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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| 83 SYFQGIHVY 91
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INDIVIDUAL ISOLATE: predicted amino acid coding sequence of SEQ ID NO:23 (HuIFNtau7).

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
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APPLICANT: MULLER, YVONNE
APPLICANT: MULLER, YVONNE
APPLICANT: KESTER, HERMANUS C.M.
APPLICANT: VISSER, JACOB
APPLICANT: VAN OOYEN, ALBERT J.J.
APPLICANT: POIN, CLAUS
TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.4%; Score 31; DB 4; Length 95; 66.7%; Pred. No. 24;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 17-OCT-1994
CLASSIFICATION: 435
                                    ATORNEY/AGENT INFORMATION:

NAME: Dehlinger, Peter J.

REGISTRATION NUMBER: 28,006

REFERENCE/DOCKET NUMBER: 5600-0001.36

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0960

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
APPLICATION NUMBER: US 07/969,890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08290978A; Patent No. 5624834; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION UNDABER: 29,959
REFERENCE/DOCKET NUMBER: 4615
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 90-4030
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7.
Fra 6; Conservative
                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20006-1812
COMPUTER READABLE FORM:
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| 83 SYFQGIHVY 91
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US-08-290-978A-5
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,467
FILING DATE: 20-Mar-1998
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Johnson, Howard M.
Pontzer. Carol H.
TITLE OF INVENTION: Interferon Tau Compositions and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 2;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/455,021
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
APPLICATION NUMBER: US 07/847,741
           PRIOR APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-0CT-1992
ATTONREY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFRENCE/POCKET NUMBER: 5600-0001.31
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0860
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 anino acids
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09-МАR-1992
11 11 07/318,050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-045-467-24; Sequence 24, Application US/09045467; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILLING DATE: 09-MAR-1992
APPLICATION NUMBER: US 07
FILLING DATE: 02-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
ORIGINAL SOURCE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-455-021B-24
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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| 83 SYFQGIHVY 91
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                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.
APPLICANT: MULLER, IVOND
APPLICANT: MULLER, IVOND
APPLICANT: MULLER, IVOND
APPLICANT: VISSER, JACOB
APPLICANT: ROLIN, CLAUS
TITLE OF INVENTION: CLONING AND EXPRESSION OF THE
TITLE OF INVENTION: EXPONENCES: IS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                          Query Match 67.4%; Score 31; DB 1; Length 452; Best Local Similarity 71.4%; Pred. No. 1.3e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY: USA

ZIP: 20006-1812
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,869
FILING DATE: 24-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION UNBER: US 08/290,978
FILING DATE: 17-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MUDARE: 17-OCT-1994
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (202) 887-1500
TELECOMMUNICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0044.00
TELEPHONE: (202) 887-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUDKESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Avenue N.W. CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08780869 Patent No. 5830737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 452 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-780-869-5
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-290-978A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|||:
203 LFDGIDI 209
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Gaps
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                                                                                                                                                                                                                                                                                         CURRENT APPLICATION PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,236
FILING DATE: March 11, 1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 4; Len
Pred. No. 1.9e+02;
                                                     APPLICANT: Xiomei, Xu
APPLICANT: Xiomei, Xu
TITLE OF INVENTION: Semaphorin K1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALLFORNIA
COUNTRY: USA
ZIP: 94010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/COCKET NUMBER: EXEL98-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-441
TELEFAX: (650) 343-434
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 634 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSURED 1. APPLICATION US/09240410
Sequence 2, Application US/09240410
Sequence 2, Application US/09240410
SECTION 0. 619754
APPLICANT: MICHALOVICH, DAVID
APPLICANT: HAYES, PHILIP DAVID
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rainer & Prestia
STREET: P.O. Box 980
CITY! Valley Forge
Sequence 2, Application US/09041236 Patent No. 6225285 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%;
75.0%;
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 6; Conserv
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|149 LFEGDEVY 156
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L. L. Change and Market

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Query Match
Best Local Similarity
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83 SYFQGIHIY 91
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FILING DATE: ...

CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UK APPLICATION NO. TO BE ASSIGNED FILING DATE: 20-JAN-1999
APPLICATION NUMBER: EP APPLICATION NO. 98300694.1
FILING DATE: 30-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESITA PAUL F
REGISTRATION NUMBER: C3,031
FELEPHONE: 610-407-0700
TELEPHONE: 610-407-0700
TELEPAX: 610-407-0700
TELEFAX: 846169
INPORMATION PROSED IN NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 aniho acids

LENGTH: 666 aniho acids
                                                             UK APPLICATION NO. TO BE ASSIGNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/08438753B
Fatent No. 5705363
GENERAL INFORMATION:
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Deblinger & Associates
STREET: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,753B
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 30-OCT-1993
ATTING DATE: 30-OCT-1992
ATTING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 4;
Pred. No. 2e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                           ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-240-410-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.4
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||| :||
181 LFEGDEVY 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
COUNTRY: US
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-438-753B-22
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predicted amino acid coding sequence of SEQ ID NO:21 (HulFNtau6).
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acid
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: 11near
MOLECULE TYPE: Protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                         ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-438-7538-22
```

65.2%; Score 30; DB 1; Length 99; 55.6%; Pred. No. 39; 2; Indels Mismatches Conservative

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Gaps

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Search completed: December 6, 2001, 07:59:55 Job time: 363 sec

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dnak-type molecula
dnak-type molecula
dnak-type molecula
dnak-type molecula
heat-shock protein
heat-shock protein
heat-shock protein
heat-shock protein
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dnaK-type molecula
dnaK-type molecula
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                                                                                         (without alignments)
7.774 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           6, 2001, 07:58:26 ; Search time 88.19 Seconds
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dnaK-type r
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    protein search, using sw model
                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T45477
T45479
T45476
T45478
H96605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S31766
JC1391
S20139
HHKW7A
A29160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S35718
I54542
                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                          1 SLFEGIDVY 9
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Match Length
                                                                                                                                 PEP1-MOD8V
                                                                                                                                                                                                                                                                                                                                                                                    pir1:*
pir2:*
pir3:*
pir4:*
                                                                              December
                                                                                                                                                                                                                                                                                                                                                                      PIR_68:*
                                                                                                                                           Perfect score:
                                                                                                                                                                                    Scoring table:
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                                                    OM protein
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30	41	89.1	645	7	151129	dnaK-type molecula
31	41	89.1	646	7	T46650	heat shock protein
32	41	89.1	647	-	HHXL70	dnaK-type molecula
33	41	89.1	647	7	S44168	dnaK-type molecula
34	41	89.1	647	7	T41121	heat shock protein
35	41	89.1	650	7	JC7088	heat shock protein
36	40	87.0	214	7	A03309	dnaK-type molecula
37	40	87.0	379	~	146588	dnaK-type molecula
38	40	87.0	467	7	T45473	heat-shock protein
39	40	87.0	467	7	T45474	heat-shock protein
40	40	87.0	641	7	JN0668	dnaK-type molecula
41	40	87.0	641	~	PC7036	heat shock protein
42	40	87.0	643	7	S25585	dnaK-type molecula
43	40	87.0	643	7	960608	dnaK-type molecula
44	40	87.0	651	~	T45517	heat shock protein
45	40	87.0	651	7	JC7132	heat shock protein
					ALIGNMENTS	
RESULT	1					
B44261						

```
RESULT 1

MATLETAR molecular chaperone HSC70 - California sea hare (fragment)

M.Alternate names: heat shock protein 70 homolog HSC70
C; Species: Aplysia californica (California sea hare)
C; Species: Aplysia californica (California sea hare)
C; Species: Aplysia californica (California sea hare)
C; Species: 04.56-1096
FX-05-1096
```

C;Accession: A44461
Kruhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1992
A;Title: Long-term sensitization training in Aplysia leads to an increase in the exprace number: A44261
A;Stetus preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-209 < KUH>
A;Note: sequence extracted from NCBI backbone (NCBIP:118951)

C;Genetics: A;Gene: HSP70a C;Function:

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diark-type molecular chaperone - mouse (fragment)
N.Alternate names: heat shock protein 68
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: A26283
R.Lowe, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A.Fitle: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000
A.Reference number: A26283; MuID:86111900
A.Accession: A26283
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208
A;Note: the authors translated the codon CTG for residue 173 as Val and CGC for resid
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heat-shock protein 70 (imported) - Eunicella cavolini (fragment)
C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
R;Borchiellini, C:; Le Parco, Y.
Submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C;Species: Chondrosia reniformis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45477
R;Borchiellini, C.; Le Parco, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1.467 <BOR>
A; Cross-references: EMBL: AF026517; PIDN: AAC05362.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Borchiellini, C.; Le Parco, Y. submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB
Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
A,Gene: Hsp70
C,Superfamily: heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.1%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.1%;
88.9%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.1
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z22983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 SLFEGIDFY 260
                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-420 <LOW>
                                                 SLFEGIDYY 294
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C;Superfamily: heat shock protein 70
C;Reywords: ATP; molecular chaperone
A; Description: involved in protein folding and assembling/disassembling of protein compl
C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: I51344
R;Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-Kilodalton heat shock polypeptides from rainbow trout: Characterization of A;Reference number: I51344; MUID:85036330
A;Accession: I51344
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C;Function:
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A;Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region. A;Reference number: PQ0138; WUID:91099690
A;Accession: PQ0138
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A; Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001
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                                                                                                                         Score 41; DB 2;
Pred. No. 0.61;
0; Mismatches
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Pred. No. 1
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A;Introns: 68/1; 137/1; 188/3; 281/3
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ilarity 88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-278 <KOT>
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Function:

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dnaK-type molecular chaperone - chicken
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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A; Molecule type: DNA
A; Residues: 1-617 <STO>
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285 SLFEGIDFY 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45478
R;Borchiellini, C:; Le Parco, Y.
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Pred. No. 1.5;
0; Mismatches 1
                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
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A;Molecule type: mRNA
A;Residues: 1-468 <BOR>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Pred. No. 1.5;
0; Mismatches
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submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
                                                                         A; Cross-references: EMBL: AF026520; PIDN: AAC05364.1
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Pred. No. 1.5;
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C;Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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Best Local Similarity 88.99
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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A; Accession: T45479
                                                                                           C;Genetics:
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probable heat shock protein [imported] - Arabidopsis thaliana probable heat shock protein [imported] - Arabidopsis thaliana (Gueen cress) (Cidate 102 Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 (Cidate 102 Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Mature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
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C; Genetics:
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Pred. No. 2.1;
0; Mismatches
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A;Experimental source: strain AX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB;
Pred. No. 2;
0; Mismatches
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C; Superfamily: heat shock protein 70
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pep1-mod8v.rpr

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dusk-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
N;Alternate names: heat shock protein 70IV; hsp70IV protein
C;Specias: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C;Accession: JC1391
R;Sconzo, G;,Scardina, G;; Ferraro, M.G.
A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
                                 R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible
A;Reference number: 136927; MUID:95080396
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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A;Residues: 1-639 <SCO>
A;Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917
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A; Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A; Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A; Experimental source: kidney; cell line CoS-1
C; Genetics:
A; Gene: hp70
C; Function:
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                                                                                                                                                               A; Accession: 136927
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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Pred. No. 2.1;
0; Mismatches
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0; Mismatches
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Pred. No.
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Best Local Similarity 88.9%;
Matches 8; Conservative
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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286 SLFEGIDEY 294
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A; Introns: 61/2
C; Function:
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A; Molecule type: mRNA
A; Residues: 1-636 <EDD>
A; Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A; Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dnak-type molecular chaperone hsp70 - green monkey

N;Alternate names: heat shock protein 70

C;Species: Cercopithecus aethiops (green monkey, grivet)

C;Species: Cercopithecus aethiops (green monkey, grivet)

C;Accession: S31766; 136927

R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.

Submitted to the EMBL Data Library, January 1993

A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein

A;Reference number: S31766

A;Reference mumber: S31766

A;Molecule type: mRNA
N'Alternate names: heat shock protein 70
C:Species: Gallus gallus (chicken)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C;Coccasion: A5646
R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 12692-12699, 1986
A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.
A;Reference number: A25646; MUID:86304452
A;Accession: A25646
A;Accession: A25646
                                                                                                                                                                                                                                                                                                                                        A) Residues: 1-634 CMOR>
A) Residues: 1-634 CMOR>
A) Residues: 1-634 CMOR>
A) Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A) Construction:
C) Function:
A) Expeription: Involved in protein folding and assembling/disassembling of protein complete S: Superfamily: heat shock protein 70
C; Superfamily: heat shock protein 70
C; Keywords: AFP; molecular chaperone
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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N,Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein c; Species: Dictyostellum discoideum
C;Species: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: A48872
R;Eddy, R.J.; Sauterer, R.A.; Condeells, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A;Tille: Aqinactin, an agonist-regulated F-actin capping activity is associated with
A;Reference number: A48872; MUID:94043116
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Score 41; DB; Pred. No. 2.1; 0; Mismatches

89.1%; 88.9%;

Conservative

280 SLFEGIDFY 288

RESULT

1 SLFEGIDVY 9

Query Match Best Local Similarity Matches 8; Conserv

A; Accession: A48872

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Score 41; DB 2; Pred. No. 2.1; 0; Mismatches

89.1%; 88.9%;

Query Match 89.1 Best Local Similarity 88.9 Matches 8; Conservative

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RESULT 2
HS72_PARLI
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                                                                                                                                                                    December 6, 2001, 08:00:50; Search time 50.21 Seconds
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P08106
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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HS71_RAT
HS71_YEAST
HS72_BOVIN
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HS70_XENLA
HS70_BLAEM
HS7D_MANSE
HS7A_DROSI
HS7X_PIG
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HS73_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HS70_CHICK
HS71_CERAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS74_PARLI
HS7A_CAEEL
HS7C_DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS70_ONCTS
HS70_PLEWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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HS70_BRUMA

    protein search, using sw model

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                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length
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                                                                                                                                                                                                                                                                                                               Perfect score:
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                                                                                                               OM protein
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                                                                                                                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                              P53421 pichia angu
P2732 lycopersico
P26413 glycine max
P19378 cricetulus
P11142 homo sapien
P87047 paracoccidi
065719 arabidopsis
                                 pichia angu
schizosacch
 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89201313; PubMed-2704388; MEDLINE-89201313; PubMed-2704388; MEDLINE-89201313; PubMed-2704388; Methstein N.M., Higashi G., Yates J., Rajan T.V.; Rothstein N.M., Higashi G., Yates J., Rajan T.V.; Moluchocerca volvulus heat shock protein 70 is a major immunogen in amicrofilaremic individuals from a filariasis-endemic area."; Mol. Blochem. Parasatol. 33:299-236(1989).

1- DISBASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.

1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
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P34931
P16627
P53623
Q10265
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88.9%; Pred. No. 0.57;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                    ASTOLORYOV STANDARD; PRT; 322 AA. BASTOLORYOV STANDARD; PRT; 322 AA. AC. P11503; PRT; 322 AA. BASTOLORYOV STANDARD; PRT; 322 AA. BASTOLORY-1989 (Rel. 12, Created) DT 01-FEB-1996 (Rel. 33, Last sequence update) DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT). ON Chocerca volvulus.
                                                                                                                                                                                                                                        ALIGNMENTS
               HS71_MOUSE
HS72_PTCAN
HS71_SCHPO
HS71_PTCAN
HS72_LYCES
HS70_SOYBN
HS7C_CHUMAN
HS7C_CHUMAN
HS7C_CHUMAN
HS7C_CHUMAN
HS7C_HOMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001023; HSP70.
Pfam: PF00112; HSP70; 1.
PROSTIE; PS001297; HSP70_1; PARTIAL.
PROSTIE; PS01039; HSP70_2; PARTIAL.
PROSTIE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J04006; AAA29417.1; -. HSSP; P19120; 1ATR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
ATP-binding; Heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 AA;
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1 SLFEGIDVY 9
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SEQUENCE
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372 AA.

PRT;

STANDARD;

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89.1%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SLFEGIDVY 9
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Q92260;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-86111900; PubMed-2868009;
Lowe D.G., Moran L.A.;
*Molecular clohing and analysis of DNA complementary to three mouse
*Molecular choing and shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
                                                                                                                                                                                                                                         la Rosa M., Sconzo G., Giudice G., Roccheri M.C., di Carlo M.; "Sequence of a sea urchin hsp70 gene and its 5' flanking region."; Gene 96:295-300(1990).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                             Paracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.1%; Score 41; DB 1; Length 372; 88.9%; Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 AA; 41347 MW; 5F8C1C590527A659 CRC64;
               01-AUG-1991 (Rel. 19, Created)
11-AUG-1991 (Rel. 19, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS73_MOUSE STANDARD; PRT; 420 AA. 061696; 061697. 061697. 061697 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT). HSP70.3 OR HSP70A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS0012; HSP70; 1.
PROSITE: PS00297; HSP70, 1.
PROSITE: PS00329; HSP70_1; 1.
PROSITE: PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 155-420 FROM N.A. MEDLINE=94357449; PubMed=8076831;
                                                                                                                                                                                                                            MEDLINE=91099690; PubMed=2269441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X16544; CAA34544.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P19120; INGJ.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.97
المالية B; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; PQ0138; PQ0138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 SLFEGIDYY 294
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                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SLFEGIDVY 9
                                                                                                                                                               NCBI_TaxID=7656;
                                                                                                                                                 Paracentrotus
                                                                                                                                                                                                                TISSUE=Gonad
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                                                                               HSP70II.
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HS73_MOUSE
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                                                                                                                                               Gene 146:273-278(1994).

Gene 146:273-278(1994).

- PEDICTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAWAGE.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene from Mus musculus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ဌ
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Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
"Molecular cloning and expression of a Penicillium citrinum
allergem with sequence homology and antigenic cross-reactivity is
a hsp70 human heat shock protein.";
Submitted (JUL-1996) to the EMBL/Genbank/DDBJ databases.
- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Pred. No. 0.76;
0; Mismatches 1; Indels
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M12571; AAA57234.1; -.
EMBL; M12572; AAA57235.1; -.
HSSP; P19120; 1ATR.
MGD; MG196244; HSP70-3.
InterPro; IPR001023; HSP70.
PFam; PF00012; HSP70-1; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
ATP-binding; Chaperone; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503 AA.
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MEDLINE-95080396; PubMed-7988690;

XMEDLINE-95080396; PubMed-7988690;

XMEDLINE-9508096; PubMed-7988690;

XMEDLINE-9508096;

XMEDLINE-9508096;

XMEDLINE-9508096;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shock; Multigene family; MHC III.
D55076A0FFAB6AB3 CRC64;
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Pred. No. 1.2;
                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.
                                                                                                                                                                                                                  638 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Cercopithecus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00297; HSP70_1; 1. PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1. ATP-binding; Chaperone; Heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X70684; CAA50019.1; -. Interpro; IPR001023; HSP70. Pfam; PF00012; HSP70; 1. PRINTS; PR00301; HEATSHOCK70.
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88.9%;
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Best Local Similarity 88.5.
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   1111111 1
289 SLFEGIDEY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111111 |
284 SLFEGIDFY 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9534;
                                                                                                                                            RESULT 6
1871_CERAE
10 72822;
20 2822;
20 2822;
20 1998
DT 15-DEC-1998
DC CECCOPITHCCU
CC CECCOPITHCE-9508
RA MAMMADIA: EDS CC CONGANELL
CC THE SEQUENCE FRO
RET THE hSC70 9
RT THE hSC70 9
RT THE hSC70 9
RT THE SCOUNCESSE
CC CONGANELL
CC CONGANELL
CC CONGANELL
CC CONGANEL
CONGANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS72_YEAST
P10592;
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ID HS72_Y
AC P10592
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-Rel. 994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (HSP70).
Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1; Length 634;
Pred. No. 1.2;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.1%; Score 41; DB 1; Length 503;
88.9%; Pred. No. 0.92;
live 0; Mismatches 1; Indels
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InterPro: IPR001023; HSP70.

Ffam: PF00012; HSP70.

PROSITE; PS00297; HSP70.1; 1.

PROSITE; PS00239; HSP70.1; 1.

PROSITE; PS01036; HSP70.2; 1.

PROSITE; PS01036; HSP70.3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                                                                      HSSP; P19120; 3HSC.
InterPro; IPR001023; HSP70.
PRINTS; PR00301; HSP70; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
ATP-binding; Chaperone; Heat shock; Allergen.
                                        entitles requires a license agreement (or send an email to license@isb-sib.ch)
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                                                                                                                                            EMBL; U64207; AAB06397.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 SLFEGIDFY 162
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NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSP70 gene.";
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P08106;
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RESULT 5

10 1-40G

MY 01-40G

MY

Matches

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Gaps

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1; Indels

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Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norbeck J., Blomberg A.; "Protein expression during exponential growth in 0.7 M NaCl medium of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                            Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.; Submitted (SEP-1994) to the SNISS-PROT data bank.

-!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE SINOPLEABMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                              В.,
                                                                                                                                                                              Slater M.R., Craig E.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                            Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender E
Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PTM: PHOSPHORYLATED.
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                           Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
 01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
AFAT SHOCK PROFEIN SSA2.
SSA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Electrophoresis 15:1466-1486(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C;
MEDLINE=95203288; PubMed=7895733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLATION, AND PHOSPHORYLATION.
                                                                                                                                                                MEDLINE=89128457; PubMed=2644626;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 91-97 AND 325-341.
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                                                                                                                                                                                                                                                                                                   SEQUENCE OF 71-638 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10592; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEPD; 9800; -.
SGD; S0003947; SSA2.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE OF 186-195
                                                                                                                                       SEQUENCE FROM N.A. STRAIN=S288C;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       database.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 639;
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                                                                                                                                                                                                                                                                                                                                   1; Indels
PRINTS: PRO0301; HEZFHOCK70.

PROSITE: PS00297; HSP70_1; 1.

PROSITE: PS00329; HSP70_2; 1.

PROSITE: PS01329; HSP70_3; 1.

Heat shock; ATP-binding; Multigene family; Acetylation; Phosphorylation.

INIT_MET 0 0 0 ACETYLATION.

MOD_RES 1 1 ACETYLATION.

SEQUENCE 638 AA; 69338 MW; 23BDDD120C194912 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; JOL1391, C11391.

HSSP; P19120; 1NGJ.

INEETPRO; IPRO01023; HSP70.

Pfam; PF000121; HSP70; 1.

PROSITE; PS00297; HSP70.1; 1.

PROSITE; PS00329; HSP70.2; 1.

PROSITE; PS01036; HSP70.3; 1.

ATP-binding; Heat shock; Multigene family, SEOUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;
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Pred. No. 1.2;
0; Mismatches
                                                                                                                                                                                                                                                                              Score 41; DB 1;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   639 AA
                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paracentrotus lividus (Common sea urchin).
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                                                                                                                                                                                                                                                                                   89.1%;
88.9%;
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88.9%;
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                                                                                                                                                                                                                                                                                                                                     8; Conservative
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Best Local Similarity
Matches 8; Conserv
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286 SLFEGIDFY 294
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  282 SLFEGIDFY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                  1 SLFEGIDVY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SLFEGIDVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paracentrotus
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ID HS74_PARLI
AC Q06248;
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cap32/34.";
EMBO J. 12:3763-3771(1993).
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SEQUENCE
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HS71_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_raxID=6239;
                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-88297155; PubMed-2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The heat shock cognate protein from Dictyostellum affects actin-polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94008983; PubMed-8404847;
Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
Noegel A.A., Schleicher M.;
                                                                                                                                                                                                                                 Gene 64:241-255(1988).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.1%; Score 41; DB 1; Length 640; 88.9%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PRO0301; HSP70-1; 1.
PROSITE; PS00297; HSP70-1; 1.
PROSITE; PS00329; HSP70-2; 1.
PROSITE; PS01036; HSP70-3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
                                                                   10, Last sequence update)
28, Last annotation update)
                                  640 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                  PRT;
                                                         (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                EMBL; M18540; AAA28078.1; -. PIR; JT0285; HHKW7A.
                                                                                         HEAT SHOCK 70 KDA PROTEIN A
                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P19120; 1NGI.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00012; HSP70: 1
                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                         characterization."
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287 SLFEGIDFY 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                               (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLFEGIDVY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=44689;
                                                                                                       HSP70A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSPB OR HSC70
                                                        01-MAR-1989
                                                                  01-MAR-1989
01-FEB-1994
                               HS7A_CAEEL
P09446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS7C_DICDI
P36415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-AX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                       HSP-1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
H87C_DICDI
1D AC P36415
DT 01-JUN
DT 01-JUN
DT 01-NU
DE HEAT S
GN HSPB C
OC EUKATY
OX NCBL T
RN (1)
RN SEQUEN
RX STRAIN
RA HAUS U
RA NOGGEL
RA NOGGEL
RT POLYME
                      HS7A_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license greement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           MEDLINE=94043116; Pubmed=8226449;

Redy R.J., Sauterer R.A., Condeelis J.S.;

Rady R.J., Sauterer R.A., Condeelis J.S.;

Rady R.J., Sauterer R.A., Condeelis J.S.;

Rady R.J., Sauterer R.A., Condeelis J.S.;

Body R.J., Sauterer R.A., Condeelis J.S.;

Body R.J., Sauterer R.A., Condeelis J.S.;

Body R.J., Sauterer R.A., Condeelis J.S.;

J. Blol. Chem. 268:2287-23274 (1993).

1- FUNCTION: A PEFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.

1- SUBCELLULAR LOCATION: CYTOPLASMIC: FOUND IN F-ACTIN-RICH REGIONS OF THE CELL CORTEX AND CELL PROTRUSIONS.

1- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSSIGIDLGTTYSCVGVWQNDRVEIIAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Y -> A (IN REF. 2).

R -> A (IN REF. 2).

S -> A (IN REF. 2).

V -> A (IN REF. 2).

Y -> A (IN REF. 2).

Y -> D (IN REF. 2).

ZE6BDC2DB96A9F5D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00301; HEATSHOCK70.
PROSITE; PR00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X75263; CAA53039.1; -. EMBL; L22736; AAA33219.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P36415; DICTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DictyDb; DD01078; hspB.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01036; HSF/L
ATP-binding; Chaperone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S37394; S37394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
341
352
640 AA;
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pep1-mod8v.rsp

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: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                             MEDLINE=91055806; PubMed=1700760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M59828; AAA63226.1; -. EMBL; M59830; AAA63227.1; -.
               Eukaryota; Metazoa;
                                                                               NCBI_TaxID=9606;
                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HEP70-1) locus.;

Anim. Genet. 25:196-196(1994).

-!-FONCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
-!-FONCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
-!-FONCTION: IN COOPERATION WITH CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION OF FOLLOWING PRANSLATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                  Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grosz M.D., Skow L.C., Stone R.T.;
"An AluI polymorphism at the bovine 70 kD heat-shock protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRESS-INDUCED DAMAGE.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.1%; Score 41; DB 1; Length 641; 88.9%; Pred. No. 1.2; 1:ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS71_HUMAN STANDARD; PRT; 641 AA.
P08107; P19790; O9UQMD; O9UQL9;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-2).
(HSPAIA OR HSPAIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shock; Multigene family. 6D548263E98780F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ANGUS;
MEDLINE=95030563; PubMed=7943958;
                                                                                                                                                                                                MEDLINE-95126904; PubMed-7826329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00297; HSP70_1; 1. PROSITE; PS00329; HSP70_2; 1 PROSITE; PS01036; HSP70_3; 1. ATP-binding; Chaperone; Heat s SEQUENCE 641 AA; 70250 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 212-641 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00301; HEATSHOCK70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U09861; AAA73914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U02891; AAA03450.1; -.
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Pfam; PF00012; HSP70; 1.
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                              TISSUE-Skeletal muscle;
                      Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P19120; INGC.
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286 SLFEGIDFY 294
                                                                                                                            SEQUENCE FROM N.A.
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                                                 NCBI_TaxID=9913;
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Homo sapiens (Human).

RESULT 12
HS71\_HUMAN
ID HS71\_H
DT 01-AUG
DT 01-FEB
DT 20-AUG
DT 20-AUG
CON (HSPALI)
OS HOMD S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.

X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.

X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)

A Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

"Structure of a new crystal form of human hsp70 ATPase domain.";

L. Acta Crystallogr. D 55:1105-1107(1999)

C. PERZISTENIP PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING

C. FUNCTION: IN COOPERATION WITH OTHER CRYPOSOL AS WELL AS WITHIN OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OF ONGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASHIC OFFORTION THAY AND THOUGH THE RANSDUCTION FROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PROCESSES THROUGH THEIR ABILITY TO RECOONIZE NONNATIVE

CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES CONFORMATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS - INDUCED DAMAGE.

C.I. INDUCTION: BY HEAT SHOCK.

C.I. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extracts
                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-86016721; PubMed=3931075;

Hunt C., Morimoto R.I.;

"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";

Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).

Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.; #Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).
Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
"Sequence of the human major histocompatibility complex class III
                                                                                                               Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-87066768; PubMed-3786141;
Drabent B., Genthe A., Benecke B.-J.;
In vitro transcription of a human hsp 70 heat shock gene by exprepared from heat-shocked and non-heat-shocked human cells.";
Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-22 AND 618-641 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF134726; AAD21816.1; -. EMBL; AF134726; AAD21815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M11717; AAA52697.1; -. M24743; AAA59844.1; -. M24744; AAA59845.1; -.
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EMBL;
EMBL;
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
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PIR; S35718; S35718.
                                                                                                                                                                                        EMBL; M35021; AAA37864.1; --
EMBL; M76613; AAA57233.1; --
PIR; JH0095; JH0095.
HSSP; P19120; INGC.
MGD; MGI:99517; HSP70-1.
InterPro; IPR001023; HSP70.
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Matches 8; Conservative
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P34930;
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Gene 146:273-278(1994).

Gene 146:273-278(1994).

- I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYEEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLTY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H871_MOUSE STANDARD; PRT; 641 AA.
P17879; Q61689; Leated)
P17879; Q61689; Last sequence update)
O1-A0G-1990 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
H8AT SHOKOK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
HSPA1 OR HSP70A1 OR HSP701 OR HCP70.1.
HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1.
Mus musculus (Mouse).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Mu
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                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
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"Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
W; 78F513118C96DE66 CRC64;
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Pred. No. 1.2;
); Mismatches 1; Indels
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
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88.9%;
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SWISS-2DPAGE; P08107; HUMAN.
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Pfam; PF00012; HSP70; 1.
                       x04677; CAA28382.1;
A29160; A29160.
X04676; CAA28381.1;
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                                                                                 A45871; A45871.
A25773; A25773.
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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HS71_MOUSE
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HS71_MOUSE
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"Complete nucleotide sequence of a porcine HSP70 gene.";

"Complete nucleotide sequence of a porcine HSP70 gene.";

"Complete nucleotide sequence of the complete of the complete nucleotide sequence of the complete nucleotide sequence of the complete of the co Gaps Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. SEQUENCE FROM N.A. MEDLINE-92175874; PubMed-1339404; Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J., ; 0 89.1%; Score 41; DB 1; Length 641; 88.9%; Pred. No. 1.2; 1:ve 0; Mismatches 1; Indels

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Biochim. Blophys. Acta 1219:64-72(1994).
Biochim. Blophys. Acta 1219:64-72(1994).
PUCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEMLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
"CDM cloning and expression of stress-inducible rat hsp70 in normal
                                                                                                                                                                                                                         Gaps
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MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
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SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
MEDILINE-34368974, Pubmed-8086479;
Lisowska 4., Krawczyk 2., Widlay W., Wolniczek P., Wisniewski J.;
"Cloning, nucleotide sequence and expression of rat heat inducible "Cloning, nucleotide sequence and expression of rat heat inducible
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                                                                                                                                                                                      89.1%; Score 41; DB 1; Length 641; 88.9%; Pred. No. 1.2; ive 0; Mismatches 1; Indels
                                                                                                                      ; Chaperone; Heat shock; Multigene family. 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HSP70-1 AND HSP70-2.
                                                                                                                                                                                                                                                                                                                                                                                641 AA
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               Interpro; IPR001023; HSP70.
Pfam: PF0012; HSP70: 1.
PRINTS: PR00301; HEATSHOCK70.
PROSITE: PS00297; HSP70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
ATP-binding; Chaperone; Heat st SEQUENCE 641 AA; 70083 MW;
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Best Local Similarity 88.9
Matches 8; Conservative
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Prints; PR00301; HSP70: 1.
PRINTS; PR00301; HSP70-1; 1.
PROSITE; PS00329; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
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D -> H (IN REF. 2 AND 3).
G -> A (IN REF. 3).
DO2D96751C868583 CRC64;
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Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                  70163 MW;
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                                                                                                     EMBL, X77208; CAA54423.1; -. EMBL, X77207; CAA54422.1; -. EMBL, X74271; CAA52328.1; -. HSSP; P19120; INGC.
                                                                                   EMBL; L16764; AAA17441.1; -.
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Best Local Similarity
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pepl-mod8v.rspt

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GenCore version 4.5
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OM protein - protein search, using sw model

December 6, 2001, 07:56:52; Search time 170.25 Seconds (without alignments) 7.732 Million cell updates/sec Run on:

1 SLFEGIDVY 9 Title: Perfect score: Sequence: Scoring table:

PEP1-MOD8V

473505 seqs, 146272329 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SP\_plant:\*
sp\_rodent:\*
sp\_vortus:\*
sp\_vertebrate:\*
sp\_unclassified:\* 1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_manmal:\*
7: sp\_mhc:\*
8: sp\_organelle:\*
9: sp\_phage:\* SPTREMBL\_17:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Q9u667 littorina p	Q9u670 littorina s	Q9u669 littorina s	Q9u665 littorina p	Q9u671 littorina s	Q9u668 littorina p	Q9u666 littorina p	P81159 aplysia cal	P81157 aplysia cal	Q90520 oncorhynchu	Q98899 fugu rubrip	Q63718 rattus norv	044350 chondrosia	044352 petrobiona	Q9nj92 guancha lac	044349 funiculina	044351 eunicella c	Q98897 fugu rubrip	Q9c7x7 arabidopsis
SUMMARIES	;	ai .	799060	090670	699060	090665	090671	Q9U668	99060	P81159	P81157	090520	668860	063718	044350	044352	Q9NJ92	044349	044351	098897	09C7X7
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di	:	Match Length DB	146	153	155	157	158	158	158	220	221	278	367	455	467	467	467	468	469	526	617
	Query	Match	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1
	,	score	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
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093147 botryllus s 093146 botryllus s 015766 dictyostell 098900 fugu rubrip 0918f9 oryalas lat	Q93601 caenorhabdi Q93240 paralichthy Q63256 rattus norv Q9qwJ5 mus musculu Q96541 setaria diq	Q9njb7 wuchereria Q9ngk9 wuchereria Q48563 brassica na Q59855 schizosacch	Q4102/ pissum satty Q9u777 stylophora Q9zs55 arabidopsis Q9lha@ arabidopsis P93937 ascophyllum Q94805 trichoplusi	Q9xzj2 crassostrea Q24952 geodia cydo Q9u9b4 mytllus edu Q44346 asbestoplum Q44347 petrosia fi Q99pm5 monosiga ov
	•		10 Q9U777 5 Q9U777 10 Q9LHA8 10 P93937 5 Q94805	
			650 650 652 653 653	
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## ALIGNMENTS

RESULT 2
090670
D 090670
AC 090670;
DT 01-MAY-2000 (TEEMBLrel. 13, Created)
DT 01-MAY-2000 (TEEMBLrel. 13, Last sequence update) 79 SLFEGIDFY 87 Ω

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SEQUENCE FROM N.A.

NCBI\_TaxID=31221;

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Bukaryota: Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa: Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
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Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaénioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_raxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hohenlohe P.A.; "Heat-shock genes in the heat-stressed genus Littorina."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191824; AAF12783.1; -HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                       Length 157;
                                                                                                                                              Hohenlohe P.A.; "Heat-shock genus Littorina."; "Heat-shock genes in the heat-stressed genus Littorina."; Submitted (oct-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191830; AAF12789.1; "HSSP; P19120; 1BA1.
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NON_TER 158 158
SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;
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PROSITE; PS01036; HSP70_3; 1.
NON_TER 1 1 157
SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       090671 PRELIMINARY; PRT; 130 cm.
090671;
00-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-UN-2001 (TIEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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Q9U668.
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                        89.1%; Score 41; DB 5;
88.9%; Pred. No. 2.1;
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
HEAT-SHOCK PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                 InterPro; IPR001023; HSP70.
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Matches 8; Conservative
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                                                                                                                             SEQUENCE FROM N.A.
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                                     Littorina plena.
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Q9U668
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Q9U671
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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.1%; Score 41; DB 5; Length 155; 88.9%; Pred. No. 2.1; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hohenlohe P.A.; "Heat-shock genus Littorina."; "Heat-shock genes in the heat-stressed genus Littorina."; Exbmitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191825; AAF12785.1; -- HSSP; P19120; 1BA1.
                                                           Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 5; Length 153;
Pred. No. 2.1;
0; Mismatches 1; Indels
                                                                                                                                                                  Hohenlohe P.A.;
Hohenlohe P.A.;
Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAF12784.1; -.
HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
PROSITE; PS01036; HSP70_3; 1.
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
       01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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89.1%; 88.9%;

Query Match
Best Local Similarity 88.9
Matches 8; Conservative

NON\_TER SEQUENCE

NON\_TER

80 SLFEGIDFY 88

1 SLFEGIDVY 9

οy g PRELIMINARY;

Q90669; Q90669;

RESULT 3 Q9U669

InterPro; IPR001023; HSP70. PROSITE; PS01036; HSP70\_3; 1.

SEQUENCE FROM N.A.

Best Local Similarity 88.9 Matches 8; Conservative

Query Match

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RESULT Q9U665

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1 SLFEGIDVY 9

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MEDLINE-93077669; PubMed-1360013;

MEDLINE-93077669; PubMed-1360013;

MEDLINE-93077669; PubMed-1360013;

MEDLINE-93077669; PubMed-1360013;

MEDLINE-93077669; PubMed-1360013;

Thong-term sensitiation training in Aplysia leads to an increase in the expression of B1P, the major protein chaperon of the ER.";

J. Cell B10.119:1069-1076(1992).

I. J. Cell B10.1 119:1069-1076(1992).

I. J. Cell B10.1 119:1069-1076(1992).

I. J. Cell B10.1 19:1069-1076(1992).

REMBL; Z16039; CAA78757.1; -...

REMBL; Z16039; CAA78757.1; -...

RESP; P19120; 1BA1.

InterPro; 1PR001023; HSP70.

REMBL; PR00319; HSP70.2; 1.

REMOSITE; PS01036; HSP70.2; 1.

REMOSITE; PS01036; HSP70.2; 1.

WHeat shock; Multigene family.

TOWLTER 220 220

SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;
                                                                            Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE-93077669; Pubmed-1360013; MEDIJNE-93077669; Pubmed-1360013; Mull D., Kennedy T., Barzilai A., Kandel E.; Kuhl D., Kennedy T., Barzilai A., Kandel E.; Lord-term sensitization training in Aplysia leads to an increase in the expression of BIP, the major protein chaperon of the ER."; J. Gell Biol. 119:1069-1076(1992).

-1. INDUCTION: BY HEAT SHOCK.
-1. SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; Z15037; CAA78755.1; -.
INTERPO: IPRO01023; HSP70.
PERM: PRO012; HSP70; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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24684 MW; FA8557F2BB85C37A CRC64;
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  01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).
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PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
NON_TER 1 1
NON_TER 221 221
SEQUENCE 221 AA; 24404 MW;
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24404 MW;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                  Aplysiidae; Aplysia.
NCBI_TaxID=6500;
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NCBI_TaxID=6500;
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                                                                            Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
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"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
"Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191829; AAF12788.1; -.
HSSP; P19120; 1BA1.
InterPro; IRR01023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                      Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191807; AAF12186.1; -...
HSSP; P19120; IBA1.
InterPro: IPR001033; HSP70.
PROSTIE; PS01036; HSP70_3; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT-SHOCK PROTEIN (FRAGMENT).
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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01-JUN-1998 (TrEMBLrel. 06, Created)
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Matches 8; Conservative
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SEQUENCE FROM N.A.
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85 SLFEGIDFY 93
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NON_TER
SEQUENCE
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Query Match

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P81159 œ

RESULT P81159 ID P8 AC P8 DT 01

Query Match

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Pfam; PF00012; HSP70; 1
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SEQUENCE
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Q63718
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                        090520 PRELIMINARY; PRT; 278 AA.
010520
01-NOV-1996 (TEMBLEEL: 01, Created)
01-NOV-1996 (TEMBLEEL: 01, Last sequence update)
01-NOV-1996 (TEMBLEEL: 01, Last sequence update)
01-JUN-2001 (TEMBLEEL: 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
01-SURATYOLUS MYKLSS (RAINDOW TROUT) (Salmo gairdneri).
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-85036330; PubMed-6092938; MEDLINE-85036330; PubMed-6092938; MEDLINE-85036330; PubMed-6092938; MEDLINE-8104014: Shock polypeptides from rainbow trout: characterization of cDNA sequences."; Mol. Cell. Biol. 4:1785-1791(1984). EMBL; K02549; AAA49562.1; HSSP; P08109; LGKR.
    Score 41; DB 5; Length 221;
Pred. No. 3.2;
0; Mismatches 1; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Y08578; CAA69892.1; -.
HSSP; P19120; 3HSC.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan: PF00012; HSP70; 1.
PRINTS: PR00301; HEATSHOCK70.
PROSITE: PS00329; HSP70_2; 1.
Heat shock: Multigene family.
        89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 88.9
Matches 8; Conservative
           Query Match 89.1
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                      139 SLFEGIDYY 147
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Q98899
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Q90520
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
D'Ambrosio E.;
D'Ambrosio E.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL. 22118; CAA81642.1; -
HSP: P08107; 1HJO.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70.
PRINTS; PR00301; HEATSHCK70.
PROSITE; PS00329; HSP70.2; 1.
PROSITE; PS01036; HSP70.2; 1.
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Bukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Chondrosida; Chondrillidae; Chondrosia.
NCBI_TaxID=68574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 11; Length 455;
Pred. No. 7.5;
0; Mismatches 1; Indels
                                                                                                                                                                   Score 41; DB 13; Length 367;
Pred. No. 5.8;
0; Mismatches 1; Indels
PRIMIS; PRO0120, HEATSHCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock.
NON TER
SEQUENCE 367 AA; 40405 MW; SCD3DDBDF6E3C2CA CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 455
455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                           Q63718 PRELIMINARY; PRT; 455 AA.
Q63718;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
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Borchiellini C., Le Parco Y.;
                                                                                                                                                                          89.1%;
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88.98;
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Best Local Similarity 88.5.
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Best Local Similarity
Matches 8; Conserv
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254 SLFEGIDFY 262
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268 SLFEGIDFY 276
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Search completed: December 6, 2001, 07:56:52
Job time: 180 sec
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252 SLFEGIDFY 260
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Eukaryota, Metazoa, Porifera, Calcarea, Calcaronea, Petrobionidae,
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
GUARNIDA lacunosa.
ENARTYOLE; Metazoa; Porifera; Calcarea; Calcinea; Clathrinida; Clathrinidae; Guancha.
NOBI_TaxID-115120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borchfallini C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026520; AAC05364.1; --
HSSP; D80109; ICKR.
InterPro; IPR00102; HSP70.
PRAM; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSTTE; PS01036; HSP70.3; 1.
NOW_TER 467 467
SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                              Query Match

89.1%; Score 41; DB 5; Length 467;
Best Local Similarity 88.9%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 1; Indels
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. EMBL, ARO26517; AACC63362.1; -. HSZP; POB109; ICKR. INTR. ITRR. IPR001023; HSZP70.
                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 AA.
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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Best Local Similarity 88.97
Matches 8; Conservative
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NCBI_TaxID=68578;
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Q9NJ92
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044352
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Borchiellini C., Le Parco Y.;

"Sponges paraphyly and the origin of Metazoa.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: ARTB2195; AARF01297.1;

InterPro; IPR001023; HSP70.

PENDLY: PS003029; HSP70.2;

PROSITE; PS003039; HSP70.2;

ROSITE; PS003039; HSP70.2;

NOW TER

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NOW TER

467 AA; 51318 MW; F36FC06CBIDEE131 CRC64;
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88.9%; Pred. No. 7.8;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 88.9
Matches 8; Conservative
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Sequence

220, 220, 1190, 1440, 160,

-08-460-806-19 -08-325-630-19 -08-483-695-40 -08-440-210-20

Sequence

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Sequence 3, Application US/08797358B
Patent No. 6268478
GENERAL INFORMATION:
APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 4; Length 643;
Pred. No. 0.63;
1; Mismatches 1; Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: CURROWN>
PRIOR APPLICATION: CURROWN>
                                     S-08-444-818-173
S-08-444-818-173
S-08-444-818-174
S-08-440-103-20
S-08-440-542-20
S-08-231-368-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:

ATTORNEY AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-CE 3165

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-949

INFORMATION FOR SED ID NO: 3:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                              US-07-965-285-40
US-08-487-231-40
US-09-201-912-40
US-08-440-103-16
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TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: California
COUNTRY: United States
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80.0%;
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COMPUTER READABLE FORM:
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Best Local Similarity 80.0
Matches 8; Conservative
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Sequence 14, Appl
Sequence 4, Appli
Sequence 2, Appli
Patent No. 5183745
Sequence 32, Appli
Sequence 32, Appli
Sequence 33, Appli
Sequence 34, Appli
Sequence 36, Appli
Sequence 2, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 81, Appli
Sequence 82, Appli
Sequence 83, Appli
Sequence 84, Appli
Sequence 86, Appli
Sequence 87, Appli
                                                                                                                                                                             (without alignments)
2.764 Million cell updates/sec
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                                                                                                                                                     December 6, 2001, 07:59:58; Search time 81.43 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-797-358B-3
US-08-441.139-14
US-09-477-046B-61
US-09-079-415-4
US-08-255-488-2
US-08-599-171A-32
US-08-6599-171A-32
US-09-69-226-32
US-09-69-226-32
US-09-69-226-35
US-09-612-38-35
US-08-867-27-71
US-08-12-184-35
US-08-12-184-35
US-08-12-184-35
US-08-12-184-35
US-08-12-373-71
US-08-12-373-71
US-08-12-373-71
US-08-12-373-71
US-08-12-373-71
US-08-262-037-89
US-08-262-037-89
US-08-262-037-89
US-08-262-037-89
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US-08-487-231-42
US-09-201-912-42
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                                                                                                                                                                                                                                                                                                                                                                                                    212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                         1 SLFEGIDAYT 10
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Match Length DB
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                                                                                                              OM protein -
                                                                                                                                                                                                                                                                                             Sequence:
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Gaps

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Sequence 2, Application US/08225488
Sequence 2, Application US/08225488
Sequence 1, Application US/08225488
GENERAL INFORMATION:
APPLICANT: Buxton, Frank
APPLICANT: Visser, Jacob
APPLICANT: Visser, Jacob
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.6%;
85.7%;
                                                                                                  72.5%;
77.8%;
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LENGTH: 495 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.6
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                          165 SLFDGISAY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:||||
| 173 EGVDAYT 179
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Patent No. 6287835
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPERENCE: 53579
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 61
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                                                                                                                                                                                      APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER INCOMPUTER FRANCE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                             ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PELLICATION.
FILLING DATE: 15-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILLING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEFHONE: 516-742-433
TELEFAN: 230 901 SANS UR
TELEFAN: 230 901 SANS UR
TELEFAN: CRARACTERISTICS:
FORTHRACTERISTICS:
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Patent No. 5773245
GENERAL INFORMATION:
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LENGTH: 646 amino acids
TYPE: amino acid
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Best Local Similarity 80.۰۰
نمر 8; Conservative
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286 SLYEGIDFYT 295
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288 SLFEGVDFYT 297
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US-09-457-046B-61
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STATE: NY
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Sequence 4, Application US/09079415
Patent No. 6013452
Patent No. 6013452
Patent No. 6013452
Patent No. 60134521h American
APPLICANT: Lehmbeck, Jan
TITLE OF INVENTION: PepE Genes Have Been Inactivated
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60134520 No. 6013452disk of No. 6013452th America, Inc.
STREET: 405 Lexington Avenue
                                           Gaps
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ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OCHENTING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,415
FILING DATE: 14-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, Carol
REGISTRATION NUMBER: 4657.204-US
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STORY
TELECOMMUNICATION STORY
INFORMATION FOR SEQ ID NO: 4:
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Pred. No. 18;
1; Mismatches
Score 37; DB 4;
Pred. No. 11;
1; Mismatches
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Fatent No. 5962283
GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Wannson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
Sequence 32, Application US/08599171A
Patent No. 5814473
GENERAL INFORMATION:
APPLICANT: WARREN, Patrick V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS: ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSE: CARCLLA, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
FILING DATE: CONCURRENTLY
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
CLASSIFICATION NUMBER:
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
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NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 331.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28,019
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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AMINO ACID
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 6; Conservative
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MOLECULE TYPE: PROTEIN
US-08-599-171A-32
                                                                                                                                                                                                                                                                                                                         CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
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34 SIFEGIRGY 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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; APPLICANT: DANCHIN, ANTOINE; GLASER, PHILLIPPE; KRIN, EVELYN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 800;
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TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
FILLOGICAL USES
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,541
FILLING DATE: 25-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.7%; Score 33; DB 6; Length 800
66.7%; Pred. No. 1.2e+02;
iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,488 FILING DATE: US/08/255,488 FILING DATE: US/0
      TITLE OF INVENTION: No. 5846802el Fungal Protease NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 2;
Pred. No. 20;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/FOCKET NUMBER: 4-19055/A/CIP
TELECOMMUICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
                                                                                            ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                   ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%;
85.7%;
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amino acid
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Best Local Similarity وه.،،
احد 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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                                    NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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721 SIFRGIQAY 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 EGVDAYT 179
                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-08-599-171A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:3:
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5183745-3

5183745-3

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Gaps

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Gaps

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Sequence 32, Application US/09412184

Facent No. 6268188

GENERAL INFORMATION:
APPLICANT: Wanson, Ronald V.
APPLICANT: Swanson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: A225 Executive Square, Suite 1400

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.7%; Score 32; DB 4; Length 303; 66.7%; Pred. No. 66; 1, Mismatches 2; Indels
                                                                                                                                                       DB 3; Length 303;
66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastESG for Windows Version 2.0
CNRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/412,184
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09010/01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,590
FILING DATE: 08-May-1996
APPLICATION NUMBER: 08/599,171
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
FILING APPLICATION DATA:
CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                         Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/POCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
                                                                                                                                                         62.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.73
Matches 6; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 303 AMINO ACID
                                                                                                                                                                           Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-412-184-32
                                                                              PROTEIN
                                      AMINO ACID
                                                            LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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34 SIFEGIRGY 42
                                                                                                                                                                                                                                    1 SLFEGIDAY 9
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                                                                          ; MOLECULE TYPE:
US-09-069-226-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-412-184-32
                                                                                                                                                           Query Match
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GAPLICANT: WARREN, PALTICK V.

TITLE OF INVENTION:
TORRESPONDENCES: 32
CORRESPONDENCE CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 303;
66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2
Pred. No. 66;
1; Mismatches
                                                  FLINE DATE: 00-may 11990
CLASSIFICATION: 435
PRIOR APPLICATION 10435
PRIOR APPLICATION NUMBER: 08/599,171
PILING DATE: 09-FEB-1996
PRIOR APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 21-January-1997
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D. Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 09010/017001
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LEMCTH: 303 amino acids
TTERE
                    APPLICATION NUMBER: US/08/646,590B
FILING DATE: 08-May-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331400-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOCTWARE: WORD PERFECT 5.1
SOCT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSITLIANON
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,171
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 331400-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-069-226-32
; Sequence 32, Application US/09069226
; Patent No. 6013509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.78;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7'
Matches 6; Conservative
  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-646-5908-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: 1
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|||| |
34 SIFEGIRGY 42
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Gaps

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APPLICANT: DEVARE, SURESH M
APPLICANT: DESAL, SURESH M
APPLICANT: CASEY, JAMES M
APPLICANT: DAMSON, GEORGE J
APPLICANT: DAMSON, GEORGE J
APPLICANT: GUTIERREZ, ROBIN A
APPLICANT: GUTIERREZ, ROBIN A
APPLICANT: STEWRRY, JAMES L
APPLICANT: RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,611
FILING DATE: 02-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,757
FILING DATE:
APPLICATION NUMBER: US/08/19,896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/US/115,030
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/572,822
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PORREMBER! Y PRISCILLA E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                      ; Sequence 30, Application US/08867611; Patent No. 6172189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 617 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
1:|||| |
34 SIFEGIRGY 42
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US-08-867-611-30
                                                                                           RESULT 11
US-08-867-611-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DESALE, S.
APPLICANT: DESALE, S.
APPLICANT: DAILEY, S.
TITLE OF INVENTION: HAVE SYNTHETIC PEPTIDE FROM NSI REGION NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: ILLINOIS
COUNTRY: U.S.
COUNTRY: U.S.
COUNTRY: IB PRO COMPATIBLE
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IB PC COMPATIBLE
COMPUTER: PC COM ; 0 ö Score 32; DB 5; Length 617; Pred. No. 1.5e+02; 1; Mismatches 2; Indels APPLICANT: CASEY, JAMES M.
APPLICANT: CASEY, JAMES M.
APPLICANT: BODE, SUZANNE L.
APPLICANT: ZECK, BILLY J.
APPLICANT: YAMGUCHI, JULIE
APPLICANT: YAMGUCHI, JULIE
APPLICANT: PRAIL, DONALD E.
APPLICANT: DESAI, SURESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: PROTEINS Score 32; DB 4; Length 617, Pred. No. 1.5e+02; 1; Mismatches 2; Indels SOFTWARE PATENTIN 1.25/MILLS
SOFTWARE PATENTIN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06965A
FILING DATE: 19920821
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGIETRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834PC.02 US-08-453-552-2
Sequence 2, Application US/08453552
Patent No. 5667992
GENERAL INFORMATION:
APPLICANT: CASEY, JAMES M.
APPLICANT: ADDE, SUZANNE L.
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: FRAIL, DONALD E. TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365 TELEFAX: 708-937-9556 INFORMATION FOR SEQ ID NO: 35: SEQUENCE CHARACTERISTICS: LENGTH: 617 amino acids TYPE: AMINO ACID 62.7%; 66.7%; 62.78; 66.78; Query Match 62.7 Best Local Similarity 66.7 Matches 6; Conservative Query Match 62.7 Best Local Similarity 66.7 Matches 6; Conservative TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US92-06965A-35 2 LFEGIDAYT 10 2 LFEGIDAYT 10 RESULT 12 PCT-US92-06965A-35 ò q

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APPLICANT: CASET, JAMES M.
APPLICANT: CASET, JAMES M.
APPLICANT: BODE, SUZANNE L.
APPLICANT: ECK, BILLY J.
APPLICANT: TAMAGUCHI, JULIE
APPLICANT: FRAIL, DONALD E.
APPLICANT: PERAIL, DONALD E.
APPLICANT: DESAI, SURESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2; Length 3011;
Pred. No. 8.7e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: .60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US93/00907
FILING DATE: 19930129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: ONE ABBOTT PARK ROAD CITY: ABBOTT PARK
                                                                                APPLICATION NUMBER: US 07/830,024
FILING DATE: 01-JAN-1992
ATTORNEY FAGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
RECISTRATION NUMBER: 33,207
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5131.PC.01
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/144,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
PCT-US93-00907-2
PCT-US93-00907-2
Sequence 2, Application PC/TUS9300907
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5131.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3011 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-710-637-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 LFSGVDAAT 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Пр
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 3011;
Pred. No. 8.7e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CASEY, JAMES M.
APPLICANT: BODE, SUZANNE L.
APPLICANT: ZECK, BILLY J.
APPLICANT: ZECK, BILLY J.
APPLICANT: FRAIL, JULIE
APPLICANT: FRAIL, DONALD E.
APPLICANT: DESAI, SURSHI M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: PROTEINS
TURBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,637
                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,552
FILIG DATE:
CLASSIPICATION: 435
                                            ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: ONE ABBOTT PARK ROAD CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D377/AP6D
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PORRABSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5131.US.D1
TELEPHONE: 708-937-6365
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5854001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7*
Matches 6; Conservative
                                                                                                                STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
    NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-453-552-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: Sit
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377 LFSGVDAAT 385
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; STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US93-00907-2
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0; Gaps Query Match
62.7%; Score 32; DB 5; Length 3011;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels

; ;

Oy 2 LFEGIDAYT 10 | | | | | | | Db 377 LFSGVDAAT 385

Search completed: December 6, 2001, 07:59:59 Job time: 367 sec

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AP000520 Homo sapi AP021056 Homo sapi AX021171 Sequence U31372 Human class L32844 Pongo pygma L32845 Pan troglod

Homo sapien Pongo pygma Pan troglod Human MHC c

Human MHC H.sapiens H.sapiens H.sapiens H.sapiens H.sapiens H.saptens H.sapiens H.sapiens

H.sapiens

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X82906 X82908 X82904 X82898 X82909

H.sapiens

X82926 X82927

**K82899** 

X82900 X82925 X82919 X82902 X82922 X82922

07-SEP-2000

PAT

Location/Qualifiers 1. .37

source

FEATURES

SUMMARIES

Gorilla gor Gorilla gor

L32845 L32855 L32849 L32847 L32851 L32843 L32843 L32863

AJ300180 Homo sapi AJ295140 Homo sapi AJ300181 Homo sapi AX105685 Sequence

Homo sap Seguence

Description

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Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
Gaudin,C. and Triebel,F.
Mutated peptide compounds, derived from hsp70, useful in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunotherapy
Patent: WO 9954464-A 3 28-OCT-1999;
ROUSSY INST GUSTAVE (FR); GAUDIN CATHERINE (FR); TRIEBEL FREDERIC (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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AX012955
AX012955.1 GI:10040205
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GORMHCIAC
GORMHIA
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ORAMCHIAB
CHPMHCIAE
HUMMHCW18
                                                                                                                                                                                                                                                                                                                                                                                                  HSB44HLA
HSB51HLA
HSHLAB18
HSHLAB35
HSHLAB37
HSHLAB37
                                                                                                                                                                                         HLACW301
ORAMHCIAC
                                                                                                                            GORMHIE
AP000520
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HSHLAB60
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                                                                                           ; Search time 1647.92 Seconds (without alignments) 370.404 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                       1472140 segs, 8248589755 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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'gene="HLA-B"
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AUTHORS
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2598. .2630,2737. .2780)
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SDHEATLRCHALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVPSG
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                                                                                                                                                                                                                                                                              HSA295141 3190 bp DNA PRI 29-NOV-2000
Homo sapiens HLA gene for MHC class I antigen, B*4701 allele, exons
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (27-OCT-2000) Cox S.T., Dept of HLA Sequencing, Anthony
Nolan Research, The Royal Free Hospital, Pond Street, Hampstead,
London, NW3 2QG, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                           B*4701 allele; HLA-B gene; human leucocyte antigen B; major
histocompatibility complex; MHC class I antigen.
                                                                                                                                 ;
                                                                                               Query Match 100.0%; Score 37; DB 6; Length 37; Best Local Similarity 100.0%; Pred. No. 0.2; Matches 37; Conservative 0; Mismatches 0; Indels
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AJ295141.1 GI:11493145
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AUTHORS
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REFERENCE
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1. .3190
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Submitted (03-NOV-2000) Cox S.T., Dept of HLA Sequencing, Anthony
Nolan Research, The Royal Free Hospital, Pond Street, Hampstead,
London, NW3 20G, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homor sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSA300180 3190 bp DNA PRI 06-NOV-2000
HOMO Sapiens HLA-B gene for MHC class I antigen, B*4006 allele.
AJ300180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'AJ300180.1 GI:11125668
.B*4006 allele; HLA-B gene; human leucocyte antigen B; major
histocompatibility complex; MHC class I antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 27.4; DE; Pred. No. 30; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         699
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2737. .2780
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                                                                                                                                                                                                                       2040. .2156
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820. .1095
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                                                                                                          1671. .1946
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                                                                                                                                                                 1947. .2039
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                                                                                                                                                                                                                                                                                                                                                                                          2631. .2736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 74.1%;
Best Local Similarity 83.8%;
Matches 31; Conservative
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RNLRGYYNDSEAGSHTLQRMYGCDVGPDGRLLRGHDQSAYDGKDYIALNEDLSSWTAA
DTAAQITQRKWEAARRAEGEGWRAYLEGICVEWIJRRYLENGKETLQRADPRYHYTHHPI
SDHEATLRCWALGFYPALITYWQROSEDQYDTELVETRPAGBRTFQKWAAVVPSG
EEQRYTCHVQHEGLEKRELILRWEPSSQSTIPIVGIVAGLAVLAVVIGAVVATVRCRR
KSSGGKGGSYSQAASSDSAQGSDVSLTA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (27-OCT-2000) Cox S.T., Dept of HLA Sequencing, Anthony
Nolan Research, The Royal Free Hospital, Pond Street, Hampstead,
London, NW3 2QG, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3196)
                                                                                                                                                                                                                                                        HSA295140 3196 bp DNA PRI 29-NOV-2000
Homo sapiens HLA gene for MHC class I antigen, B*1501101 allele,
                                                                                                                                                                                                                                                                                                  AJ295140
AJ295140.1 GI:11493143
B*1501101 allele; HLA-B gene; human leucocyte antigen B; major
histocompatibility complex; MHC class I antigen.
                                                                                                             Gaps
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                                                                            Length 3190;
                                                                                                             Indels
                                                                                                             9
                                                                            DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Cox,S.T.
Confirmatory sequence of HLA B*1501101
                                                                           Score 27.4; Di
pred. No. 30;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .3196 // Organism="Homo sapiens" // db_xref="taxon:9606" // chromosome="fp21.31" // cell_line="Pp"
                665
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                   Б
                1023
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98. .170
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570. .814
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/gene="HLA-B"
                                                                              74.1%;
83.8%;
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                                                                              Query Match 74.1
Best Local Similarity 83.8
Matches 31; Conservative
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HSA295140
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              (101. .173,174. .302,303. .572,573. .816,817. .1092,
. .1667,1668. .1943,1944. .2036,2037. .2153,2154. .2594,
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303. .572
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1093. .166
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                join(101
1093. 16
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gene	exon		SGD	-		_	•	intron	exon	intron	exon	intron	-	introp	exon	-	intron	exou	intron	exon	gene
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sequences."
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Matches 29; Conservative
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                                                                                                                 31
                                                                          CAAT_Signal
BASE COUNT
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                                            misc_feature
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AP000520/c
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Vallejo,A.N. and Pease,L.R.
Structure of the MHC A and B locus promoters in hominoids. Insights on the evolution of the class I MHC multigene family 95221896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                class I gene promoter; germline; major histocompatibility complex. Gorilla gorilla (individual_isolate Shamba).
Gorilla gorilla gorilla Eukaryota; Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                     Patent: WO 0125271-A 25 12-APR-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Fibroblast growth factor-5 (fgf-5) is a tumor associated t-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GORMHIE 190 bp DNA PRI 03-AUG-1995
Gorilla gorilla (clone ShA7), MHC class I Gogo-A gene promoter.
L38651
L38651.1 GI:632919
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                                                                                                                                                                                                                                   30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="synthetic construct"
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10 c 7 g 3 t
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                                                                       Length 3199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 27;
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Pred. No. 2.8e+02;
                                                                         DB 9;
                                                                                                                                              64 GGGCGTCGACGGACTCAGAATCTCCCCAGACGCCGAG 100
                                                                                                                               1 gggcaagcttggactcagaatctccccagacgccgag 37
                                                                      Score 27.4; DB red. No. 30; 0; Mismatches
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/organism="Gorilla gorilla"
/isolate="Shamba"
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                299
                                                                                                                                                                                                                      AX105685 27 bp DNA
Sequence 25 from Patent WO0125271.
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100.0%; Pre
0; }
              1021
                                                                                                                                                                                                                                                                                                                                 artificial sequence.
1 (bases 1 to 27)
Hanada,K.I. and Yang,J.C.
/gene="B*1517"
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                                                                       74.1%;
83.8%;
                                                                                                                                                                                                                                                                                                     synthetic construct.
                                                                                                                                                                                                                                                                                                                    synthetic construct
              922 c
                                                                 Query Match
Best Local Similarity 83.88
Matches 31; Conservative
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Best Local Similarity 100.
Matches 27; Conservative
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ACCESSION
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AUTHORS
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AX105685
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E 1 (sites)
S hina, S., Tamiya, G., Oka, A. and Inoko, H.
Shina, S., Tamiya, G., Oka, A. and Inoko, H.
Homo sapiens 2, 229, Slibb genomic DNA of 6p21.3 HLA class I region
L Published Only in DataBase (1999) In press
E 2 (bases I to 100000)
Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
S Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
L Submitted (21 SEP-1999) to the DDBJ/EMBL/GenBank databases. Mika
Hirakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
Japan (E-mail:mikaetokyo.jst.go.jp,
URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
Fax:81-3-5214-8470)
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5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan
For further infomation about this sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
Location/Qualifiers
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    .190
/note="sequence shown is the 5'-proximal promoter region
between the NFKB site and the first ATG"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP000520 100000 bp DNA PRI 30-MAR-2000
Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
section 19/20.
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/note="match HLA-H (M31944) with account of intervene
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Phone:+81-463-93-1121, Fax:+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                              Length 190;
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                                                                                  8. .19
/note="interferon responsive element"
                                                                                                                                                                                                                                                                                                     Score 26; DB 9; Len
Pred. No. 2.6e+02;
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/note="985L;The location is
PCR primers."
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/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
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                                                                                                                                  86. .95
/note="Enhancer B"
111. .116
a 62 c 45 g
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85.3%;
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Gaps

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exon

22-AUG-1995

BASE COUNT ORIGIN

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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artificial sequence.
1 (bases 1 to 39)
Braud, V.M., O, Allan, D.S., Ogg, G.S. and Mcmichael, A.J.
H.a-e binding
Patent: WO 9928748-A 22 10-JUN-1999;
BRAUD VERONIQUE M (GB); CALLAGHAN CHRISTOPHER A O (GB); ALLAN DAVID 5 J (GB); ISIS INNOVATION (GB); OGG GRAHAM S (GB); MCMICHAEL ANDREW J (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete nucleotide sequence of a gene encoding a functional human class I histocompatibility antigen (HLA-CW3)
EMBO J. 3 (4), 879-885 [1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zemmour,J. and Parham,P.
Distinctive polymorphism at the HLA-C locus: implications for the
expression of HLA-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (bases 1 to 165)
Smith, K.D. and Lutz, C.T.
Direct Submission
Submitted (11-JUL-1995) Kelly D. Smith, Pathology, University of Iowa, 200 Hawkins Dr., Iowa City, IA 52242, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 165)
McCutcheon,J.A., Gumperz,J., Smith,K.D., Lutz,C.T. and Parham,P.
Low HLA-C expression at cell surfaces correlates with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human class I major histocompatibility antigen (HLA-Cw3) gene,
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                                                                                                                                                                                                                                                                                                                                                                     Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Pred. No. 7.5e+02;
0; Mismatches 1;
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J. Exp. Med. 181 (6), 2085-2095 (1995)
95279935
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c42"

    .39
/organism="synthetic cc/db_xref="taxon:32630"

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88. .160
/gene="HLA-Cw3"
                                                                                                                                                                                                                                                                    /note="primer"
                                                                                                                                                                                                                                                                                                                                                                     68.6%;
96.3%;
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U31372.1 GI:951147
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Best Local Similarity
Matches , 26; Conserv
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Kikkwa,E., Twata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram,S. and Inoko,H.
Molecular Gynamics of MrG genesis unraveled by sequence analysis of
the 1,796,938-bp HLA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submission Submission Submitted (29-JAN-1999) to the DDBJ/EMBL/GenBank databases. Takashi Shiina, Tokai University School of Medicine, Department of Molecular Life Science 2; Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mail:tshiina@is.icc.u-tokai.ac.jp, Tel:81-463-94-8884)
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                 AB023056 162227 bp DNA PRI 20-NOV-1999
Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
clone:544A6, complete sequence.
AB023056
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Pred. No. 19;
0; Mismatches 2; Indels 0;
                                                                                                                              DB 9; Length 100000;
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                          /db_xref="GDB:127895"
25903 a 23050 c 23320 g 27727 t
                                                                                                                            Score 25.8; DE Pred. No. 23; 0; Mismatches
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Sequence 22 from Patent WO9928748.
                                                                                                                                                                                                                               DD 16168 TGGGACTCAGATTCTCCCCAGACGCCGAG 16140
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                          9 ttggactcagaatctcccagacgccgag 37
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Shiina, T. and Takishima, N.
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Best Local Similarity 93.1%;
Matches 27; Conservative (
                                                                                                                            Query Match 69.7%;
Best Local Similarity 93.1%;
Matches 27; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="6p21.3
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synthetic construct
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Query Match 68.6%;
Best Local Similarity 96.3%;
Matches 26; Conservative C
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135. .141
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/note="B"
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CHPMHCIAC
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class I gene promoter; major histocompatibility complex.
Pongo pygmaeus.
Pongo pygmaeus.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Pongo.
1 (bases I to 184)
Vallejo, A.N. and Pease, L.R.
Structure of the MHC A and B locus promoters in hominoids. Insights on the evolution of the class I MHC multigene family
95221896
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/germline
| 1. .184
/note="5" proximal promoter region between transcription
factor site NFkB and first ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132845.
132845.1 GI:625016
Lisss I gene promoter; major histocompatibility complex.
Pan troglodytes.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes (clone K1811) MHC class I Patr-B gene, promoter
region.
                                                                                        Gaps
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Pongo pygmaeus (clone C632) MHC class I Popy-A gene, promoter
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                                                            Score 25.4; DB 9;
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Pred. No. 4e+0
0; Mismatches

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    /cell_line="CP81"

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/note="Enhancer B; B
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133. .139
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/number=1
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Best Local Similarity 96.3
Matches 26; Conservative
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/cell_type="EBV-transformed B-lymphoblastoid cell"
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9. .20
/bound_moiety="interferon responsive element"
84. .94
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Class I gene promoter; major histocompatibility complex.
Pan troglodytes.
Pan troglodytes.
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
I (bases I to 186)
Vallejo,A.N. and Pease,L.R.
Structure of the MHC A and B locus promoters in hominoids. Insights on the evolution of the class I MHC multigene family
1 (bases 1 to 186)
Vallejo,A.N. and Pease,L.R.
Structure of the MHC A and B locus promoters in hominoids. Insights on the evolution of the class I MHC multigene family
J. Immunol. 154 (8), 3912-3921 (1995)
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/note="5' proximal promoter region between transcription factor site NFkB and first ATG"
9. .20
/bound_moiety="interferon responsive element"
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Pan troglodytes (clone T1725) MHC class I Patr-B gene, promoter
region.
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1. 186
1. Garain troglodytes"

Ab_xref="taxon:9598"

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122849.1 G1:625033
Gorilla gorilla.
Gorilla gorilla.
Gorilla gorilla.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
1 (bases I to 186)
Vallejo, A.N. and Pease, L.R.
Structure of the MHC A and B locus promoters in hominoids. Insights on the evolution of the class I MHC multigene family
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Gorilla gorilla (clone 0520) MHC class I Gogo-A gene, promoter
region.
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Query Match 68.6%; Score 25.4; DB 9; Length 186; Best Local Similarity 96.3%; Pred. No..4e+02; Matches 26; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 96.3%; Pred. No. 4e+02;
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159 GGACTCAGATTCTCCCCAGACGCCGAG 185 11 ggactcagaatctccccagacgccgag 37 q

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Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen; PCR; primer; amplification; ss.
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                   Compugen Ltd.
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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AAT74985
AAI63980
AAN70225
AAT61639
AAC00214
AAC00214

    nucleic search, using sw model

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                                                                                                                                                                               The invention relates to a mineral of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response. Comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may cancer of head and neck, particularly kidney cancer). The peptides may cancers of head and neck, particularly kidney cancer). The peptides may estimulate inmunogenicity and high specifically interleukin-2, interferon-gamma and tumony necrosis factors (specifically interleukin-2, interferon-gamma and tumour necrosis factors). The meland identifies peptides with high immunogenicity and high specificity for particular HiA (human leucocyte in a cellular should identifies peptides with high immunogenicity and high specificity for particular HiA (human leucocyte in a cellular should the propertion of the cellular should the content of the cellular should the cellular should the cellular should be content of the cellular should the cellular should be content of the cellular should be cont
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                                                                                                                                                           The invention relates to a method of identifying peptides, derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating a subject having a neoplasm expressing fibroblast growth factor-5 (FGF-5), e.g. prostate, breast, bladder, or pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reverse RT-PCR primer for cloning human leucocyte antigen-A3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 37; DB 21; Length 37; 100.0%; Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37 BP; 9 A; 12 C; 11 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gggcaagcttggactcagaatctccccagacgccgag 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA alleles for the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                 Example 7; Page 24; 56pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD03948 standard; DNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-2000; 2000WO-US26689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.0
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-290607/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanada K, Yang JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200125271-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
AAD03948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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The present invention relates to a method 10. Liealing a subject maying modulating an immune response to FGF-5 or FGF-5 comprises modulating an immune response to FGF-5 or FGF-5 expression or activity. FGF is a timour associated antigen (TAA). The method is useful for treating or preventing a neoplasm such as prostate carcinoma. Dreast carcinoma, bladder carcinoma, pancreas carcinoma, and renal cell carcinoma (RCC) and diseases such as Hippel-Lindau disease, horseshoe kidneys, adult polycystic kidneys and acquired renal cystic carcinoma (RCC) and disease such as Hippel-Lindau disease, horseshoe kidneys, adult polycystic kidney desses as immunogen in the production of antibodies, which are useful in quantitative immunoassays that determine concentrations of antigen-bearing substances in biological sample, the antibodies may also be used to treat FGF-5 expressing or overexpressing tumours by decreasing FGF-5 activity, as diagnostic agents to monitor the profession or regression of an FGF-5 connection of an FGF-5 charactured or sequence is reverse RT-PCR primer used for cloning therapy for the treatment of neoplasm. FGF-5 cDNA is also useful in gene therapy. The present sequence is reverse RT-PCR primer used for cloning hunchduce HLA-A3 into non-HLA-A3 gene from autologous 1764 RCC to introduce HLA-A3 into non-HLA-A3 expressing cells. The HLA-A3 gene was then subcloned into retroviral vector pRx-TRES-BSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein-encoding gene 33 cDNA clone HTXDC77, SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDshimer; disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine stind disorder; pregnancy related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                             The present invention relates to a method for treating a subject having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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carcinoma, comprises modulating an immune response to FGF-5 or modulating FGF-5 expression or activity \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.0%; Score 27; DB 22; Length 27; Best Local Similarity 100.0%; Pred. No. 0.018; Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human secreted protein preca
/transl_except= (pos: 74..76, aa: Xaa)
/transl_except= (pos: 89..91, aa: Xaa)
/transl_except= (pos: 104..106, aa: Xaa)
/transl_except= (pos: 113..115, aa: Xaa)
/transl_except= (pos: 270..172, aa: Xaa)
/transl_except= (pos: 269..271, aa: Xaa)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ggactcagaatctcccagacgccgag 27
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                                                                                                                                                     Example 3; Page 24; 101pp; English
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WO200077022-A1
                  11-JUN-1999;
               21-DEC-2000
       sig_peptide
         mat_peptide
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HLA-E; human leukocyte antigen-E; interaction; natural killer cell; NK cell; T cell; CF94/NKG2+ cell; targeted killing; CD8+ T cell; cancer; CD4/NKG2 receptor; bone marrow transplantation; treatment; detection; autoimmune disease; lymphoma; leukemia; infection; pregnancy; PCR primer; transplantation; immunodeficiency; immunosuppressive; cytostatic; ss.
                                                                                                                                                                                                                                                                                                               HLA-B*0702/mouse CD80 chimeric DNA PCR primer 3.
AAX78122 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9928748-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1998;
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                                                                                                                                                                                                                                                                  19-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                     AAX78122;
                                                                                                                                               AAX78122
                                     QQ
                                                                                                                                                                                                                     AAEO08345-AAD08394 represent CDNAs corresponding to 50 human secreted protein genes and AAEO3998-AAEO3947 represent the proteins they encode. AAEO3996 AAEO3997 represent the protein step encode. CAAEO3996 AAEO3996 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. CC therapy. Pathological conditions can be diagnosed by determining the early of the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the can include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental conditions and include developing products for the diagnosis or treatment of allergies, hematropoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., hematroid arthritis), inflammation, allergies, neurological disorders, diseases, atherosclerosis, cardiovascular disorders (e.g., Alzheimer's disease, cardiovascular disorders, espesis, diabetes, atherosclerosis, cardiovascular disorders, anglogenic disorders, kidney disorders, edisorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to continue of primary tissues, to regenerate tissues, to identify their collure of content ligands or binding partners, and in chemotraxis, and can be used as a food additive or preservative to modify storage properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention.
     /transl_except= (pos:323..325, aa:Xaa)
/transl_except= (pos:338..340, aa:Xaa)
/transl_except= (pos:347..349, aa:Xaa)
/transl_except= (pos:346..388, aa:Xaa)
/transl_except= (pos:419..421, aa:Xaa)
/transl_except= (pos:512..514, aa:Xaa)
/note= "Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome -
                                                                                                                                                                                                                                                                                                               /product- "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1441 BP; 299 A; 403 C; 412 G; 283 T; 44 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 513; 614pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2000; 2000WO-US15136
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                                                                                                                                                                                                                  65..118
/*tag= b
119..517
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-367020/38.
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98WO-GB03686. 97GB-0025764

(first entry)

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This invention describes a novel method to identify the interaction between human leukocyte antigen E (HLA-E) and natural killer (NK) cells and/or a subset of T cells, and to target or isolate those cells. Cells and/or subset of T cells, and to target or isolate those cells. Identifying the presence of, separating, killing or inactivating claim or inactivating a sample with HLA-E under CF94/NKG2+ cells compruses (a) contacting a sample with HLA-E under CF binding conditions and (b) detecting binding, separating cells bound to HLA-E surgeted killing on bound cells. The HLA-E property CF binding to CD94/NKG2 receptors on NK cells and a subset of CD8+ T CF compounds, such as antibodies, that interfere with interaction of CF CD94/NKG2 and HLA-E binding can be tailored for specific CD94/NKG2.

CC COMPOUNDS, such as antibodies, that interfere with interaction of CF CD94/NKG2 and HLA-E binding can be tailored for specific CD94/NKG2.

CC CD94/NKG2 and HLA-E binding can be tailored for specific CD94/NKG2.

CC CD94/NKG2 and HLA-E binding can be tailored for specific CD94/NKG2.

CC CD94/NKG2 and HLA-E binding can be tailored for specific CD94/NKG2.

CC CD94/NKG2 and HLA-E binding can be tailored for specific CD94/NKG2.

CC CD94/NKG2 and HLA-E binding can be tailored for specific CD94/NKG2.

CC CD94/NKG2 and HLA-E binding contification of NK cells or a sub population of NK cells or cells, or as up population of NK cells or as a permit of the placental infertion immunodeficiency, and autoimmune collection immunosation of CD4/NKG2 and autoimmune collection immunosation of CD4/NKG2 and autoimmune the invantion have immunosation of CD4/NKG2 and autoimmune immunosation and autoimmune im
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention have immunosuppressive and cytostatic activity. This sequence represents a PCR primer used in the construction of a chimeric DNA containing the leader segment of human HLA-B*0702 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte antigen E binding interaction with CD94/NKG2+ cells
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                                                                                                                                                   Allan DSJ, Braud VM, McMichael AJ, O'Callaghan CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39 BP; 8 A; 14 C; 12 G; 5 T; 0 other;
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(ISIS-) ISIS INNOVATION LTD.
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Gaps

70.8%; Score 26.2; DB 22; Length 1441; 92.6%; Pred. No. 0.072; ive 2; Mismatches 0; Indels 0;

Query Match 70.8 Best Local Similarity 92.6 Matches 25; Conservative

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Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ds.
297, ggactcagattctccccagacgccgag 323
                                                                                                                                                                                Human polynucleotide SEQ ID NO 352,
                                                                                 AA163980 standard; DNA; 3357 BP.
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                                                                                                                                              22-0dr-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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22-AUG-2000
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23-AUG-2000
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                                                                 AA163980
                                              RESULT
                                                                                                This is the histocompatibility antigen (HLA-A2) template. This is fused at the amino terminus to gp350/220 peptide sequence from Epstein Barr virus (EBV). This is used in creating a fusion protein comprising a fusion protein comprising a non-virally encoded cell membrane molecule and a targeting ligand. The fusion protein usually comprises a major histocompatibility complex (MHC) class I or II molecule or beta2 microglobulin and a targeting ligand or one member of a high affinity binding pair, preferably avidin. The HLA-A2 is a MHC class I antigen. The fusion protein on the surface of a gene delivery vehicle can be used in a method for targeting such a gene delivery vehicle to a selected cell type in a warm blooded animal. The pathogenic agents include parasites, bacteria and viruses, cancer and tumour cells. The method can also be used to generate an immune response against an immunogenic portion of an antigen.
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                                                                                                                                                                                                                                                                                                               major histocompatibility complex; MHC; fusion protein; gene delivery;
inhibit; pathogen; expression cassette; avidin; Epstein-Barr virus;
                                             Gaps
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                                                                                                                                                                                                                                                                               Human HLA-A2 template for construction of a fusion protein.
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        Score 25.4; DB 20;
Pred. No. 0.092;
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 Query Match
68.6%; Score 25.4; D
Best Local Similarity 96.3%; Pred. No. 0.09
Matches 26; Conservative 0; Mismatches
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                                                                 11 ggactcagaatctcccagacgccgag 37
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95US-0009411.
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The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM43447)-AAM3660) useful for preventing, treating cor ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, cone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -
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HLA-B 27.
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Pred. No. 0.18;
0; Mismatches 1;
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ID AAN70225 standard; DNA; 3874 BP
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200005-0256719.
200005-021479.
200005-0251866.
200005-0251869.
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2000US-0250160.
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96.38;
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                                                                                                     20000S-0250391.
20000S-0251030
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Best Local Similarity 96.3
Matches 26; Conservative
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                                                          17-NOV-2000;
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic predisposition to seronegative spondyloarthropathies (SNSA)
                                                                                                                                                                                              33' flanking region diagnostic for genetic predisposition to SNSA"
                                                          /*tag= a
/note= "HLA-B27 3' flanking region, downstream a
3' untranslated region"
                                                                                                                                                                                                                                                              /noté= "absence of cytosine at this site is indicative of a predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting pre-disposition to seronegative spondylarthropathies from the absence of a C residue at a specific position in the 3'-flanking region of the HLA B27 allele
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                                                                                                          /note= "3' flanking region diagnostic for predisposition to SNSA" 4270..4556
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                          Location/Qualifiers
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sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riethmuller G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Length 3874;
Ankylosing spondylitis; rheumatic disorder; diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25.4; DB Pred. No. 0.18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lang M,
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518..590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT61639 standard; DNA; 6553 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dorner C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.6%;
Best Local Similarity 96.3%;
Matches 26; Conservative
                                                                                                                                                                                                                       ,..3041
                                                                                                                                                                                                                                                                                                                                                                                                                 85DE-3545576.
85DE-3542024.
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2450..2566
/*tag= e
3009..3041
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                                                                                                                           /*tag= b
1090..1506
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1932..2357
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3148..3191
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                                                                                                 /*tag= a
720..989
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P-PSDB; AAP70155.
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                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1986;
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01-JAN-1985;
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                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    24-JUN-1987
                                                                                                                                                                                                                                                                                                                     EP226069-A
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Gaps

AAT61639 RESULT

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from ollgo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
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                                                                                                                                                                          diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 529 BP; 97 A; 174 C; 169 G; 83 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 21;
Pred. No. 0.2;
1; Mismatches 1
                                                              Giordano J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein 5' EST, SEQ ID NO: 210.
                                                                                                                                                                                                      Claim 1; SEQ ID 212; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 ggactcagaatctccccagacgccgag 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A,
                                                              Duclert A,
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92.68;
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   99US-0122487
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Matches 25; Conservative
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                                                                                          WPI; 2000-500381/45.
P-PSDB; AAG00208.
                                                              Dumas Milne Edwards
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                                (GEST ) GENSET
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 26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 447 BP; 83 A; 150 C; 132 G; 70 T; 12 other;
                                                                                                                                                                                                                       Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein 5' EST, SEQ ID NO: 212.
                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 3766; 71pp + CD-ROM; English.
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1; Mismatches
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gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.6%;
92.6%;
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                                                                                                                         21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                   WPI; 2000-500381/45.
P-PSDB; AAG03762.
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nes 25; Conserv
                                                                                                                                                                                        (GEST ) GENSET
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                               Homo sapiens
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correspond to 5'ESTs and for

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or poly4+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy and chromosome mapping procedures. They are used to obtain
  obtaining cDNAs and genomic DNAs that correspond to 5^{\circ}ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                      upstream regulatory sequences and to design expression and secretion
                                                                               Claim 1; SEQ ID 210; 71pp + CD-ROM; English.
genomic DNAs that
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nes 24; Conserv
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Best Local Si
Matches 24;
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Sequence 432 BP; 81 A; 149 C; 124 G; 62 T; 16 other;

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                      Gaps
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66.5%; Score 24.6; DB 21; Length 432; 88.9%; Pred. No. 0.29;
                      Indels
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                     2; Mismatches
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens. EP1033401-A2

AAC00213 standard; cDNA; 358 Human; 5' EST; gene therapy; 06-OCT-2000 AAC00213; RESULT 12 

Human secreted protein 5' EST, SEQ ID NO: 211. (first entry)

BP

; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.

Homo sapiens.

EP1033401-A2

06-SEP-2000

21-FEB-2000; 2000EP-0200610.

99US-0122487 26-FEB-1999;

(GEST ) GENSET

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures Giordano J; Duclert A, Dumas Milne Edwards J, WPI; 2000-500381/45. P-PSDB; AAG00207.

Claim 1; SEQ ID 211; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. ESTs sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are

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often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
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                                                                                                                                                                                                                                                             Score 24; DB 21; Length 358;
Pred. No. 0.51;
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7
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88.9%;
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Matches 24; Conservative
                                                                                                                                                                                                          Sequence 358 BP;
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures Claim 1; SEQ ID 8354; 71pp + CD-ROM; English. expression and secretion vectors. 

Duclert A, Giordano J;

Dumas Milne Edwards J, WPI; 2000-500381/45

(GEST ) GENSET

21-FEB-2000; 2000EP-0200610.

06-SEP-2000.

99US-0122487

26-FEB-1999;

Sequence 527 BP; 95 A; 176 C; 160 G; 71 T; 25 other;

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2000US-0229513.
2000US-0230437.
2000US-0230438.
2000US-0231242.
2000US-0231243.
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20000S-0231968.
20000S-0232397.
20000S-0232398.
20000S-0232399.
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2000US-0236370.
2000US-0236802.
2000US-0237037.
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200005-0237038.
200005-0237040.
200005-0239935.
200005-0239935.
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2000US-0241785
2000US-0241786
2000US-0241787
2000US-0241808
2000US-0241809
2000US-0244617
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2000US-0246475.
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2000US-0246528.
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2000US-0246609.
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2000US-0234997.
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2000US-0235836.
2000US-0236327.
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2000US-0246525.
2000US-0246525.
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2000US-0231413
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2000US-0232080
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2000US-0233065
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2000US-0249211
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21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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20 - OCT - 2000;
01 - NOV - 2000;
08 - NOV - 2000;
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29-SEP-2000;
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27-SEP-2000;
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20-0CT-2000;
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20-0CT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                             cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antialergic; hepatotropic; antidiabetic; antialergic; hepatotropic; antidiabetic; antibacter; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ds.
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Human; antlarthritic; antirheumatic; antiproliferative; vasotropic;
                                            ;
  DB 21; Length 527;
                                            5
                                          1; Mismatches
    Score 24; L
Pred. No. 0.
                                                                              Human polynucleotide SEQ ID NO 353
64.98;
88.98;
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2000US-018464.
2000US-0186350.
2000US-0189874.
2000US-0199076.
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2000US-0209467.
2000US-0214886.
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2000US-0216647.
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2000US-0217496.
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2000US-0220963.
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2000US-0225447.
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2000US-0225759.
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                                                                                                                                                                                                                                                                                                            (first entry)
                                          24; Conservative
Query Match
Best Local Similarity
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24 - FEB - 2000;
02 - MAR - 2000;
17 - MAR - 2000;
11 - MAR - 2000;
19 - MAY - 2000;
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14 - AUG - 2000;
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14-JUL-2000;
26-JUL-2000;
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                                            Matches
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XXX AA763981

XXX AAA16

XXX XXX AA16

XXX XXX B Hums

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cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antialergic; hepatotropic; antidiabetic; antibammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ds.
                                                                                                                               Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
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2000US-0180628.
2000US-0184664.
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19-MAY-2000;
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28-JUN-2000;
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06-SEP-2000;
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22-AUG-2000;
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24-FEB-2000;
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                AAI63979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human polynuclectides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating or ameliotal conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addisson's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative collits; (c) cardiovascular disorders such as myocardial ischemias, chimund healing, controlly a finence of a myocardial ischemias, chimund healing, controlly a finence of a myocardial ischemias, chimund healing, controlly a finence of a myocardial ischemias, controlly and controll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders
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ID AA163979 standard; DNA; 3372 BP.
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2000US-0250391.
2000US-0251030.
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2000US-0251990
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Matches 25; Conservative
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The invention relates to human polynucleotides (AAIG3803-AAIG4012) and
the encoded proteins (AAM43497-AAM43660) useful for preventing, treating
cor ameliorating medical conditions e.g. by protein or gene therapy. The
genes were isolated from a range of human tissues disclosed in the
correction. The nucleic acids, proteins, antibodies and (ant)agonists
are useful in the diagnosis, treatment and prevention of: (a) cancer,
correct and ovarian cancer and other cancers of the adrenal gland,
concer, bone marrow, breast, gastrointestinal tract, liver, lung, or
cuogenital; (b) immune disorders e.g. Addison's disease, allergies,
autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
colitis; (c) cardiovascular disorders such as myocardial ischaemias;
colitis; (c) neurological diseases e.g. cerebral anoxia and
colitis; (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal
and parasitic infections.
Conte: The sequence data for this patent did not form part of the
content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders
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                                                                                                     2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
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2000US-0251989.
2000US-0251990.
2000US-0254097.
2001US-0259678.
                       2000US-0250391.
2000US-0251030.
2000US-0251988.
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488781/53.
                       01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
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01-DEC-2000;
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Search completed: December 6, 2001, 10:01:23 Job time: 4267 sec

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Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 10, Appl
Sequence 19, Appl
Sequence 19, Appl
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72.065 Million cell updates/sec
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Sequence 3, Ag
Sequence 3, Ag
Sequence 4, Ag
Sequence 1, Ag
Sequence 1, Ag
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                 1 gggcaagcttggactcagaatctccccagacgccgag
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PCT-US34-06422-1
PCT-US32-0703-1
US-09-813-819-3
US-09-039-555B-19
US-09-078-459-3
US-09-078-459-3
US-09-102-204-3
US-09-104-308-3
US-09-104-308-3
US-09-104-308-3
US-09-104-308-3
US-09-104-308-3
US-09-104-308-3
US-09-549-108-4
US-09-549-108-4
US-09-549-106-4
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US-08-938-858-1
US-09-198-955A-13
US-09-198-955A-14
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US-09-248-528-1
US-09-549-108-1
                                                                                                                                                                                                                                     351203 seqs, 113238999 residues
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US-08-480-525-1
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                                                                              6, 2001, 08:50:16
                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                    - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                     Title:
Perfect score:
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                                                                                                                                                                  Sequence:
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Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	SPONDY LOARTHROPATH I ES · AND	6553; ; 0; Gaps 0;
29 18.4 49.7 1516 3 US-09-248-528-3 30 18.4 49.7 1516 4 US-09-549-108-3 31 18.4 49.7 1516 4 US-09-549-108-3 32 18.4 49.7 1516 4 US-09-549-108-3 33 18.4 49.7 1516 4 US-09-549-106-3 34 18.4 49.7 1517 3 US-09-549-106-2 35 18.4 49.7 1517 4 US-09-549-106-2 36 18.4 49.7 1517 4 US-09-549-106-2 37 18.4 49.7 1517 4 US-09-549-106-2 38 18.4 49.7 1517 4 US-09-549-106-2 39 18.4 49.7 1517 4 US-09-549-106-2 40 18.4 49.7 441529 4 US-09-103-840A-1 41 18.2 49.2 27 1 US-09-103-840A-1 42 18.2 49.2 1161 2 US-08-561-151-2 43 18.2 49.2 1161 2 US-08-661-857-151 44 18.2 49.2 1161 2 US-08-616-857-151	NETIC SATIVE Clark	Query Match 68.6%; Score 25.4; DB 1; Length 6 Best Local Similarity 96.3%; Pred. No. 0.075; Matches 26; Conservative 0; Mismatches 1; Indels QY 11 ggactcagaactcccagacgccgag 37

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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: PCT/US94/06422
FILING DATE: JUNE 7, 1994
CLÁSSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/073,830
FILING DATE: 07-JUN-1993
CLÁSSIFICATION
CLÁSSIFICATION:
APPLICATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4066PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%; Score 19.2; D
87.5%; Pred. No. 23;
tive 0; Mismatches
                                                                                         PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 ctcagaatctccccagacgccgag 37
                                         E: FLOPPY DISK
IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 758-4800
TELEFRAX: (212) 751-6849
INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS:
        ZIP: LULD.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.50,
Thes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEIC ACID
                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: ...
STRANDEDNESS: DOUE
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PCT-US92-07103-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
                             Sequence 1, Application US/08480525

Fatent No. 5556754

GENERAL INFORMATION:
APPLICANT: SINGER, DINAH, S.; KOHN,
APPLICANT: LEONARD; MOZES, EDNA; SAJI, MOTOVASU;
APPLICANT: LEDLEY, FRED, D
TITLE OF INVENTION: METHODS OF TREATING
TITLE OF INVENTION: APPCINANCES: 38
CORRESPONDENCE: MORGAN EINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.2; DE
Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/073,830

FILING DATE: 07-JUN-1993

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI:

REGISTRATION NUMBER: P-37,341

REFERENCE/DOCKET NUMBER: 2026-4066

TELEPHONE: (212) 758-4800

TELEPHONE: (212) 758-4809

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1088 CTCAGCTTCTCCCCAGACTCCGAG 1111
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Best Local Similarity 87.5%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: UNKNOWN
US-08-480-525-1
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
RESULT 2
US-08-480-525-1
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Gaps
                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9207103
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology; Forsyth Dental
TITLE OF INVENTION: NOVEL STRAIN OF CHLAMYDIA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                            ó;
Length 1419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07103
FILING DATE: 19920824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MIT-5643A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .J920824
N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,998
FILING DATE: 23-AUG-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brook, David E. REGISTRATION NUMBER: 22,592
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METHODS OF TREATING AUTOIMMUNE DISEASES AND TRANSPLANTATION FEJECTION

Sequence 1, Application PC/TUS9406422
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS OF TREAT
TITLE OF INVENTION: AUTOIMMURE DISEAR
TITLE OF INVENTION: REJECTION
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK

RESULT 3 PCT-US94-06422-1

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Patent No. 6033856
GENERAL INFORMATION:
APPLICANT: Keerner, Kathrin
APPLICANT: Radlack, Hans-Harald
APPLICANT: Radlack, Hans-Harald
TITLE OF INVENTION: PROMOTER OF THE CDC25B GENE, ITS
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,660B
FILING DATE: 09-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 96/06943
FILING DATE: 07-MAR-1996
PRIOR APPLICATION NUMBER: 95/06466
FILING DATE: 29-MAR-1995
PRIOR APPLICATION NUMBER: 94/1366
FILING DATE: 29-MAR-1995
PRIOR APPLICATION NUMBER: 94/1366
FILING DATE: 26-MG-1994
ATTONINY/AGERY INFORMATION:
MAND: ATTONINY/AGERY INFORMATION:
                                                                                                         DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
CELL CYCLE REGULATED REPRESSOR
AND DNA ELEMENT
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.8%; Score 18.8; 76.7%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 GGCCAACGTCGGACTCAGAGTCTTCCCTGA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lowen, Cara Z.
REGISTRATION NUMBER: 38,227
REFERENCE/DOCKET NUMBER: 47211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS:
                                                                                                                              STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 270 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 76.7
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
APPLICANT: MULLER,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                 USA
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US-09-039-555B-19/c
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                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-793-660B-10
                                                                                                                                                                                               COUNTRY:
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APPLICANT: MERKULOV, Gennady et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001177
CURRENT APPLICATION NUMBER: US/09/813,819
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                    ANTI-SENEE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia sp.
STRAIN: novel
POSITION IN GENOME:
CHROMOSOME/SEGRENT: 165
PUBLICATION INFORMATION:
AUTHORS: Stills Jr., Harold F.
TITLE: Isolation of an Intracellular Bacterium
JOURNAL: Infect. Immun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 GCCACACUGGGACUGAGACACUGCCCAGACUCCUA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ggcaagcttggactcagaatctccccagacgccga 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.4%; Score 19; DB Best Local Similarity 81.5%; Pred. No. 40; Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.4%; Score 19; DB Best Local Similarity 62.9%; Pred. No. 28; Matches 22; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3730 GCAAGTTTGGCTTCACAATTTCCCCAG 3704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 gcaagcttggactcagaatctccccag 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-793-660B-10/C
S. Sequence 10, Application US/08793660B
Patent No. 6214614
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(17138)
COTHER INFORMATION: n = A,T,C or G
US-09-813-819-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09813819 Patent No. 6294368
                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1510 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
(617) 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); DATE: August 24-1991
PCT-US92-07103-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: rRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-813-819-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 17138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
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Sequence 41, Application US/08678039A

Batent No. 5858662

GENERAL INFORMATION:
APPLICANT: Morris, Colleen A.
TITLE OF INVENTION: Diagnosis of Williams Syndrome and
TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C. STREET: 555 Thirteenth Street, N.W., Suite 701 East STRETT: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Mashington
STATE: DC
COUNTRY: U.S.A.
ZIP: DC
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/678,039A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REPEDEDAND NUMBER: 38,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.3%; Score 18.6; C
72.7%; Pred. No. 38;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 AAGCAGGAGGCGGACGTCTCCGGACGCCGAG 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 aagettggactcagaatetececagaegecgag 37
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                                                REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2323
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: Coding Sequence
LOCATION: 1...849
GTHER INFORMATION:
US-09-078-459-3
                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 72.7
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3262 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-678-039A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: XU, SHUANG-YONG
APPLICANT: MAUNUS, ROBERT E.
APPLICANT: LUNNEN, REITH D.
APPLICANT: LUNNEN, REITH D.
APPLICANT: ALLEN, RACHEL
TITLE OF INVENTION: AND PRODUCING THE Age! RESTRICTION
TITLE OF INVENTION: BNONUCLESE IN E. COLI
CORRESPONDENCE ADDRESS:
ADDRESSEE: AND MESSE:
ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWAREN APPLICATION DATA:
APPLICATION NUMBER: US/09/039,555B
FILING DATE: 16-MAR-1998
CLASSIFICATION 514
PRIOR APPLICATION BATA:
APPLICATION NUMBER: D19710643.9
FILING DATE: 14-MAR-1997
ATONNEY/AGENT INFORMATION:
APPLICATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: 2000 base pairs
TYPE: nucleic acid
STRNDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.8%; Score 18.8; Dest Local Similarity 76.7%; Pred. No. 36; Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gggcaagcttggactcagaatctccccaga 30
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09078459
Patent No. 5885818
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-09-039-5558-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beverly
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SULT 8 -09-078-459-3

RESULT

ŏ QQ TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO HYPOTHETICAL: 1
ANTI-SENSE: NO
ORIGINAL SOURCE

NAME: Williams, Gregory D REGISTRATION NUMBER: 30901 FILING DATE:
ATTORNEY/AGENT INFORMATION:

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Sequence 3, Application US/09104308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-104-308-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jones, Brian E.
APPLICANT: Van Der Kleij, Wilhelmus A.H.
APPLICANT: Van Solingen, Piet
APPLICANT: Weyler, Walter
TITLE OF INVENTION: No. 6190899el Cellulase Producing
TITLE OF INVENTION: Actinomycetes, Cellulase Produced Therefrom
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                   Length 3262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 421;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                   Score 18.6; DB 2;
Pred. No. 46;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TESTER OF WARSE
SOFTWARE: FASTER OF WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,204
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/974,041
FILING APPLICATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC539
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7555
TELEPAX: 650-846-7555
TELEPAX: 650-846-7555
TELEPAX: 043 DEED NO: 35 DEDUCTED TO THE TELEPAX: 051 DEDUCTED TO THE TELEPAX: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 GGCCACACTGGGACTGAGACACGGCCCAGACTCCTA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gggcaagcttggactcagaatctccccagacgccga 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.4; DB Pred. No. 42; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 615 GGCAAGCGTGGACTTTCAGTCTCCATTGACCCC 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Genencor International, Inc
925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                              2 ggcaagcttggactcagaatctccccagacgcc 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-102-204-3
; Sequence 3, Application US/09102204
; Patent No. 6190899
; GENERAL INFORMATION:
                                                                                                                                                                                                                                       50.38;
72.78;
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                                                                                                                                                                                                                                   Query Match 50.3:
Best Local Similarity 72.7'
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 base pairs
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Best Local Similarity 69.4
Matches 25; Conservative
   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 About
STREET: 925 CITY: Palo Alto
                                                               ; NAME/KEY: CDS
; LOCATION: 96..2036
US-08-678-039A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-102-204-3
                                   FEATURE:
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RESULT 11 US-09-104-308-3

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Sequence 3, Application US/09321981

Patent No. 6287839

GENERAL INFORMATION:
APPLICANT: Genor International, Inc.
TITLE OF INVENTION: No. 6287839e1 Cellulase Producing Actinomycetes,
TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing Same
FILE REFERENCE: GG540-2

CURRENT APPLICATION NUMBER: US/09/321,981

CURRENT FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 09/104,308

PRIOR FILING DATE: 1999-06-24

PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1999-06-34

NUMBER: 08/974,042

NUMBER: OSEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3
                   APPLICANT: Jones, Brian E.
APPLICANT: Van Der Kleij, Wilhelmus A.H.
APPLICANT: Van Solingen, Piet
APPLICANT: Weyler, Walter
TITLE OF INVENTION: No. 6187577el Cellulase Producing Actinomycetes,
TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,308
FILING DATE: 24-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,042
FILING DATE: 19-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 GGCCACACTGGGACTGAGACACGGCCCAGACTCCTA 309
                                                                                                                                                                                                                              ADDRESSEE: Genericar International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: California
CONNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TELEPHONE: 650-846-7555
TELEPAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stone, Christopher L. REGISTRATION NUMBER: 35,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
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Matches 25; Conservative
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                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor
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GENERAL INFORMATION:
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 09/248,528
                     PRIOR APPLICATION NUMBER: 09/:
PRIOR FILING DATE: 1999-02-10
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APPLICANT: Oriel, Patrick J
APPLICANT: Padmakumar, Rugmini
APPLICANT: Rim, Sang H
TITLE OF INVENTION: Method for Producing Amide Compounds Using a Nitrile
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
FILE REFERENCE: MSU 4.1-486
CURRENT APPLICATION NUMBER: 2000-04-13
PRIOR APPLICATION NUMBER: 60/083,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oriel, Patrick J
APPLICANT: Padmakumar, Rugmini
APPLICANT: Rim, Sang H
TITLE OF INVENTION: Method for Producing Amide Compounds Using a Nitrile
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
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LOCATION: (1)..(497)
OTHER INFORMATION: nucleotides 17 - 513 of rRNA sequence
OTHER INFORMATION: X60643/Genbank
                                                                                   ; OTHER INFORMATION: Nearest "neighbor" = Streptomycetes; OTHER INFORMATION: thermovebaceous US-09-321-981-3
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CURRENT APPLICATION NUMBER: US/09/248,528C
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 60/083,485
EARLIER FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: X60643/Genbank
DATABASE ENTRY DATE: 1997-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09248528C Patent No. 6153415
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Patent No. 6214603
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Best Local Similarity 69.4%;
Matches 25; Conservative
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Matches 25; Conservative
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                                TYPE: DNA
ORGANISM: Unknown
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          LENGTH: 463
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APPLICANT: Oriel, Patrick J
APPLICANT: Padmakumar, Rugmini
APPLICANT: Endmakumar, Rugmini
APPLICANT: Rim, Sang H
APPLICANT: Rim, Sang H
TITLE OFINNEWINON: Method for Producing Amide Compounds Using a Nitrile
TITLE OFINNEWINON: Hydratase from a Thermophilic Bacillus
FILE REFERENCE: MSU 4.1.489
CURRENT APPLICATION NUMBER: US/09/549,111
CURRENT APPLICATION NUMBER: 00/04.13
PRIOR APPLICATION NUMBER: 09/248,528
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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LOCATION: (1)...(497)
OTHER INFORMATION: nucleotides 17 - 513 of FRNA sequence
OTHER INFORMATION: X60643/Genbank
PUBLICATION INFORMATION:
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Pred. No. 43;
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                                                                                                                                                                     NAME/KEY: IRNA
LOCATION: (1)..(497)
COTHER INFORMATION: nucleotides 17 - 513 of
OTHER INFORMATION: X60643/Genbank
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: X60643/Genbank
US-09-549-108-4
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US-09-549-111-4
; Sequence 4, Application US/09549111
; Sequence 5, Application US/09549111
; Sequence 5, Application US/09549111
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Best Local Similarity 69.4%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 69.4%;
Matches . 25; Conservative
PRIOR FILING DATE: 1999-02-1
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus smithii
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602650569 601436104 AU088719

602713810 602184126 602525283 60257118 602636421 AL533479 344381 BA 340902 BA AU106135

Anopheles Au106172 Au106177 Au106184

602696375 174173 BA

AU106243 AU106245

Perfect score:

Sequence:

OM nucleic

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Scoring table:

Searched:

Database

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 719)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Micheel J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Location/Qualifiers

Location/Qualifiers

1. 719

Arrafe—Haxon:9606

Alab_Most="NAMGE:487499"

//lab_host="NAMGE:487499"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG721571 719 bp mRNA EST 08-MAY-2001
602695180F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4827499 5',
                                                        BE476868 BG536621 AA102697 BG340457 BG546413 BG751030 BG755440 BF568512
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AL533479 A
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AU106135 A
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AU106245 B
BCB18707 B
BG718363 B
BE486369 A
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BC78369
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BG721571
BG721571.1 GI:14000758
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TITLE
JOURNAL
COMMENT
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BET170215 PCL0440 M
BF806991 QV4-C1015
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BF724208 Dx02b09.7
BG108345 602240354
                                                                                                  Search time 2220.1 Seconds
(without alignments)
179.088 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                     6, 2001, 08:50:16
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Maximum Match 100%
Listing first 45 summaries
                                                                        nucleic search, using sw model
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Maximum DB seq length: 2000000000
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AU106142 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC05779, mRNA sequence.
AU106142
AU106142.1 GI:13555663
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#RC09410, mRNA sequence.
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Pred. No. 4.4;
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69.7%; Score 25.8; D
Best Local Similarity 81.1%; Pred. No. 4.7;
Matches 30; Conservative 0; Mismatches
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/db_xref="taxon:9606"
/clone="HRC05779"
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l Similarity 96.3%;
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S. Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S., Okubo , K., Suyama, A. and Sugano, S. Tructural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries (The Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries (The Structural Size of Virology (Trobia) (Trobia)
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| RS | Claudio,J.O., Tang,H., Khan,E.M., Voralia,M., Li,Z., Cukerman,E., Franciso-Pabalan,O., Liew,C.C. and Stewart,A.K. | The transcriptional phenotype of myeloma cells | Contact: A. Keith Stewart, M.D. | Contact: A. Keith Stewart, M.D. | Oncology Research | Network | GlO University Ave., 5-126, Toronto, Ontario, MSG 2M9, Canada | Tel: (416) 946-4639 | Fax: (416) 946-6546 | Email: K.stewarteutoronto.ca | PCR PRImers | PCR 
                                                                                                                                                                                                                                                                 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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DEFINITION PCL0440 Myeloma (PCL) CDNA library Homo sapiens CDNA, mRNA
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BACKWARD: 5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3'
Seq primer: 5'-GAAATTAACCCTCACTAAAGG-3'
Location/Qualifiers
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Pred. No. 4.4;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone="HRC09410"
/clone="HRC09410"
/clone=lib="Sugano Homo sa
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/db_xref="taxon:9606"
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Best Local Similarity 96.3%;
Matches 126; Conservative
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                                                                                   /cell_type="myelona"
/dev_stage="myelona"
/dev_stage="myelona"
/dev_stage="plasma cell leukemia"
/dev_stage="myelona"
/dev_stage="plasma cell leukemia dev_stage="plasma cell leukemia yestelle"
/dev_stage="myelona"
/dev_
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2-QV4-CI0151-091100-522-h06&t3-2000-11-09&t4-1)
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QV4-CI0151-091100-522-h06 CI0151 Homo sapiens CDNA, mRNA sequence.
BF806991 GI:12135980
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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/clone_lib="Myeloma (PCL) cDNA library"
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Pred. No. 5.
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                                                              /tissue_type="Blood"
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96.3%;
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Best Local Similarity 96.33
Matches 26; Conservative
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LOCUS

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/db_xref="taxon:9606"
/clone="IMAGE:4690512"
/clone="IMAGE:4690512"
/clone="IMAGE:1690512"
/clone="IMAGE:1690512"
/lab host="DHIOB (TI phage-resistant)"
/lab host="DHIOB (TI phage-resistant)"
/note="Organ: lung: Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcaggcc); Site_2: Site (ggccattatggcc); S' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-ACGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCATG-GT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T): Average insert size 1.9
kb (range 0.5-4.0 kb): 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 490)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Onpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM150B row: d column: 01

High quality sequence stop: 462.

ES

Location/Qualifiers
                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="cr01511"
/dov_stage="Adult"
/note="Organ: colon_ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG537751 490 bp mRNA EST 03-APR-2001 602566102F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4690512 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25.4; DB 11;
Pred. No. 5.9;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                           low stringency conditions."
102 c 110 g 51 t
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/organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.3%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG537751
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Matches

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Lower sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 652)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: gapbs:r@mall.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10021 row: k column: 13

High quality sequence stop: 649.
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs:r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG325639 721 bp mRNA EST 27-FEB-2001
602424355F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:4562485 5',
                                     BG108345 652 bp mRNA EST 30-JAN-2001
602280354F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4368132 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25.4; DB 11; Length 652; Pred. No. 6.6;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BG325639
BG325639.1 GI:13132076
                                                                                                                  BG108345
BG108345.1 GI:12602191
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96.3%;
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                                                                                              mRNA sequence.
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Best Local Similarity
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                                                                                                                                                                                           human.
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ORIGIN
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JOURNAL
COMMENT
                                                                   DEFINITION
                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                  REFERENCE AUTHORS TITLE JOURNAL COMMENT
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KEYWORDS
SOURCE
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                      BG108345
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                                                                                                                                              VERSION
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RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Addult"
/lab_host="EMDH10B"
//lab_host="EMDH10B"
//lab_host="EMDH10B"
//lab_host="EMDH10B"
//lab_host="EMDH10B"
//note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
tissue was pooled from 10 individuals ranging in age from
tissue was pooled from 10 individuals ranging in age from
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pcMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the SuperScript Plasmid System
full details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adapter [5'-pGACTAGTTCGCGAGGGGCGCCC(T)15-3'
]. Not I/blunt end inserts were cloned into the Not I/EcoR
V sites in the vector. EST analysis was performed on the
unamplified library at the NIH Intramural Sequencing
Center (NISC)."
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BX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 550)
                                                                                                                                                                                                                                                                                       BF724208 550 bp mRNA EST 05-JAN-22001 bx02b09.yl Human Iris cDNA (Un-normalized, unamplified): BX Homo sapiens cDNA clone bx02b09 5', mRNA sequence.
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                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wistow.G.J., Bernstein,S., Behal,A. and Smith,D.
NEIBANK: EST analysis and bioinformatics for ocular genomics Invest. Optithalmol. Vis. Sci. 41 (2000) In press
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Fax: 301 496 0078
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                      Score 25.4; DB 11; Length 490;
Pred. No. 6.3;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: graeme@helix.nih.gov
Plate: 02 row: b column: 09
Seq primer: MI3RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Iris"
                                                                                                                       11 ggactcagaatctccccagacgccgag 37
                                                                                                                                                   1 GGACTCAGATTCTCCCCAGACGCCGAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="bx02b09"
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BF724208.1 GI:12040117
                        ch 68.6%;
il Similarity 96.3%;
26; Conservative (
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Matches 26; Conservative
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                                                    Best Local Similarity
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                             Query Match
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source

FEATURES

BASE COUNT

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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

DEFINITION

RESULT BF724208

ACCESSION

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Gaps

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Indels

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us-09-673-795-3.rst

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AL549560
AL549560.1 GI:12885667
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AL537221
AL537221.1 GI:12800714
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96.3%;
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Best Local Similarity 96.3
Matches 26; Conservative
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AUTHORS
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VERSION
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AL537221
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                                                                                                                                                                                                                                                                         / Organism="Homo sapiens"
// Laxon:9606"
// Laxon:1008
// Laxon:
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/clone="IMAGE:4360404"
/clone=lib="NIH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 761)
NIH-MCC http://mgc.ncl.nih.gov/.
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Contact: Robert Strausberg, Ph.D.
Email: Gapbs.rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML274 row: m column: 14
High quality sequence stop: 714.
Location/Qualifiers
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 6.7;
0; Mismatches 1; Indels 0
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Location/Qualifiers
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96.38;
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Matches 26; Conservative
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BF969741
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COMMENT
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/u.each="taxon:9606"
/db_xref="taxon:9606"
/clone=icsDl0144fP01"
/clone=ilb="TITINELO6_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/fotce="vector: pcwvsporT 6; Site_1: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcwvsporT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filangeliletech.com URL : http://fullength.invitrogen.com"
61 a 251 c 270 g 119 t nothers
primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

251 c 255 g 107 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL537221 891 bp mRNA EST 13-FEB-2001 AL537221 LTI_FL013_FBrn1 Homo sapiens cDNA clone CSODF019YC10 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL549560 802 bp mRNA EST 16-FEB-2001
AL549560 LTI_NFLO06_PL2 Homo sapiens cDNA clone CSODI044YP01 5
prime, mRNA sequence.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                        Length 763;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Oppublished (2001)
                                                                                                                                                                                                                  Query Match 68.6%; Score 25.4; DB 11;
Best Local Similarity 96.3%; Pred. No. 6.8;
Matches 26; Conservative 0; Mismatches 1;
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Pred. No. 6.8;
0; Mismatches 1;
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/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="blu10B (phage-resistant)"
/lab_host="blu10B (phage-resistant)"
/note="Grgan: prostate; Vector: pOTB7; Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhol sites using the following 5' adaptor: GGCAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

88 a 304 c 322 g 148 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE894912 1139 bp mRNA EST 20-OCT-2000 601436104F1 NIH_MGC_72 Homo sapiens CDNA clone IMAGE:3921072 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1139)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.htcolumn: 01
Plate: LLAM9753 row: h column: 01
High quality sequence stop: 432.
Location/Qualifiers
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Pred. No. 7.2;
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/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                        /clone="IMAGE:4761328"
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96.38;
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Best Local Similarity
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                             /clone="CSODFOLDYCIO"
/clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note--Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the
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                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 891)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Thanil: cgapbs-r@mail.nih.gov
Thanil: cgapbs-r@mail.nih.gov
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602650569F1 NIH_MGC_40 Homo saplens cDNA clone IMAGE:4761328 5'
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
http://image.lnl.gov
http://image.lnl.gov
High quality sequence stop: 837.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Pred. No. 6.9;
0; Mismatches 1; Indels 0
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/db_xref="taxon:9606"
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96.38;
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ORGANISM
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KEYWORDS
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KEYWORDS
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Oryza sativa.

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Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; Ehrhartoideae; Oryzeae; Oryza.

El (bases 1 to 486)

Sasaki.T. and Yamamonto.K.

Rice cDNA from etiolated shoot (2000)

Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Stree Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = KGP.

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/organism="Oryza sativa"
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/db_xref="taxon:4530"
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AX012956 Sequence Description

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AX012956 Sequence M24048 Chimpanzee M24044 Chimpanzee X13116 Chimpanzee X13116 Chimpanzee X13116 Chimpanzee M307679 Pan troglod AR073931 Sequence G07078 human STS W Z22651 H. Sapiens H L42345 Homo Sapien X3435 H. Sapiens M X60253 G. gorrilla M AF157406 Gorrilla M AF1574045 Homo Sapien AF157317 Homo Sapien AF150937 Homo Sapien AF150937 Homo Sapien AF150937 Homo Sapien AF1501557 Homo Sapien AF1501557 Homo Sapien AF1501657	PAT 07-SEP-2000  Vertebrata; Euteleostomi; ; Hominidae; Homo. hsp70, useful in cancer NE (FR); TRIEBEL FREDERIC
AX012956 CHPMHCAE CHPMHCAE CHPMHCAB AR075099 G07078 HSHLAB5A HSHLAB5A HUMHLAB44A- HSHLAB7X GGB0201 HUMMHBAAA HUMHBABAB HUMHBABA HUMHBABAB AY07140 HUMHBBAB AY07140 HUMHBBAB AY07140 HSA29439 HSA29439 HSA29439 HSA29439 HSA29439 HSA29439 HSA29439 HSA30936	PA444.  Craniata; Ve; Catarrhini; crived from hs T-1999; UDIN CATHERINE
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Barham,P., Lawlor,D.A., Lomen,C.E. and Ennis,P.D.

Diversity and diversification of HLA class I alleles
J. Immunol. 142, 3937-3950 (1989)

By 25215

Draft entry and computer-readable sequence for [1] kindly submitted by P.D.Ennis, 14-APR-1989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="VWPDSDAASPRKEPRTPWIEQEGPEYWDRETQISKTNAQTYRVG
LRNLLEXYNOSEAGSHTWQTWFGCDVGPDGRLLRGYRQYAYDGKDYIALNQDLSSWTA
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ISDHEATLRCWALLGFYPAETILTWQRDGEDQTQDTELVETRAGDRTFQKWAAVVVPS
GEEQRYTCHVQHEGLPKPLTLRWEPSSQSTIPIVGIVAGLAVAAVWCR
RKSSGRGGSYSQAASSDSAQGSDYSTTA"
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cell surface antigen; cell surface glycoprotein; class I gene;
lntegral membrane protein; major histocompatibility complex.
Chimpanzee (Tank) EBV-transformed B lymphoblastoid cell, cDNA to
                                                                                                                                                                                                                                                        complete cds, clone 18
                                                                                                                 Gaps
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RESLANLRGYYNOSEAGSHIIORWYGCDMGPDGRLLRGYEGYYOKBYIALNQDLSS
WTAADTAAQ!TQRKWEAARWABQLRALLGGTVCWARLRRYLEGYRYERYGKHYTHIPISDHEATLRGWALGFYPREITTRWABCLRALLGGTVGTVGTGTVGTRYFRAGDRTFQKWAAVV
VPSGEEQRYTCHVQHEGLPKPLILRWEPSSQSTIPIVGIVAGLAVTRGAVAAV
MCRKKSGGGGGGGSYSQAASSDSAQGSVVLTA"
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untegral membrane protein; major histocompatibility complex.
Chimpanzee (Kasey) EBV transformed B lymphoblastoid cell, cDNA to
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                                                                                    Pan troglodytes
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 929; 930 to 1359)
Parham, P., Lawlor, D. A., Lomen, C.E. and Ennis, P.D.
Diversity and diversification of HLA class I alleles
J. Immurol. 142, 3937-3950 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-FEB-1989) to the EMBL/GenBank/DDBJ databases Position 617 is c in [1], [3] and u in [2].
                                                                                                                                                                                                                                                                                                              Computer-readable copy of sequence [1] kindly submitted P.D.Ennis 14-APR-1989.
Location/Qualifiers
1. -1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1359;
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                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pan troglodytes"/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. .1359
/product="MHC Chla mRNA"
<1. .929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        970 PCTGCATCTCAGTCCCTCACAGACAGCTGTC 939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MHC ChlA chain"
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/protein_id="AAA87971.1"
/db_xref="GI:176825"
/translation="MQVTAPRTVLLLLSAALALTETWAGSHSMKYFYTAVSRPGRGEP
                                                                                                                                                                                                                                          RNLRGYYNQSEAGSHIIQRMYGCDMGPDGRLLRGYEQYAYDGKDYIALNQDLSSWTAA
                                                                                                                                                                                                                                                          DTAAQITQRKWEAARWAEQLRAYLEGTCVEWLRRYLENGKETLQRADPPKTHVTHHPI
SDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVPSG
EEQRYTCHVQHEGLPKPLTLRWEPSSQSTIPIVGIVAGLAVLAVVVIGAVVAAVWGRR
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1 (bases 1 to 39)
van der Bruggen, P., Mandruzzato, S. and Boon-Falleur, T.
Isolated cytolytic T cells which are specific for complexes OF HLA-
B35 molecules and the peptide PHE Pro Ser Asp Ser Trp Cys Tyr PHE,
and uses thereof
Patent: US 5952228-A 4 14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                         RFISVGYVDDTQFVWFDSDAASPREEPRAPWIEQEGPEYWDRETQISKTNAQTYRESL
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                                                                                                                                                                                                                                                                                                                       73. .1086
/note="MHC class I protein mature peptide"
74. .343
                                                                  'note="MHC class I protein signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27.2; DB Pred. No. 0.11;
              /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                     1. .1089
/note="MHC class I protein"
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Sequence 4 from patent US 5952228.
AR073931
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15 c 7 a
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                                                                                                                                                          /codon_start=1
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/number=5
1013. .1045
/number=6
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435 c
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90.6%;
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Best Local Similarity 83.3%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1046. .1093
/number=7
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/number=2
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/number=3
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/number=4
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Best Local Similarity
Matches 29; Conserv
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BASE COUNT 328
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                                                  sig_peptide
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TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                               SDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVPSG
EEQRYTCHVQHEGLPKPLTLRWEPSSQSTIPIVGIVAGLAVLAVVVIGAVVAAVWCRR
KSSGGKGGSYSQAASSDSAQGSDVSLTA"
                                                                                                                                                                                                                                                                          /translation="MQVTAPRTVLLLSAALALTETWAGSHSMKVFYTAVSRPGRGEP
RFISVGYVDDTQFVWFDSDAASPREEPRAPWIEQEGPEYWDRETQISKTNAQTYRESL
                                                                                                                                                                                                                                                                                                            RNLRGYYNQSEAGSHIIQRMYGCDMGPDGRLLRGYEQYAYDGKDYIALNEDLSSWTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein surface antigen; cell surface glycoprotein; integral membrane protein; major histocompatibility complex.

P. troglodytes male B-cell (cell line Colin) cDNA to mRNA.

Bun troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

I (bases 1 to 1517)

Lawlor, D.A., Warren, E., Ward, F.E. and Parham, P.

Comparison of class I MHC alleles in humans and apes

10201944
                                                                                                                                                                                                                                                                                                                                DTAAQITQRKWEAARWAEQLRAYLEGTCVEWLRRYLENGKETLQRADPPKTHVTHHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Authorin copy of sequence [Immunol. Rev. (1990) In press] kindly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                       to 338)"
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                                                                                                                                                                                                                                                                                                                                                                                                                     /product="ChLA-B2 mature protein (AA 1-338)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHPMHCBAB 1517 bp mRNA PRI 16
Pan troglodytes MHC class I protein mRNA (MHCPATRB5)
M30679
                                                                                                                                                   /product="leader peptide (AA -24 to -1)"
1. 1089
/note="ChLA-B2 protein precursor (AA -24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195. .101i
/note="transmembrane domain"
                                                                                                                                                                                                                                                        db_xref-"SWISS-PROT:P13751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27.2; DB Pred. No. 0.11;
                              /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1012. 1086
/note="cytoplasmic domain"
1495. 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1130 TCTGCATCTCAGTCCCTCACAAGACAGCTGTC 1099
                                                                               /tissue_type="lymphocyte"
/cell_line="Hugo-EBV"
/clone="p2B2."
                                                                                                                                                                                                                        /protein_id="CAA31508.1"
/db_xref="G1:38209"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343. .618
/note="alpha-2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="alpha-3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="alpha-1 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note-"polyA signal"
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="polyA site"
433 c 449 g
                                                                  /chromosome="5
                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.6%;
90.6%;
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Matches 29; Conservative
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CHPMHCBAB/C
                  source
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ORIGIN
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VERSION
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TITLE
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FEATURES
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Direct Submission
Submitted (27-APR-1993) Steinle A., University of Munich, Institute
of Immunology, Goethestrasse 31, W-8000 MUENCHEN 2, GERWANY
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Steinle-A., Reinhardt,C., Nossner,E., Uchanska-Ziegler,B., Ziegler,A. and Schendel,D.J.
Mcroheterogeneity in HiA-B35 alleles influences peptide-dependent allorecognition by cytotoxic T cells but not binding of a peptide-restricted monoclonal antibody Hum. Immunol. 38 (4), 261-269 (1993)
2 (bases 1 to 1270)
Steinle,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /germline
/haple="A24 Cw4 B35 DR3 DGw2, A2 Cw6 B13 DR7 DGw2"
/clone="Ty4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-1994
                                                                                                                                                                                                                                                 Prepared with primer pairs derived from M12678 -- Unigene. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="lymphoblastoid B-cell line"
1. .1089
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;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26.2; DB 11;
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="HLA-B35"
/function="peptide presentation"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                   ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
179. 293
179. 196
complement(274. 293)
a 104 c 94 g 126
                                              Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/isolate="TL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ctagateteagteecteacaaggeagetgte 36
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/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSHLA35A 1270 bp
H.sapiens HLA-B35 mRNA.
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                              72.8%;
90.3%;
                                                                                                                                                Buffer:
MGC12: 1.5 mM
KC1: 50 mM
Tris-HC: 10 mM
PH: 9.3
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222651.1 GI:297142
HLA-B35.
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Best Local Similarity 90.3:
Matches 28; Conservative
                                                                                                                                                                                                                                                                               .427
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                                    Protocol:
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                                                                                                                                                                                                             Unknown.
Unknown.
Unclassified.
Unclassified.
I (bases 1 to 39)
Van der Bruggen, P., Mandruzzato, S. and Boon-Falleur, T.
Nucleic acid molecule encoding a bifunctional protein, the protein
so encoded uses thereof
Patent: US 595313-A 4 21-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eutaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Ostelchithyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                                             28-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.3%; Score 26.4; DB 6; Length 39; Best Local Similarity 83.3%; Pred. No. 0.34; Matches 30; Conservative 0; Mismatches 6; Indels
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Whitehead Institute for Biomedical Research
Verbridge Center, Cambridge MA 02142 USA
191: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu
                                                                                                                           PAT
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                      1 gccctctagatctcagtccctcacaaggcagctgtc 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR075099 39 bp DNA
Sequence 4 from patent US 5955313.
AR075099
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Primer B: AGAGTTGCAGCTCAGTGCA
STS size: 115
PCR Profile:
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Polymerization:
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human STS WI-9014.
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HSHLAB27X/C
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            /product="HLA-B35 variant"
/product="HLA-B35 variant"
/protein_id="CAA80366.1"
/db_xref="G1:297143"
/db_xref="SWISS-PROT:P30474"
/db_xref="SWISS-PROT:PROT!PARTEVELELMGAVALTETWAGSHSMRYFYTAMSRPGRGEP
//LTANS1ation="MRYTAPRTVLLLLMGAVALTETWAGSHSMRYFYTAMSRPGRGEP
RFIAVGYVDDTQFVRFDSDAASPRTEPRAPWIEQEGPEYWDRNTQIFKTNTQTYRESL
RNLRGYYNQSEAGSHIIQRWYGCDLGPDGRLLRGHDQSAXDGKDYIALNEDLSSWTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RETAVGYVDDTQEVREDSDAASPRTEPRAPWIEQEGPEYWDRWTQIFKTNTQTYREUL
RIALRYYNQEBAGSHIIQRWTGCDVGPDGRLLRGYDQDAYDGKDYIALNEDLSSWTAA
DTAAQITQRKWEBARVAEQDRAYLEGICVESILRYLENGKETLQRADPRYHWTHHPI
SDHEYTLRCWALGFYPAELTLTWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVPSG
EEQRYTCHVQHEGLPKRLJLIWEPSSQSTVPIVGIVAGLAVLAVVIGAVVARWRR
KSSGGKGGSYSQAACSDSAQGSDVSLTA"
                                                                                                                                       DTAAQITQRKWEAARVAEQRRAYLEGICVEWILRRYLENGKETLORADPPKTHVTHHPV
SUBEATLEGRALGFPPALITLIWQRGGEDQTQDTELVETRPAGDRTFQKWAAVVVPSG
EEQRYTCHVQHEGLEKPLILEWEDSSQSTIPIVGIVAGLAVLAVVVIGAVVATVMCRR
KSSGGKGGSYSQAASDSAQGSDVSLTA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( hases 1 to 1270)

Zhao, W., Fernandez-Vina, M.A. and Stastny, P.

Novel HiA-B allele part B*5101 and part B*4402

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMHLAB44A 1270 bp mRNA PRI 18-JAN-1996
Homo sapiens lymphocyte antigen HLA-B*4402 and HLA-B*5101 mRNA,
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Pred. No. 0.32;
0; Mismatches 3;
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/protein_id="AAB59610.1"
/db_xref="GI:1160934"
                                                                                                                                                                                                                                                                                 /product="HLA-B35 variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .72
73. .1086
/standard_name="HLA-B35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="leukocyte"
                                                                                                                                                                                                                                                                     /evidence=experimental
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/gene="HLA-B*4402"
/replace="tgca"
141. .311
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Homo sapiens cDNA to mRNA.
Homo sapiens
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90.3%;
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/number=2
                                                                                                                                                                                                                                                                                                                      388 c
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Best Local Similarity 90.39
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1272)
Del Porto, P. D'Amato, M., Fiorillo, M.T., Tuosto, L., Piccolella, E. and Sorrentino, R.
Identification of a novel HLA-B27 subtype by restriction analysis of a cytotoxic gamma delta T cell clone
J. Immurol. 153 (7), 3093-3100 (1994)
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Direct Submission
Submitted (10-MAY-1994) D'Amato M., Institute of Cell Biology-CNR, Immunobiology, Viale Marx 43, Rome, Italy, 00143
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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233453
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HLA-B27 antigen; human leukocyte antigen.
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/isolate="Ci"
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309. .311
/gene="HLA-B*4402"
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/gene="HLA-B*4402"
165. .167
/qene="HLA-B*4402"
                                                                /gene="HLA-B*4402"
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                                                                                                                                                                                                                                                                                                                                                /replace="gat"
344. .619
/number=3
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                                  /replace="cca'
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Best Local Similarity 90.3%;
Matches 28; Conservative (
                                                                                    /replace="g"
206
                                                                                                                                    /replace="c"
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/number=5
1013. .1045
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/number=4
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1046. .108
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/translation="WOYTAPRTLILLISAALALTETWAGSHSMRYFHTAMSRPGRGEP
RFITYGYVDDTQFVWFDSDAASPRKEPRTPWIEQEGPEYWDRETQISKTNTOTYRVGL
GTLRGYYNQSEDGSHTIQRWYGCDMGPDGRLIRGYSQLAYDGKDYLALNEDLSSWTAA
                                                                                                                                                       DTAAQITQRKWEAARAAEQERAYLEGLCVEWIRRYLENGKETLORADPPKTHYHHPI
SDHRATLRCWALGRYPAEITLTWORDGEDQTQDTELVETRPAGDRTFOKWAAVVVPSG
EEQRYTCRVQHEGLPEPLTLRWEPSSQSTIPIVGIVAGLAVLVVTVAVVAVVAAVWCR
RKSSGGKGGSYSQAASSDSAQGSDVSLTA"
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Gorilla gorilla MHC class I heavy chain antigen (Gogo-B) mRNA,
Gogo-B*0301 allele, complete cds.
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/db_xref="G1:22872"
/db_xref="SNISS-PROT:P30382"
                                                                                                                                                                                                                                                                                                      chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26.2; DB Pred. No. 0.32;
                                                                                                                                                                                                                                                /gene="MhcGogo-B0201"
73. 1089
/gene="MhcGogo-B0201"
/product="Mhc class I heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           620. .895
/gene="MhcGogo-B0201"
/note="alpha 3"
                                                                                                                                                                                                                                                                                                                         74. .343
/gene="MhcGogo-B0201"
/note="alpha 1"
                                                                                                                                                                                                                                                                                                                                                                                         344. .619
/gene="MhcGogo-B0201"
/note="alpha 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1016. .1048
/gene="MhcGogo-B0201"
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/gene="MhcGogo-B0201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="cytoplasmic 1"
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/gene="MhcGogo-B0201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="cytoplasmic 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="transmembrane"
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387 c
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90.3%;
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1049. .10
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Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gorilla.
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                                                                                                                                                                                                                                       sig_peptide
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AF157406/c
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BASE COUNT
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                                                                                                                                                                                                                                       /db_xref="SPTEMBL:029846"
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DTAAQITQRKWEAARYAEQIRAYLEGECVEWLRRYLENGKETLQRADPFKTHYTHPI
SDHBATLKCKWALGFYPAETITTWQRDGEDQTQDTELVETRPAGDRFFGWAAVVVPSG
EDRAYTCHVQHEGLERELIAWEPSSGSTVPIVGIVAGLAVLAVVVIGAVVAAVWCRR
KSSGGKGGSYSQAACSDSAQGSDVSLTA"
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B locus allele; Class I major histocompatibility gene; heavy chain;
major histocompatibility gene; peptide binding protein;
transplantation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
1 (bases 1 to 1273)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-JUN-1991) D.A. Lawlor, Stanford Univ School of Medicine, Dept of Cell Biology, Stanford Ca 94305, USA 2 (bases 1 to 1092)
Lawlor, D.A., Warren, E., Taylor, P. and Parham, P. comparison to human and chimpanzee class I and or himpanzee class I berry, Med. 174 (6), 1491-1509 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGB0201 1273 bp mRNA PRI 07-FEB-
G.gorilla MhcGogo-B0201 gene for Mhc class I heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/cell_line="0ko B lymphoblastoid cell line"
/clone_lib="0KB192"
                                                                                                                                                                                       /product-"human lymphocyte antigen HLA-B27"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26.2; DB 9;
Pred. No. 0.32;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="MhcGogo-B0201"
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                                                                                                     /tissue_type="blood"
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/cell_line="Ci"
2. 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                       /dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /isolate="Oko"
                                                                     /clone="M13Ci"
                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.8%;
90.3%;
                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.8
Best Local Similarity 90.3
Matches 28; Conservative
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Gorilla gorilla
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LOCUS
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FEATURES
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KEYWORDS

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RESULT

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TITLE

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'qene="HLA-A"
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Best Local Similarity 90.3
Matches 28; Conservative
                      . 903
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                                                                                                                                                                                                                                                                                                                                                                                                         /product_"MHC class I heavy chain antigen"
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/dbrotein_id="RAF80149.1"
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SDHEATLECWALGFYPAETTLTWQRGCEDOTQDTELVETRPAGDRTFOKWAAVVVPSG
EEQRYTCRVQHEGLPEPLTLRWEPSSQSTIPIVGIVAGLAVLVVTVAVVAVVAVVAVVACR
RKSSGGKGGGSGSQASSDSAQGSDVSLTA"
                                                                                            Divater, J.A. and Watkins, D.I.
Direct Submission
Submitted (09-JUN-1999) Wisconsin Regional Primate Research Center,
University of Wisconsin-Madison, 1220 Capitol Court, Madison, WI
Gorillas with Spondyloarthropathies Express an MHC Class I Molecule with Only Limited Sequence Similarity to HLA-B27 that Binds Peptides with Arginine at P2
J. Immunol. 166 (5), 3334-3344 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arnot, D., Lillie, J.\dot{w}, Auffray, C., Kappes, D. and Strominger, J.L. Inter-locus and intra-allelic polymorphisms of HLA class I antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMMHBIAW3 1323 bp mRNA PRI 07-JAN-1995 Human MHC class I HLA-A (A28,-B40,-Cw3) cell surface antigen mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell surface antigen; cell surface glycoprotein; class I gene; integral membrane protein; major histocompatibility complex. Homo sapiens cDNA to mRNA.
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Pred. No. 0.32;
); Mismatches 3;
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    1273
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    /db_xref="taxon:9593"

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/cell_line="lymphoblastoid"
/map="6p21.3"
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                                                                                                                                                                                                                                                                                                                                /allele="Gogo-B*0301"
                                                                                                                                                                                                                   Location/Qualifiers
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/note="G00-119-310"
1. .1323
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M27540
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90.3%;
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Best Local Similarity
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HUMMHBIAW3/c
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RFISVGYVDDTQFYCKTORDSDAASPREBERAPWIEQEGPEYWDRNTGICKTUTGEBER RRLEGYYNDDTQFYCKTUTGDAASPREBERAPWIEQEGPEYWDRNTGICKTUTGTBESL RNLRGYYNGSBAGSHFWQTWYGCDVGPDGRLLRGHNOFAYDGKDYTALNEDLSSWTAA DTAAQITQRKWEAARVAEQLRTYLEGTCVEWLRRYLENGKETLQRADPPKTHVTHPI SDHEATLRCWALGFYPAEITLWQRDGEDQTQDTELVETRPAGDRTFQKWAANVVPSG EEQRYTCHVQHEGLFRPLTRWEPSSQSTVPIVGIVAGLAVVVIGAVVAAVWCRR KSSGGRGSYSQAASSDSAQGSDVSLTA"
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GYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHDQYAYDGKDY IALNEDLRSWTAADTAA
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ATLTQKWALGAYPAEITLTWQRDGEDOTQDTELVETRPAGDRTFQKWAAVVPSGEEQR
YTCHVQHEGLRKPLTEWBESSOSTVPIVGIVAGAVAAVWCRRKSSG
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Catarrhini; Hominidae; Homo.
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B*39011 allele; HLA-B39; cell surface antigen; cell surface glycoprotein; class I gene; integral membrane protein; major histocompatibility complex.
Homo sapiens (individual_isolate H.A.A.) cDNA to mRNA.
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/protein_id="AAB59484.1"
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Full cDNA sequence of a novel HLA-B39 variant
Unpublished (1995)
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Homo sapiens MHC HLA-B39 mRNA, complete cds.
L42024
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Pred. No. 0.32;
0; Mismatches
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1. .160
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Mammalia, Eutheria, Primates,
1 (bases 1 to 1357)
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88. .1176
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Gaps

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Search completed: December 6, 2001, 09:57:30 Job time: 4034 sec

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Human polynucleoti
Human polynucleoti
Sequence of genomi
pHLA-B7 expression
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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36
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			-	. Human polynucleot	Human polynucleot	Human EST-derived	Human oligonucleot	Human HLA-G gene e	Human HLA-G gene e	HLA-G 3-5 from whi	Human HLA-G gene D	gene	Human HLA-G gene I	Human HLA-G gene	Human secreted pro	Human gene signatu	Human bone marrow	Human biallelic po	Human sulfonylurea	Human ORFX ORF183	Castor bean calret	cDNA encoding mur	Mouse MT4-MMP (2)	Human cDNA sequenc	BAC containing rep	Primer for amplify	Lung cancer associ	DNA encoding human	Aspergillus oryzae	Human olfactory re		Clone 16467945.0.8
AAC07491 AAH02916	AAI63974	AAI63975	AAT20964	AAI61063	AAI59277	AAH98676	AAZ25761	AAZ25752	AAZ25751	AAT03428	AAZ25757	AAZ25758	AAZ25755	AAZ25756	AAC79821	AAT24989	AAH89966	AAX12144	AAA76194	AAC74628	AAF29743	AAA14339	AAA13378	AAH18414	AAF22287	AAA47587	AAF18009	AAS09957	AAF12553	AAH31904	AAH31616	AAF74495
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69.4 69.4	φ.		٠					57.8							55.6	54.4				•	53.3	53.3	53.3	53.3	53.3	52.8	52.8	52.8	52.8	52.8	52.8	52.8
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## ALIGNMENTS

RESULT

Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen; PCR; primer; amplification; ss. Human HLA allele amplification primer 3P2-X. BP. AAZ22706 standard; DNA; 36 (first entry) 15-FEB-2000 AAZ22706; AAZ22706 

Homo sapiens Synthetic.

WO9954464-A1

28-OCT-1999

99WO-FR00957 98FR-0005033 22-APR-1999;

22-APR-1998;

(INSR ) INST ROUSSY GUSTAVE

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Triebel F, Gaudin C;

WPI; 2000-013251/01.

Identifying mutant peptides from heat-shock protein 70, for treatment

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has The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response (e.g. AAV44199 and AAV4200). Identification of the hsp70 peptides that have at least cone mutation or alteration compared with the native sequence, and induce tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, that induces cellular stress, are used for treatment of cancer. The peptides may also be used to increase the proportion of tumour-specific cytocoxic T lymphocytes in a cell culture and/or induce these cells to secrete cytotoxic factors (specifically interleukin-2, interferon-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HiA (human leucocyte antique) allels. The primars AAZ22706 were used to PCR amplify
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 36; DB 21; Best Local Similarity 100.0%; Pred. No. 2.2e-06; Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA alleles for the method of the invention
                                                              Example 7; Page 24; 56pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV21517 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-1997;
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of cancer
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 AAV21517

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; proliferative disorder; cancer; tumour; foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; pregnancy-related disorder; endoctine disorder; infection; wound healing; vulnerary; cell culture; chemoctaxis; food additive; gene therapy; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                         Gaps
        This antisense primer and a sense primer (see AAV21516) were designed for the PCR amplification of HLA-B35 cDNA. The PCR product was cloned into PCDNA3, and used with plasmids containing DNA from BB49-SCCHN head and neck squamous cell carcinoma cells to cotransfect COS-7 cells. Transfectants were tested to determine if they could stimulate tumour necrosis factor production by CTL clones 328a/69 and 328a/121. A 2649 bp cDNA clone (see AAV21515) was obtained that codes for a novel tumour rejection antigen precursor that is processed to an antigenic peptide (see AAW5127) that can be used to develop products for the diagnosis and trearment of conditions characterised by HLA-B35 positive cells,
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/note= "Xaa equals any of the naturally occurring
L-amino acids"
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0
                                                                                                                                                                                                                                                                                   Score 26.4; DB 19; Length 39;
Pred. No. 0.028;
0; Mismatches 6; Indels
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pos:89..91, aa:Xaa)
pos:104..106, aa:Xaa)
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(pos:269..271, aa:xaa)
(pos:275..277, aa:xaa)
(pos:323..325, aa:xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (pos:338..340, aa:Xaa)
(pos:347..349, aa:Xaa)
(pos:386..388, aa:Xaa)
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..514, aa:Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pos:113..115, aa:Xaa
                                                                                                                                                                                                                                   Sequence 39 BP; 8 A; 15 C; 7 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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/transl_except= (pos:89
/transl_except= (pos:10
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/transl_except= (i
/transl_except= (i
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                                                                                                                                                                                                                                                                                   73.3%;
83.3%;
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119..517
/*tag= c
                                                                                                                                                                                                                                                                                                                     30; Conservative
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Best Local Similarity
                                                                                                                                                                                                    e.g. tumours.
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Human polynucleotide SEQ ID NO 352.
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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                                                                                                                                              Homo sapiens.
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01-SEP-2000;
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                                                                                                                                                                                                      02-AUG-2001
 The genes and their secreted protein rangments or variants.

The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in so angule or by determining the presence of mutations in the new genes. Specific uses are described for each of the 50 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental aborders, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rhematoid arthritis), inflammation, allergies, neurological disorders, eig., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, allergies, neurological disorders, schizophrenia, asthma, allergies, nadiofections. The proteins can also be used to ald wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleyateling symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked in manners associated with the disorders mentioned above, and contracted and additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleyateling symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked in manners.
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                                                                                                                                                                                                                                                                                                                                   AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein genes and AAE03898-AAE03947 represent the proteins they encode. AAE03948-AAE03996 represent human secreted protein fragments or variants.
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                                                                                                                                                                                                                                            Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1441;
/product= "Mature human secreted protein"
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                                                                                                                                                                                                                                                                            disease, botulism, cancers and Scimitar syndrome
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Pred. No. 0.065;
0; Mismatches
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                                                                                                                                                                                                                                                                                                         Claim 1; Page 513; 614pp; English.
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                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                99US-0138629.
                                                                                   01-JUN-2000; 2000WO-US15136
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Matches 28; Conservative
                                                                                                                                                                         Rosen CA, Ruben SM,
                                                                                                                                                                                                     2001-367020/38
                                                                                                                                                                                                                  P-PSDB; AAE03930
                           WO200077022-A1.
                                                                                                                11-JUN-1999;
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Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; antibacterial; Virucide; fundicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiallergic; hepatotropic; antidiabetic; antibacterive; antiuneer; vulherargy; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiavastic; neurological disease; infection; human; ds.
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2000US-0246611.
2000US-0246613.
2000US-0249207.
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2000US-0239937.
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2000US-0256719
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                                                                     14 · SEP - 2000;
21 · SEP - 2000;
21 · SEP - 2000;
25 · SEP - 2000;
26 · SEP - 2000;
27 · SEP - 2000;
29 · SEP - 2000;
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20-oct-2000;
20-oct-2000;
20-oct-2000;
20-oct-2000;
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20-oct-2000;
20-oct-2000;
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08-NOV-2000;
08-NOV-2000;
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05-DEC-2000;
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13-OCT-2000;
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02-OCT-2000;
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08-NOV-2000;
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08-NOV-2000;
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The invention relates to human polynuclectides (AAIG3803-AAI64012) and the encoded proteins (AAM43497-AAM4360) useful for preventing, treating cor ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, c. g., breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thirroiditis, diabetes mellitus, conting disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

CNOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly con my mypo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antilnflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                            New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.8%; Score 26.2; DB 22; Length 3357; 90.3%; Pred. No. 0.075;
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 352; 664pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3357 BP; 647 A; 949 C; 1036 G; 725 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                                              Barash SC, Ruben SM
                   2000US-0251856.
2000US-0251868.
2000US-0251869.
                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
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                                                                           08-DEC-2000; 20000S-0251989.
08-DEC-2000; 20000S-0251990.
11-DEC-2000; 20000S-0254097.
05-JAN-2001; 20010S-0259678.
2000US-0251479
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                                                                                                                                                                                                                                                                       WPI; 2001-488781/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 28; Conserv
                   08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                Rosen CA,
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AA163981/c
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WO200155308-A2

Homo sapiens.

PR 29-SEP-2000; 2000US-0236368.  PR 29-SEP-2000; 2000US-0236369.  PR 02-CCT-2000; 2000US-0237037.  PR 02-CCT-2000; 2000US-0237037.  PR 02-CCT-2000; 2000US-0237037.  PR 02-CCT-2000; 2000US-0239937.  PR 13-CCT-2000; 2000US-0239937.  PR 20-CCT-2000; 2000US-0241785.  PR 20-CCT-2000; 2000US-0241809.  PR 20-CCT-2000; 2000US-0241809.  PR 20-CCT-2000; 2000US-0241809.  PR 20-CCT-2000; 2000US-0241809.  PR 20-CCT-2000; 2000US-0246674.  PR 20-CCT-2000; 2000US-0246679.  PR 20-CCT-2000; 2000US-0246679.  PR 20-CCT-2000; 2000US-024652.  PR 20-CCT-2000; 2000US-024929.  PR 20-CCT-2000; 2000US-02492	WPI; 2001-488781/53.
40-US01309 18-US01309 18-O180628 18-O180628 18-O186464 18-O186480 18-O2186350 18-O2186350 18-O2186350 18-O2186350 18-O2186360 18-O2186360 18-O218630 18-O218630 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O225266 18-O223286 18-O223286 18-O233286 18-O233286 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233386 18-O233428	3-023
7. JAN-2001. 2001WO  8. 31-JAN-2001. 2001WO  8. 44-FEB-2000. 2000US  8. 44-AR-2000. 2000US  8. 15-MAR-2000. 2000US  8. 16-MAR-2000. 2000US  9. 17-JUN-2000. 2000US  9. 18-JUN-2000. 2000US  9. 18-JUN-	29-SEP-2000; 29-SEP-2000;
C X F X X X X X X X X X X X X X X X X X	2 2

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The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes ware isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antigaonists or useful in the diagnosis, treatment and prevention of: (a) cancer, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, cutoimmune haemolytic anamia, autoimmune thyroiditis, diabetes mellitus, collitis; (c) cardiovascular disorders such as myocardial ischemenias; (c) mutiple sclerosis, rheumatoid arthritis and ulcerative (c) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.

CC on the sequence data for this patent did not form part of the correct or true was obtained in electronic format directly and from WIPO at ffp. Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
               New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of genomic DNA encoding human histocompatibility antigen
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Length 3357;
                                                             Disclosure; SEQ ID NO 353; 664pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ankylosing spondylitis; rheumatic disorder; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3357 BP; 645 A; 947 C; 1035 G; 730 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.8%; Score 26.2; DB 22;
90.3%; Pred. No. 0.075;
itive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ctagatctcagtccctcacaaggcagctgtc 36
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518..590
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Best Local Similarity 90.39
Watches 28; Conservative
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THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, e.g. for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /.cap. ...
/note= "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
Tn903"
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                     DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "pBR322 backbone contg. bacterial origin of
                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                              Meo T, Riethmuller G;
                                                                                                                                                                                                                                                                                                                  72.8%; Score 26.2; DB 8; Length 3874; 90.3%; Pred. No. 0.077; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                          Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region of HLA-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/note= "SV40 polyA signal sequence"
complement (1412..1560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "HLA-B7 open reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "SV40 small t intron"
complement (1561..1794)
                                                                                                                                                                                                                                                                                                                                                                             3272 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 3242
                                                                              Lang M,
                                                                                                                                                                                                                                                                                                                                                                6 ctagatctcagtccctcacaaggcagctgtc 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chain mRNA" complement (1795..2880)
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/note= "3' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (1410..1177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..354
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replication"
355..1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                        Szots H, Weiss E, Dorner C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ75974 standard; cDNA; 4059
              85DE-3545576.
85DE-3542024.
                                                                                                                                                                           Claim 1; p6; 13pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                          Local Similarity 90.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHLA-B7 expression vector.
                                                (BEHW ) BEHRINGWERKE AG.
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                                                                                                WPI; 1987-171469/25.
P-PSDB; AAP70155.
          21-DEC-1985;
01-JAN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ75974
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It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic ribosomal subunits when located within a mRNA mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HIA-B7 stop codon on this biscistronic mRNA to be recognised by the ribosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "ppR322 backbone contg. bacterial origin of replication, it represents nucleotides 2244-3193"
                                                 sequences. The oligonucleotide removes a polyadenylation signal sequence originally found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
Tn903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "murine encephalomyocarditis CAP-independent
translational enhancer (EMCV-CITE); taken from
nucleotides 255-843 of cloned EMCV genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "multiple cloning site, forms a junction between the HLA-B7 sequence and the EMCV-CITE sequence, and is used to facilitate subcloning 1889..2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "encodes beta-2 microglobulin; this cDNA is deriv. from chimpanzee (differs to the human cDNA by only 4 bases)"
 region of a synthetic oligonucleotide which modifies this regulatory sequence to effect higher level of expression of downstream
                                                                                                                                                                                                                                                                                            /*tag= e
/note= "encodes putative HLA-B7 heavy chain mature
peptide"
                                                                                                                                                                                                                                                                                                                                                                           untranslated sequence of HLA-B7 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "synthetic linker to facilitate cloning
                                                                                                                                                                      /*tag= c
/note= "HLA-B7 heavy chain open reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "3' untranslated region of the beta-2 microglobulin mRNA"
                                                                                                                                                                                                                                       /note= "encodes putative signal peptide of HLA-B7 heavy chain"
                                                                                                                      /*tag= b
/label= consensus_Kozak_signal_seguence
                                                                                    in the RSV DNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "synthetic linker"
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                                                                                                                                                                                                                                                                                                                                                                                               chain mRNA"
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                                                                                                                                                                                                                                                                        607..1620
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                                                                                                    531..534
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/note=
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3112..3
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/note=
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/note=
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                                                                                                                                                                                                         sig_peptide
                                                                                                    misc_signal
                                                                                                                                                                                                                                                                          mat_peptide
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                                                                                                                                                       CDS
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     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This HLA-B7 antigen encoding plasmid was developed to incorporate many advantageous features, eg. the kanamycin resistance gene. The eradication of two open reading frames encoding portions of SV40 viral proteins lowers the risk of tumourigenicity. The vector may also operate as a cassette into which cistrons may be inserted and removed at will for the transcription and subsequent translation of peptides of interest. The vector is used partic. for the treatment of neoplastic disease, eg. melanoma, and provides enhanced gene delivery and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
"Rous sarcoma virus LTR promoter domain, derived
for the Schmidt-Rupin strain nucleotides
8673-9146. This region also includes a 56 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7; light beta-2 microglobulin; class I major histocompatibility complex MHC; bicistronic mRNA; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
        /*tag= g
/note= "Rous sarcoma virus 3' LTR promoter region"
3416..4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                          New vectors for gene therapy, partic for tumours - comprising genetic material encoding one or more cistron(s) which express immunogenic or therapeutic peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26.2; DB 16;
Pred. No. 0.078;
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                                                                                                                                                                                                                                                                                                          Nabel GJ;
                                                                   /*tag= h
/note= "pBR322 backbone"
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complement (2886..3415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 42-43; 50pp; English.
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                                                                                                                                                                                                                                                                                                          Nabel EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.8%;
                                                                                                                                                                                       94WO-US06069
                                                                                                                                                                                                                       93US-0074344
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/note=
                                                                                                                                                                                                                                                         UNMI ) UNIV MICHIGAN.
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Best Local Similarity
                                                                                                                                                                                                                                                                        (VICA-) VICAL INC
                                                                                                                                                                                                                       07-JUN-1993;
                                                    misc_feature
                                                                                                                                                                                     27-MAY-1994;
                                                                                                                  WO9429469-A.
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AAQ75973;

Key

AAQ75973/c

RESULT

Matches

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WO9429469-A.

Lew D,

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Genetic predisposition to seronegative spondyloarthropathies (SNSA) is detected by determining the absence of a cytosine nuclectide in the 3% flanking region (see also AATG1647 + 48) of an HIA-B gene at a position corresponding to nuclectide 4495 of the HIA-B27 consensus sequence given in AATG1639. Probes and primers (see also AATG1640-46) based on this region can be used in diagnostic assays to detect the genetic predisposition to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA from B27+ normal individuals who are resistant to such diseases.
/note= "3' flanking region diagnostic for genetic
predisposition to SNSA"
4270..4556
                                                                                /*tag= b
/note= "3' flanking region diagnostic for genetic
predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human breast cancer related protein coding sequence SEQ ID NO: 42.
                                                                                                                                                        d
"absence of cytosine at this site is
indicative of a predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting pre-disposition to seronegative spondylarthropathies from the absence of a C residue at a specific position in the 3'-flanking region of the HLA B27 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Length 6553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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Pred. No. 0.085;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              (CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 52-56; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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90.3%;
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                                                                                                                                                                                                                                                                                                                    96WO-US13256
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/note=
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                                                                                                                                     misc_difference
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                                                                                                                                                                                                                                                                              13-MAR-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ryan DB;
                                                         mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The PHLA-B7/Deta-2 microglobulin plasmid expression vector, in addition
to the kanamycin resisitance gene, contains the plasmid DNA encoding the
heavy (human HLA-B7) and light (beta-2 microglobulin) proteins of a
class I major hisotocompatibility complex (MHC) antigen. The plasmid is
designed to express these two proteins via a bicistronic mRNA in
designed to express these two proteins via a bicistronic mRNA in
c eukaryotic cells. Initiation of transcription of the mRNA is dependent
on a Rous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long
terminal repeat. Termination of transcription is dependent upon the
plyadenylation signal sequence deriv. from the bovine growth hormone
c plyadenylation signal sequence deriv. from the bovine growth hormone
gene. Bukaryotic cell translation of the heavy chain is regulated by the
controlled by the CITE Finally the replication of the plasmid in
bacterial cells is controlled by the presence of a bacterial origin of
replication. The vector is used partic. for the treatment of neoplastic
in the controlled by the CITE factor.

c replication and provides enhanced gene delivery and expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "HLA-B27 3' flanking region, downstream of
3' untranslated region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Relter's syndrome; arthritis; acute anterior uveitis; diagnosis;
                                                                                                                                                                                                                                                                                               New vectors for gene therapy, partic for tumours - comprising genetic material encoding one or more cistron(s) which express immunogenic or therapeutic peptide(s)
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Pred. No. 0.081;
0; Mismatches 3; Indels 0:
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                                                                                                                                                                                                                         Nabel GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 ctagatctcagtccctcacaaggcagctgtc 36
                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 41-42; 50pp; English.
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3968..6653
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                                                                                                                                                                                                                     Marquet M, Nabel EG,
                                                                                94WO-US06069.
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Best Local Similarity 90.3%;
Matches 28; Conservative (
                                                                                                                      93US-0074344
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                                                                                                                                                          (UNMI ) UNIV MICHIGAN. (VICA-) VICAL INC.
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                                                                         27-MAY-1994;
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                                   22-DEC-1994.
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KW HLA B2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T lymphocyte; sterile inflammatory disease; autoimmune disorder; GVHD; immunodeficiency disease; cancer; graft-versus-host-disease; psoriasis; rheumatoid arthritis; asthma; genetic disease; cytokine gene; Jurkat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides methods to identify a therapeutic or prophylactic agent that modulates a T lymphocyte population found in a subject having a sterile inflammatory disease, autoimmune disorder, immunodeficiency disease, cancer or graft-versus-host-disease (GVHD). The methods can be used to identify therapeutic or prophylactic agents that modulate T lymphocyte populations in subjects having a sterile inflammatory disease
                                                                                                                                                                                                                                     New polynucleotides encoding breast tumor specific proteins, useful for prevention, treatment and diagnosis of breast cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Studying changes in gene expression in T lymphocytes used to identify therapeutic or prophylactic agents which modulate T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the coding sequences for a number of breast cancer related proteins. These can be used in vaccinations against, diagnosis of and treatment of cancer, particularly breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 509;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T lymphocyte cDNA sequence ID No: 29 of W09957130.
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Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                               Claim 25; Page 132-133; 165pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 ATCTCAGTCCCTCACAAGACAGCTGTC 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.6%;
96.3%;
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99US-0140903
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                           99US-0158980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENE LOGIC INC
                                                                                                                                Yuqiu J, Mitcham JL;
                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-023547/02.
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  23-JUN-1999;
                        12-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ38041;
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NAME OF THE PARTY 
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cc (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, allergic rhinitis, cardiac and renal reperfusion injury, thrombosis, cadult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, lymphocytopenias, autoimmune lymphoproliferative syndrome, severe combined immunodeficiency syndrome, wasvere combined immunodeficiency syndrome, Maxia-telangiectasia, Cartilagerain hypoplasia, immunodeficiency with thymoma and leukocyte adhesion deficiency 1), cancer (15 T lymphocyte leukemia/lymphoma's are listed in the specification), immunodeficiency disease, autoimmune disorder (20 clisted in the specification) or a genetic disease. The methods can also be used to identify an agent that induces the differentiation of cuiescent pre-, cortical or medullary T lymphocytes into a differentiated T lymphocyte subpopulation. The methods are especially useful for identifying cytokine genes, genes encoding cell surface receptors and genes encoding intermediary signaling molecules. Sequences compared to the specification of the sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           нuman; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 456 BP; 94 A; 109 C; 99 G; 136 T; 18 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25.2; DB Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 ctagatctcagtccctcacaaggcagctgt 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%;
90.0%;
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Best Local Similarity 90.09
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Tue Dec 11 08:46:11 2001

Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cereproprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuloer; vulnerary; anticonvulsant; antibacterial; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ds.

Homo sapiens

Human polynucleotide SEQ ID NO 346.

(first entry)

22-0¢T-2001

AAI63974;

AAI63974 standard; DNA; 4756 BP.

RESULT 14 AAI63974/C

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cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAS with intact 5' ends and can therefore be used to obtain full length cDNAS and genomic DNAS. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
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                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in t diagnosis, treatment and screening of vascular diseases caused by arterioscierosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequences, proteins encoded by them and antibodies against them useful in diagnosis and treatment of vascular disease caused by
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                                                                                                                                                 21; Length 439;
                                                                                                                                                                                                                                                                                                                                                                              Human shear stress-response coding sequence SEQ ID NO: 85.
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                                                                                              Sequence 439 BP; 93 A; 110 C; 147 G; 85 T; 4 other;
                                                                                                                                       Ouery Match
69.4%; Score 25; DB 21
Best Local Similarity 84.8%; Pred. No. 0.17;
Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                             4 ctctagatctcagtccctcacaaggcagctgtc 36
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ekine S, Nakamura Y, Sugano S;
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                                                                        expression and secretion vectors.
                                                                                                                                                                                                                                                                                          AAH02916 standard; DNA; 1817
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P-PSDB; AAB90793.
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2000US-0224518.
2000US-0224519.
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                                                                   WO200155308-A2.
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAR-2000;
07-JUN-2000;
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Score 25; DB 22; Length 1817; Pred. No. 0.22; 0; Mismatches 5; Indels (

69.4%; 84.8%;

Ouery Match 69.4 Best Local Similarity 84.8 Matches 28; Conservative

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2000US-0234998
2000US-0235484
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08-SEP-2000;
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14-SEP-2000;
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21-SEP-2000;
21-SEP-2000;
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26-SEP-2000;
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The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating crameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
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cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acids and polypeptides, useful for dlagnosing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating and/or preventing human diseases and disorders -
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Best Local Similarity 84.8%; Pred. No. 0.26;
Matches 28; Conservative 0; Mismatches
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              2000US-0249265.
2000US-0249297.
2000US-0249299.
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2000US-0250160.
2000US-0250391.
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2000US-0256719.
2000US-0251479.
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2000US-0251990.
2000US-0254097.
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fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective, antialergic; hepatotropic; antidiabetic; antilnflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ds.
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2000US-0186628.
2000US-0186564.
2000US-0186350.
2000US-0198174.
2000US-0198123.
2000US-029467.
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2000US-0225759.
2000US-0226279.
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200005-0231414.
200005-0232080.
200005-0232081.
200005-0232991.
                                                                                                                           17-JAN-2001; 2001WO-US01309.
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2000us-0228924.
2000us-0229287.
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                                                                                   WO200155308-A2
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04-FEB-2000; 2

16-MAR-2000; 2

16-MAR-2000; 2

17-MAR-2000; 2

19-MAR-2000; 2

19-MAR-2000; 2

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19-MAR-2000; 2

11-JUL-2000; 2
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14 - AUG - 2000;
18 - AUG - 2000;
22 - AUG - 2000;
22 - AUG - 2000;
30 - AUG - 2000;
31 - SEP - 2000;
30 - SEP - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-SEP-2000;
3-SEP-2000;
2-SEP-2000;
-SEP-2000;
                                                                                                        02-AUG-2001
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2000US-0233065.
2000US-0234274.
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2000US-0234998.
2000US-0235884.
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25-SEP-2000; 2
25-SEP-2000; 2
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29-SEP-2000; 2
20-OCT-2000; 2
20-OCT 17-NOV-2000; 17-NOV-2000;

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OR OB-DEC-2000; 2000US-0251990.

PR 108-DEC-2000; 2000US-0251990.

PR 108-DEC-2000; 2000US-0251990.

PR 108-DEC-2000; 2000US-0251970.

PR 65-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (HUMA-) HUMAN GENOME SCI INC.

XX WPI; 2001-488781/53.

New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders - treating and/or preventing human polynucleotides (AAIG3803-AAIG4012) and the encoded proteins (AAM4)3497-AAM4360) useful for preventing, treating CC or ameliorating medical conditions e.g. by protein or gene therapy. The specification The nucleic acids, proteins, antibodies and (antibodois care useful in the diagnosis, treatment and prevention of; (a) cancer, c.g. bone, bone marrow, breast, gastrointestinal tract, liver, lung, or uropential, (b) immune disorders e.g. Addison's diabetes mellitus, cutoimmune haemolytic aneamia, autoimmune thyroiditis, diabetes mellitus, colinis; (c) cardiovascular disorders such as myocardial isochaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and on parastic infections.

CC toli solitis; (c) cardiovascular diseases such as wiral, bacterial, fungal and parastic infections.

CC tolitis; (c) cardiovascular diseases such as wiral, bacterial, fungal and parastic infections.

CC tolitis; (c) cardiovascular diseases such as viral, bacterial, fungal and parastic infections.

CC printed specification, but was obtained in electronic format directly from WIPO at ftp.WiPo.int/Pub/published_pct_sequences.
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Query Match 69.4%; Score 25; DB 22; Length 4756; Best Local Similarity 84.8%; Pred. No. 0.26; Antches 28; Conservative 0; Mismatches 5; Indels

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Search completed: December 6, 2001, 10:01:25 Job time: 4269 sec

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Sequence 8 Sequence 1 Sequence 8 Sequence 1

US-08-588-983-11 US-08-588-976-8

Sequence 1 Sequence 5 Sequence 4 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2

US-09-338-907-73 US-09-338-907-183 US-09-157-17-130 US-09-257-584-5 US-09-257-584-4 US-09-257-584-4 US-09-257-584-4 US-09-257-584-1 US-09-287-251-25 US-08-937-250-2 US-08-993-260-2 US-08-588-976-19 US-08-588-976-19 US-08-588-983-19 US-08-588-976-19 US-08-588-976-11 US-08-588-976-11 US-08-588-976-11

Sequence 3

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SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.3
Best Local Similarity 83.3
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2297
22911
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23111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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TOPOLOGY:
US-08-718-964-4
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70.117 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1,
Sequence 1,
Sequence 1,
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Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           351203 seqs, 113238999 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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36
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Perfect score:
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Sequence 4, Application US/08718964

Sequence 4, Application US/08718964

Patent No. 5932694

GENERAL INFORMATION:
APPLICANT: Wan der Bruggen, Pierre; Mandruzzato, Susanna;
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Boon-Falleur, Therry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding A Functional
TITLE OF INVENTION: Protein, The Protein So Encoded And Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: New York City
STATE: New York City
STATE: New York
STATE: New York
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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83.3%; Pred. No. 0.0053;
iive 0; Mismatches 6;
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CONTRING DATE: 26-September-1996
CLASSIFICATION 536
PRICATION S36
PRICATION DATA:
APPLICATION NUMBER: 08/669,590
FILING DATE: 24-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5932694man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5442.1
TELEPHONEY: (212) 688-9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3844
INFORMATION FOR SEQ ID NO: 4:
SEDENTIAL SAME SEG ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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4 GCCCGAATTCTCTCAGTCCCTCACAAGGCAGCTGTC 39

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                                                             APPLICANT: van der Bruggen, Pierre; Mandruzzato, Susanna;
APPLICANT: van der Bruggen, Pierre; Mandruzzato, Susanna;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding A Functional
TITLE OF INVENTION: Protein, The Protein So Encoded And Uses Thereof
CORRESPONDENCE & G
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P..
STREET: 555 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-842-341-4
; Sequence 4, Application US/08842341
; Patent No. 5955313
; GENERAL INFORMATION:
APPLICANT: van der Bruggen, Pierre; Mandruzzato, Susanna;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding A Functional
TITLE OF INVENTION: Protein, The Protein SO Encoded And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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ZIP: 10.103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gccctctagatctcagtccctcacaaggcagctgtc 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/059,964A
FILING DATE: US/08/059,964A
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/718,964
FILING DATE: 26-September-1996
APPLICATION NUMBER: 08/669,590
FILING DATE: 24-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 595228man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5442.1
TELECOMMUNICATION INFORMATION:
Sequence 4, Application US/09059964A
Patent No. 5952228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 688-9200 TELEFRAX: (212) 838-3884 INFORMATION FOR SEO ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREFT: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 39 nucleotides
TYPE: nucleic acid
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Best Local Similarity
Matches 30; Conserv
                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nuclei
STRANDEDNESS:
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APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Nabel, Gary
APPLICANT: Nav, Denise
APPLICANT: Marquet, Magda
TITLE!OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.3%; Score 26.4; DB 2; Best Local Similarity 83.3%; Pred. No. 0.0053; Matches 30; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gecetetagateteagteceteacaaggeagetgte 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GCCCGAATTCTCTCTCAGTCCCTCACAAGGCAGCTGTC 39
                                                          OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURREWY APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 24-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/718,964
FILING DATE: 26-September-1996
APPLICATION NUMBER: 08/669,590
FILING DATE: 24-UUNE-1995
ATORNEY AGENT INFORMATION:
NAME: Hanson, NO. 595313man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10D 5442.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/564,313
FILING DATE: 01-DEC-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.1
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08564313 Patent No. 5910488
                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 883-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 39 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01
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Db 1755 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FASTEDO Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,313
FILING DATE: 01-DEC-1995
CLASSIFICATION 514
PROG APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-UUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISTAGLSEN, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-564-313-1/c
; Sequence 1, Application US/08564313
; Patent No. 5910488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29,655
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REFERENCE/DOCKET NUMBER: VI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                        Query Match 72.8%;
Best Local Similarity 90.3%;
Matches 28; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
CLONE: HLA-B7 and Beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
    STRANDEDNESS: double TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                      TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                 FRAGMENT TYPE:
CRIGINAL SOURCE:
STRAIN: HLA-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
COUNTRY: USA
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-564-313-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Regents of the University of Michigan
APPLICANT: Regents of the University of Michigan
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marquet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: VICAL.033CP1
TELECOMMUTCATION:
TELEPHONE: 619-235-8550
TELEPHONE: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VICAL.033VPC
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/ACENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
PCT-US94-06069-2
Sequence 2, Application PC/TUS9406069
GENERAL INFORMATION:
REGISTRATION NUMBER: 29,655
                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 4059 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.39
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-235-0176
                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: HLA-B7
                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
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ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                           Indels
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GENERAL INFORMATION:
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Nabel, Gary
APPLICANT: Marquet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
Score 26.2; DB 5;
Pred. No. 0.015;
                                           0; Mismatches
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LENGTH: 6553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                         ADDALL
STREET: 4300 TITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches '28; Conserv
                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9 1
US-08-406-057-1/C
                                                                                                                                                                                                                                                           COUNTRY:
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                                               Gaps
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                                             0
Query Match 72.8%; Score 26.2; DB 2; Length 4965; Best Local Similarity 90.3%; Pred. No. 0.015; Matches 28; Conservative 0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                            APPLICANT: Lew, Denise
APPLICANT: Marquet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        Vical Incorporated
Regents of the University of Michigan
Nabel, Elizabeth
Nabel, Gary
                                                                                                                                                                                                                                                                                                                                                                                SSEE: Knobbe, Martens, Olson and Bear
F: 620 Newport Center Drive 16th Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISTABLSON, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033VPC
TELEPHONE: 619-235-8550
TELEFRAX: 619-235-0176
                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ctagatctcagtccctcacaaggcagctgtc 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
                                                                                                                                                     RESULT 7
PCT-US94-06069-1/c
Sequence 1, Application PC/TUS9406069
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.8%;
90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-B7 and Beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.8
Best Local Similarity 90.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA ZIP: 92660 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                            APPLICANT:
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PCT-US94-06069-1
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RESULT

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Sequence 1. Application US/0852942

Farent No. 253442

GENERAL INFORMATION:

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DNA (genomic)
                                                                                                                                                TOPOLOGY: linear; MOLECULE TYPE: CDNA to mRNA US-08-958-316-1
                                                                                                                                                                                                                                                     Query Match 57.8%;
Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206-622-4900 TELEPAX: (206)-682-6031 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1928 base pairs
                                                                                      LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-675-816-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKMAN, ELIANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON. CORRESPONDENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 2; Length 440;
2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE PATENTIN STILEM:

SOFTWARE PATENTIN RELEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/958,316

FILING DATE: 27-0CT-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 94 03179

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REFERENCE/POCKET NUMBER: 24,618

TELECOMMUNICATION INFORMATION:
                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20.8; D
Pred. No. 2.2;
0; Mismatches
                                                                                                                    PRIOR APPLICATION 1973
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILIND DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-331-0
TELECOMMUNICATION: INFORMATION:
                                                              APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 CTCAGTCCCACAGGGCAGCTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08958316
Patent No. 6291659
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 ctcagtccctcacaaggcagctgt 35
                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR:
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.8%;
Best Local Similarity 91.7%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRGINIA
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
US-08-406-057-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-958-316-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Sequence 4, Application US/08675816
Sequence 4, Application US/08675816
Betent No. 6171864
GENERAL INFORMATION:
APPLICANT: Coughlan, Sean J.
APPLICANT: Winfrey, Jr., Ron J.
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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Score 20.8; DB 4; Length 440;
Pred. No. 2.2;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 701...
STREET: 701...
CITY: Seattle
STATE: Washington
COMPIRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 53.3%; Score 19.2;
1. Similarity 87.5%; Pred. No. 14,
21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Seed and Berry STREET: 701 Fifth Ave. Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: No. 6171864tenburg, Carol
                                                                                                                                      278 CTCAGTCCCACACAGGGCAGCTGT 255
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TELECOMMUNICATION INFORMATION:
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USA
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STATE: PA
COUNTRY:
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US-09-276-993-5
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Patent No. 6063760
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: Of MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                        TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS TITLE OF INVENTION: OF MAKING THE SAME NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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Pred. No. 34;
0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 TCTTCATCACAGACTCTCTCAAGCAAGCTGT 885
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLUCA: MARK
REGISTRATION NUMBER: 33,229
REFERENCE/POCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEFRAX: (215) 568-3100
TELEFRAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                  Sequence 5, Application US/08859167
Patent No. 6037461
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
                                                           GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 50.6%;
Best Local Similarity 74.2%;
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: both
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                          19103
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US-08-859-167-5
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-08-859-167-5
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Retandez-Alnemri, Teresa

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: GENERAL AND COMPOSITIONS FOR AND METHODS

TITLE OF INVENTION: OF MAKING THE SAME

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801r1s

STREET: One Liberty Place, 46th floor

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                               APPLICATION NUMBER: US/09/109,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDER-ECCT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276
                                                                                                                                                                                                                                                          FILLING DATE:
ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION UNDRER: 33,229
REFERENCE/DOOKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEFRAN: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09276993
Patent No. 6207801
                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: WINDOWS SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%;
74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.69
Best Local Similarity 74.23
Matches 23; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 32..988
US-09-109-273-5
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MOLECULE TYPE: CDNA
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FEATURE
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Sequence 29, Application US/08888497

GENERAL INFORMATION:

APPLICANT: Tischfield, Jay A.

APPLICANT: Sellhamer, Jeffrey J.

TITLE OF INVENTION: Broaded Thereby, Antisense A2 Nucleotide

TITLE OF INVENTION: Broaded Thereby, Antisense Sequences and Nucleotide

TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences

TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

TORRESPONDENCES A4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA

STREET: 200 East Broward Boulevard

CTTY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18.2; DB; Pred. No. 34; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTOKNEY/ABCHT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REGISTRATION NUMBER: 1N21044-5
REFECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              855 TCTTCATCACAGACTCTCTCAAGCAAGCTGT 885
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APPLICATION NUMBER: US/08/651,405
                   REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.6%;
Best Local Similarity 74.2%;
Matches 23; Conservative
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1828 base pairs
                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: 32..988
US-09-276-993-5
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                        TOPOLOGY: both
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CLASSIFICATION:
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                                                                                                                                                                   Length 1828;
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                                                                                                                                                                     Query Match 50.6%; Score 18.2; Dest Local Similarity 74.2%; Pred. No. 37; Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                          Search completed: December 6, 2001, 08:52:36 Job time: 140 sec
                                                                                                                                                                                                                                                         823 CTCTACATCAGAGTCCCTCTCTAGGATTCTG 793
                                                                                                                                                                                                                                      4 ctctagatctcagtccctcacaaggcagctg 34
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                    CDS
233..643
                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                ; NAME/KEY:
; LOCATION:
US-08-888-497-29
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us-09-673-795-4.rni

Tue Dec 11 08:46:11 2001

RC2-IT004 QV3-HT026 601146750

50 RC1-CT019 zb55f05.s1

nc72b02.r RCO-GN027 IL3-MT026

OV4-EN004 MR4-UM002 PM0-ET015

RC6-ST017 RC3-CT021

CM3-UM003 RC6-HT014 RC1-CT020 CM2-CN006

CM3-MT011 CM2-CN006 RC3-CT021 IL2-ST016 CM1-DT000 PM4-UM005

QV1-ET006

Perfect score:

Title:

Sequence:

1

nucleic

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Scoring table:

Searched:

Database

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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-mRO-HT0559-020
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria: Primates; Catarrhini: Hominidae: Homo.

I (bases 1 to 317)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magal,M.A., activa,M.A., Bordin,S., Costa,F.F.,

Nagal,M.A., de Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.F.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

'M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                         BF875422 QV3-ET010
BF770493 RC2-IT004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE708567 317 bp mRNA EST 12-SEP-2000
MRO-HT0559-020800-032-d06 HT0559 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                              AL545658 AAA468055 n
BIO52969 R
BIO20663 I
AW389745 R
AW376423 R
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AW796825 C
AW366718 F
AW376219 F
BG978500 C
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20202663
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                                                                                                                              AL54568
AA468055
BIO20669
BIO20663
AW389745
AW36423
AW36423
AW796825
AW366718
AW376219
AW376219
                                         BF875422
BF770493
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BI017003 PM3-ET020
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                            /note="Organ: head_neck; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORBSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 347)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., Bordin,S., Costa,F.F.,
Aggal,M.A., da Silva,W. Jr., Zago,M.A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0559-290 500-026-h05&t3=2000-05-29&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 347.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_ll="HT0559"
/dev_strage="Adult"
/dot_strage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products
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MRO-HT0559-290500-026-h05 HT0559 Homo sapiens cDNA, mRNA sequence.
BE708216
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                              /organism="Homo sapiens"/db_xref="taxon:9606"
High quality sequence start: 5
High quality sequence stop: 317.
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/dev_stage="Adult"
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Fax: +55-11-2707001
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derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases I to 399)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Gordin, S., Costa, F.F., Nagai, M.A., Bordin, S., Costa, F.F., Brunstein, A., Geolivelra, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brehtani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1st2=PM1-CN0098-020101-002-f02&t3=2001-01-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 398.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG978548 399 bp mRNA EST 12-JUN-2001
PM1-CN0098-020101-002-f02 CN0098 Homo sapiens CDNA, mRNA sequence.
BG978548
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509–010, Sao Paulo-SP,
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Fax: +55-11-2707001
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Length 399;

DB 11;

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of colon tumor

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

MEDLINE JOURNAL

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TITLE

RESULT 4 BF083691/c

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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-CT0255-
Seq primer: puc 18 forward
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW361438 559 bp mRNA EST 04-FEB-2000 RC3-CT0255-031099-011-e09 CT0255 Homo sapiens CDNA, mRNA sequence.
  AW973450 489 bp mRNA EST 02-JUN-2000
EST385443 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence.
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1 (bases 1 to 559)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LLCR Human Cancer Genome Project
Unpublished (1999)
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                               Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
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/clone_lib="MAGE resequences, M
/note="Vector: pBluescriptSKm"
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Laboratory of Cancer Genetics
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77.2%;
Best Local Similarity 93.5%;
Matches 29; Conservative
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/organism="Homo sapiens"
/db_xref="Haxon:9606"
/db_xref="Laxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR2-CT0456-190
900-003-c078513-2000-09-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 475.
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1 (Dases I to 476)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Rogal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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MRZ-CT0456-190900-003-c07 CT0456 Homo sapiens CDNA, mRNA sequence.
BF083691.1 GI:10877430
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                             Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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0; Mismatches
    Pred. No. 1;
0; Mismatches
                                                                       398 CTACATCTCAGTCCCTCACAAGACAGCTGTC 368
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  90.98;
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Best Local Similarity 90.98
Matches 30; Conservative
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Gaps

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High quality sequence start: 52 High quality sequence stop: 541.

BASE COUNT

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Matches

AW973450

RESULT

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Location/Qualifiers

FEATURES

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1...323
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/clone_lib="Er0207"
/dev_stage="Adult"
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/note="Organ: lung_tumor; Vector: puc18; Site_1: Smal;
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derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 323)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-ET0207-Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence start: 11
Location/Qualifiers
BI017003
PM3-ET0207-300301-012-a04 ET0207 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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0; Mismatches
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ilarity 90.6%;
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Best Local Similarity 90.6%;
Matches 29; Conservative
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Fax: +55-11-2707001
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//16 - Ludwig Institute for Cancer Research) profiles
//16 - Ludwig Institute for Cancer Research) profiles
//18 - Ludwig Institute for Cancer Research) profiles
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 237)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Negal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deOliveira,P.S., Matsukuma,A., Bala,G.S., Simpson,D.H.,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR4-UM0115-040
500-203-f08&t3=2000-05-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 34
High quality sequence stop: 237.
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AW806440
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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0; Mismatches 2;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                          stringency conditions.
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RESULT AW806440

ð a VERSION KEYWORDS

REFERENCE AUTHORS

MEDLINE JOURNAL

COMMENT

TITLE

FEATURES

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us-09-673-795-4.rst

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AIB01734 LOCUS DEFINITION

RESULT

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ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Irissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 546)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 541)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1662 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 249.
Location/Qualifiers
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90.6%; Pred. No. 2.5;
iive 0; Mismatches
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/clone="IMAGE:1992738"
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Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-refmail.nh.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 556 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 222.
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/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DHIOB"
/ince="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                       AI801734 479 bp mRNA EST 14-DEC-1999 to94f10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185963 3' similar to 9b:M12678 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2705 ALPHA (HUMAN);, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 479)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 2.5;
0; Mismatches 3;
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                  390 TCTGCATCTCAGTCCCTCACAAGACAGCTGTC 421
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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90.68;
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Unpublished (1997)
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Best Local Similarity 90.6
Matches 29; Conservative
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FEATURES

BASE COUNT ORIGIN

RESULT 10 AI290139 LOCUS

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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Tel: +55-11-2704922
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Matches 28; Conserv
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                     /note="Organ: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpsone@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-HT0469-
010200-012-c04&t3=2000-02-01&t4-1)
Seq primer: puc 18 forward
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Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW607375 174 bp mRNA EST 23-MAR-2000 RC4-HT0469-010200-012-c04 HT0469 Homo sapiens cDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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                found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1199 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 154.
Location/Qualifiers
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HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
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Pred. No. 2.5;
0; Mismatches 3;
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/db_xref="taxon:9606"
/clone_lib="HT0469"
/dev_stage="Adult"
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High quality sequence stop: 174.
Location/Qualifiers
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90.6%;
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Best Local Similarity
Matches 29; Conserv
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AUTHORS
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/note="Organ: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORBSTSS PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions. 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM2-HT0657-150
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM2-HT0657-150
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 215.
1. 376
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1 (bases 1 to 376)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baila,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                               BE183227 . 376 bp mRNA EST 22-JUN-2000
CM2-HT0657-150400-156-h06 HT0657 Homo sapiens CDNA, mRNA sequence.
BE183227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
tissue mRNA and cDNA amplification were performed under low stringency conditions." 60\ c=37\ g=40\ t
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                      Length 174;
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                                                                                                                                                           Score 27;
Pred. No.
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ilarity 93.3%;
Conservative
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85.7%;
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B-8 B*0801 ALPHA (HUMAN);, mRNA sequence
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Job time: 2369 sec
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/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
35 a 37 c 48 g 39 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001

Email: asimpsondludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0199-
220999-013-E06&t8=1999-09-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 128
High quality sequence stop: 159.
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zb55f05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:307521 3' similar to gb:M28204 HLA CLASS I HISTOCOMPATIBILITY
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                                                                                                                                                               AW752350 159 bp mRNA EST 28-APR-2000
RC1-CT0199-220999-013-E06 CT0199 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                          350 rggarcrcagrccrcacaagacagcrgrc 321
7 tagatctcagtccttcacaaggcagctgtc 36
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87.98;
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Homo sapiens

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostoml;

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 442)

S Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

(S Hillier,L., Lennon,G., Becker,M., Dandue,T., Favello,A., Gish,W., Hawkins

M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore, B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,

Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,

Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.

Genome Res. 6 (9), 807-828 (1996)

RE Gonome Res. 6 (9), 807-828 (1996)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St., Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 537 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 270.
Location/Qualifiers
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Best Local Similarity 87.9
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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us-09-673-795-4.rst

Tue Dec 11 08:46:12 2001

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

December 6, 2001, 07:56:53 ; Search time 170.25 Seconds (without alignments) 7.732 Million cell updates/sec Run on:

PEP1-MOD8F 48 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1 SLFEGIDFY 9

Sequence:

473505 seqs, 146272329 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_17:\* Database :

sp\_archea:\*
sp\_barchea:\*
sp\_lungi:\*
sp\_lunan:\*
sp\_lunan:\*
sp\_nammal:\*

sp\_vertebrate:\*
sp\_unclassified:\* sp\_organelle:\* sp\_phage:\* sp\_rodent:\* sp\_plant:\* sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	7 littorina p	O littorina s	9 littorina s	_	1 littorina s	8 littorina p	6 littorina p	P81159 aplysia cal	20 oncorhynchu	99 fuqu rubrip		0 chondrosia	2 petrobiona	2 guancha lac			97 fuqu rubrip	x7 arabidopsis	093147 botryllus s
Descr	60	069n670	699n60	Q90665	Q9u671	09u60	999n60	P8115	990520	668860	963718	044350	044352	Q9nj92	04434	04435	098897	Q9c7x7	09314
di di	090667	090670	699060	Q90665	090671	090668	Q9U666	P81159	090520	668860	963718	044350	044352	Q9NJ92	044349	044351	098897	Q9C7X7	093147
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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5 Q93146 5 O15766 13 Q918P9 5 Q93601 13 O93240 11 Q62256 11 Q90WJ5 5 Q90KR9 5 Q90KR9 10 Q48563 3 O59855 10 Q41027 5 Q90777 10 Q92285 10 Q92885 10 Q92885	m H wwwww
	.9 467 .9 467 .9 467 .9 639
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## ALIGNMENTS

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Gaps
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
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"Heat-shock genes in the heat-stressed genus Littorina.";
"Bubmitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191828; AAF12787.1;
HSSP; P19120; 1BA1.
InterPro; IPR01023; HSP70.
PROSITE; PS01036; HSP70.
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146 AA; 16607 MW; C3F3556AlAF43BBB CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                         PRT; 146 AA.
                                                                                                              PRELIMINARY;
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SEQUENCE FROM N.A.
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Q9U670 PRELIMINARY; PRT; 153 AA. Q9U670; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 79 SLFEGIDEY 87 1 SLFEGIDFY 9 ~ RESULT Q9U670 ID Q9U AC Q9U DT 01: g δ

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

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Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels
                               Littorina plena.
Sukaryota, Metazoa, Mollusca, Gastropoda; Caenogastropoda;
Neotaenloglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID-31219;
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                                                                                                                                  Hobeliohe P.A.;
Hoteliohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
Bubmited (OCT-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AF191801; AF12789.1;
HSSP; P19120; 1BA1.
InterPro; 1PR01023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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Bukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglosas Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
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"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191824; AAF12783.1;
EMSP; P19120; 1BA1
Interpro; IPR001023; HSP70.
PRINTS; PR001001; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                              157 157
157 AA; 17834 MW; E8F743382B285EB2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT_SHOCK PROFIEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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HEAT-SHOCK PROTEIN (FRAGMENT)
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Matches 9; Conservative
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                                                                                                                      SEQUENCE FROM N.A.
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85 SLFEGIDFY 93
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NON_TER
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090668;
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Q9U671
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                                       Littorina scutulata.
Bukaryota: Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglosas; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID-31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 48; DB 5; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0: Indels
                                                                                                                                       Hohenlohe P.A.;
Hohenlohe P.A.;
Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAR12784.1;
HASS; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31221;
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SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
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   HEAT-SHOCK PROTEIN (FRAGMENT).
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Best Local Similarity 100.vv
School 9; Conservative
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Q90669; Q90669;

RESULT Q9U669

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RESULT Q9U665 ID Q9U AC Q9U DT 011

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Gaps

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Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                   MEDLINE-93077669; PubMed=1360013;
MEDLINE-93077669; PubMed=1360013;
Kuhl D., Kennedy T., Barzilai A., Kandel E.;
"Long-term sensitization training in Aplysia leads to an increase in the expression of BlP, the major protein chaperon of the ER.";
J. Cell Biol. 119:1069-1076(1992).
--- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
--- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
HSSP; P19120; LBA1.
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090520;
01-NOV-1996 (TERMELrel. 01, Last sequence update)
01-NOV-1996 (TERMELrel. 01, Last sequence update)
01-NOV-1996 (TERMELrel. 17, Last annotation update)
01-JUN-2001 (TERMELrel. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
Oncorlynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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"70-Kilodalton heat shock polypeptides from rainbow trout:
characterization of cDNA sequences.";
Mol. Cell. Biol. 4:1785-1791(1984).
EMBL; K02549; AAA49562.1;
HSSP; P08109; ICKR.
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220 AA; 24684 MW; FA8557F2BB85C37A CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
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MEDLINE=85036330; PubMed=6092938;
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
NON_TER 220
SEQUENCE 220 AA; 24684 MW;
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
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Pfam; PF00012; HSP70; 1.
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Matches 9; Conservative
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                                                                                                                               Aplysiidae; Aplysia.
NCBI_TaxID=6500;
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278 AA;
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                          Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                   Hohenlohe P.A.; "Heat-shock genus Littorina."; "Heat-shock genes in the heat-stressed genus Littorina."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191827; AAF12786.1; "HSSP; P19120; 1BAL. InterPro; PR0010123; HSP70. PRINTS; PR001011; HEATSHOCK70. PROSITE; PS01036; HSP70_3; 1.
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"Heat-shock genes in the heat-stressed genus Littorina.";
"Bubmitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191829; AAF12788.1; -.
HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AA; 17868 MW; D2ECE71042EC44CB CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT-SHOCK PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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Best Local Similarity 100.00
Best Local 9; Conservative
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                                                                     Littorina plena.
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252 SLFEGIDFY 260
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                                                                                                                                                                                                    NCBI_TaxID=68578;
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ID 044350
AC 044350;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                          Gaps
                                                                                                                                                                                                                                                                                                                              Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontides;
Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 48; DB 13; Length 367; Best Local Similarity 100.0%; Pred. No. 0.23; Matches 9; Conservative 0; Mismatches 0; Indels 0
                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lim E.H.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 198578; CAA69892.1; ...
InterPro; 1PR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PROSITE; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_1; 1.
PROSITE; PS01036; HSP70_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 367 367 367 SEQUENCE 367 AA; 40405 MW; 8CD3DDBDF6E3C2CA CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
                                                                                                                                                                                                                    01-FBB-1997 (TrEMBLrel. 02, Created)
01-FBB-1997 (TrEMBLrel. 02, Last sequence update)
01-FBB-1997 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
      Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 AA
                                                                                                                                                                                                    367 AA
                        0; Mismatches
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PRINTS; PR00301, HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
  100.0%;
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                        9; Conservative
                                                                                                                                                                                                      PRELIMINARY;
      Best Local Similarity
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                                                                                      NCBI_TaxID=10116;
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                                                                1 SLFEGIDFY 9
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Bukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
Petrobiona.
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Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Chondrosida; Chondrillidae; Chondrosia.
NCBI_TaxID=68574;
                                          Query Match
100.0%; Score 48; DB 11; Length 455;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 48; DB 5; Length 467; 100.0%; Pred. No. 0.31; ative 0; Mismatches 0; Indels
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467 AA; 51707 MW; ODBE6920F2E6EA96 CRC64;
50404 MW; 0F45F12CBA1E2971 CRC64;
                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Alcyonaria, Funiculinidae,
Funiculina.
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                                                                                                                                                                                                                                                                                                                               Guancha lacunosa.
Bukaryota; Metazoa; Porifera; Calcarea; Calcinea; Clathrinida;
Clathrinidae; Guancha.
NCBI_TaxID=115120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

100.0%; Score 48; DB 5; Length 467;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                              Query Match 100.0%; Score 48; DB 5; Length 467; Best Local Similarity 100.0%; Pred. No. 0.31; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Borchiellini C., Le Parco Y.;
"Sponges paraphyly and the origin of Metazoa.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF182195; AAF61297.1;
InterPro: IPR001023; HSP70.
Print: PF000123; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS00329; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
BORCHiellini C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026516; AAC05361.1; -.
HSSP; P08109; 1CKR.
InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
NON_TER 1 1
NON_TER 467 467
SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;
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467 AA; 51318 MW; F36FC06CBIDEE131 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEWBLrel. 15, Created)
01-0CT-2000 (TrEWBLrel. 15, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
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252 SLFEGIDFY 260
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252 SLFEGIDFY 260
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SEQUENCE
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DR Pfam; PF00012; HSP70; 1.

DR PRINTS, PR00301; HSP702.1.

DR PROSITE; PS00329; HSP70_2; 1.

A 18 FT NOW_TER 468 468

Query Match

Query Match

A 2 100.0%; Score 48; DB 5; Length 468; Best Local Similarity 100.0%; Pred. No. 0.31; Matches 9; Conservative 0; Mismatches 0, Indels 0; Gaps

Qy 1 SLFEGIDFY 9

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| Db 253 SLFEGIDFY 261

Search completed: December 6, 2001, 07:56:53

Job time: 181 sec
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Appli Appli Appli Appli Appli Appli Appli

Sequence 9, Sequence 9, Sequence 7, Sequence 7, Sequence 7, Sequence 9, Sequence 9, Sequence 7, Sequence 7, Sequence 7, Sequence 7,

Sequence 15, Appl Sequence 7, Appli

Sequence 9, 1 Sequence 15,

-08-613-009A-15

-08-483-577A-9

Appli

Appli Appli Appli Appli

Sequence 7, Sequence Sequence Sequence

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US-08-487-890A-7
US-08-487-890A-9
US-08-478-435-7
US-08-337-483-7
US-08-337-483-9
US-08-478-373-9
US-08-478-373-9
US-08-474-671-9
US-08-474-671-9
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US-08-474-671-9
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COMPUTER READABLE FORM:
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Best Local Similarity 80.0
Matches 8; Conservative
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US-08-797-358B-3
RESULT
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Sequence 107, App
Sequence 5, Appli
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19, APP1
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                                                                                                                6, 2001, 07:59:57; Search time 81.43 Seconds
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-441-139-14
US-08-487-800A-19
US-08-377-483-19
US-08-474-671-19
US-08-474-671-19
US-08-474-671-19
US-08-474-671-19
US-08-478-713-19
US-08-897-438-19
US-08-911-311-8
US-08-911-311-8
US-08-478-431-107
US-08-478-431-107
US-08-478-411-107
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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51
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COMPUTER: IBM PC compatible

COMFRATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/797,358B

FILING DATE: 11-Feb-1997

CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/011,491

FILING DATE: 12-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathry A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-CE 3165

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPAX: (619) 535-9001

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 643;
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                                                                                                                                                                                                                                                       ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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Pred. No. 0.41;
1; Mismatches
ALIGNMENTS
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-797-358B-3
                                                                                                   Sequence 3, Application US/08797358B Patent No. 6268478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 643 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: California
COUNTRY: United States
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Length 36;
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                                                                                                                                                                         COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC COMPUTER: DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
CLASIFICATION: 435
PRIOR APPLICATION AAA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/148,968
FILING DATE: SOWOV-1993
APPLICATION NUMBER: US 08/148,968
FILING DATE: SOWOV-1993
ATTORNEY AGENT INFORMATION:
NAME: STEWART, MICHAELI
REGISTRATION NUMBER: 1038-466 MIS:jb
TELECOMMUNICATION INFORMATION:
mut FULLNUM CALLON INFORMATION:
mut FULLNUM CALLON INFORMATION:
mut FULLNUM CALLON INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Wang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Michin, Andrew
APPLICANT: Telens, Transferrin Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1;
Pred. No. 3.6;
1; Mismatches
    NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 Unviersity Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08478435
Patent No. 5922323
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-487-890A-19
                                                                                                                STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 FEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||: |||
28 FEGVAIYT 35
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US-08-478-435-19
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                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Wittrup, Dr. Karl D.

APPLICANT: Modern Dr. Karl D.

APPLICANT: Robinson, Anne S.

TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:

ADDRESSEE: ACULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFPICATION: A35
PFLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DiG191io, Frank S.
REGISTRATION NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID SANS UR
INFORMATION POS SEQ ID SANS UR
SECONTENT SEQ 100: 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08487890A
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Klein, Andrew
APPLICANT: Klein, Michel
                                                                                                                                 Sequence 14, Application US/08441139
Patent No. 5773245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.3%;
80.0%;
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Best Local Similarity 80.0*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-441-139-14
                                                                                                                                                                                                                                                                                                                                                                                       Garden City
11111:1 11
288 SLFEGVDFYT 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11:1111 11
286 SLYEGIDFYT 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino
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                                                                                   RESULT 2
US-08-441-139-14
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Gaps

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66.7%; Score 34; DB 2; 75.0%; Pred. No. 3.6;
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELEPAX: (416) 595-1163
INFORMATION FFOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1038-463 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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APPLICATION NUMBER: US/08/478,373 FILING DATE: 07-UNN-1995 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: US 08/337,483 FILING DATE: 08-NOV-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116 FILING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08478373 Patent No. 5922841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loosmore, Sheena
Harkness, Robin
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.v.
                                                                                                                                                                                                                      single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                       linear
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28 FEGVAIYT 35
                                                                                                                                                                                                                 STRANDEDNESS:
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US-08-337-483-19
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US-08-478-373-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LOOSMOTE, Sheena
APPLICANT: LOOSMOTE, Robin
APPLICANT: Schrywers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                     PRIOR APPLICATION 1973.

APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY AGWART, MICHAELI
NAME: SLEWART, MICHAELI
NAME: SLEWART, MICHAELI
NAME: SLEWART, MICHAELI
NAME: (460 595-1163
TELECOMMUNICATION NUMBER: 1038-462 MIS:VG
TELECOMMUNICATION NUMBER: 1038-462 MIS:VG
TELECOMMUNICATION NUMBER: 1038-462 MIS:VG
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 and no acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB;
Pred. No. 3.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
CITY: Toronto
                                                                APPLICATION NUMBER: US/08/478,435 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-08-337-483-19
Sequence 19, Application US/08337483
Patent No. 5922562
GENERAL INFORMATION:
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75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.7
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 FEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111: 111
28 FEGVAIYT 35
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                                           0; Gaps
Length 36,
                                              1; Indels
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COMPUTER: IEM PC Compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Wurdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
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Gaps
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                                                            Length 36;
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Pred. No. 3.6;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-Ping
APPLICANT: Windin, Andrew
APPLICANT: Klein, Michel
ITILE,OF INSTITON: Transferrin Receptor Genes
CORRESPONDENCES: 160
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,577A
FILIG DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                   Score 34; DB 3;
Pred. No. 3.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIORIAPPLICATION PATA:
APPLICATION NAMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIORIAPPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIORIAPPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTOCNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-511
TELEPHONE: (416, 595-1155
TELEPHONE: (416, 595-1155
TELEPHONE: (416, 595-1155
TELEPHONE: (416, 595-1163
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08483577A Patent No. 6015688 GENERAL INFORMATION:
APPLICANT: LOSSMORE, Sheena
                                                   66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.78;
75.08;
                     Query Match
Best Local Similarity 75.0%
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                               3 FEGIDIYT 10
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28 FEGVAIYT 35
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Pred. No. 3.6;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,671
FILING DATE: 07-001-1995
CLASSIFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING APPLICATION NUMBER: US 08/175,116
FILING APPLICATION NUMBER: US 08/148,968
FILING APPLICATION NUMBER: 1038-465 MIS:VG
TELERCOMOTONICATION INFORMATION:
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APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schrywers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Mindin, Andrew
APPLICANT: Klein, Michel
ITTLE OF INVENTION: Transferrin Receptor Genes
WUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08474671
Patent No. 6008326
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                           LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                             Query Match
Best Local Similarity 75.0%
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single;
TOPOLOGY: linear
US-08-474-671-19
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STREET: Surranty: Toronto
                                                                                                                                                                                                                                                                                                                                    3 FEGIDIYT 10
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28 FEGVAIYT 35
                                                                                                         ; TOPOLOGY:
US-08-478-373-19
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111: 111 28 FEGVAIYT 35

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Pred. No. 36;
1; Mismatches 1; Indels
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: McDonell, Michael W.
TITLE OF INFORTON: Recombinant Feline Herpes virus
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSE: John P. White
STREET: JiB5 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
                                                                                                                                                                                                                                                                                    COMPUTER: TOOSY
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: EL 30 466 DXS
COMPUTER: EL 30 466 DXS
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 26-OCT-1995
CLIASSIFICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/329,883
FILING DATE: 26-OCT-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 39118-PCT
TELECOMMUNICATION INMBER: 39118-PCT
TELECOMMUNICATION INMBER: 39118-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Roger K. Maes and Stephen J. Spatz
TITLE OF INVENTION: Recombinant Poxvirus
TITLE OF INVENTION: Vaccine Against
TITLE OF INVENTION: Felline Rhinotracheitis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08911321 Patent No. 6010703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212)278-0400
TELEFAX: (212)391-0525
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.78;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.7
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
PCT-US95-13975-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 FEGIDIYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                       APPLICANT: LOOSMOZE, Sheena
APPLICANT: LOOSMOZE, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Murdin, Andrew
APPLICANT: Millin, ANDRESSE:
ADDRESSE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-JUN-1995
PRIOR APPLICATION UNDER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION UNDER: US 08/175,116
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                   US-08-897-438-19
Sequence 19, Application US/08897438
; Patent No. 6262016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.7%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 FEGIDIYT 10
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Gaps

MELLUS.
COMPUTER: IBM COMPC...
OPERATING SYSTEM: MS-DOS
....MARARE: Wordperfect 5.1

RESULT 10 PCT-US95-13975-72 ; Sequence 72, Application PC/TUS9513975

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Length 911;
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                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LOOSMOTE, Sheena
APPLICANT: LOOSMOTE, Sheena
APPLICANT: Barkness, Robin
APPLICANT: Barkness, Robin
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Wand, Yan-Ping
APPLICANT: Wandin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER: OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; I
Pred. No. 1.2e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                             FILING DATE: 07-JUN-1993
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
APTORIEY/AGENT INFORMATION:
NAME: STEWART: Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 M:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 107:
SEGUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
STRANDEDNESS: single
TOPPICE INFORMATION
TOPPICES: 100-107:
TOPPICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-UN-1995
CLASSIPICATION: 435
PROM APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107, Application US/08478435 Patent No. 5922323 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0°,
....nes | 6; Conservative
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US-08-487-890A-107
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Pred. No. 54;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LOOSMOIR, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Schryvers, Anthony
APPLICANT: Gray-Oven, Scott
APPLICANT: Yang, Yan-Pling
APPLICANT: Murdin, Andrew
APPLICANT: Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/096,183
FILING DATE: JULY 26, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-166
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (517) 347-4103
TELEFAN: (517) 347-4103
TELEFAN: (517) 347-4103
TELEFAN: (517) 347-4103
TELEFAN: No. 6010703e
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION:
; IDENTIFICATION METHOD: Deduced Sequence
; OTHER INFORMATION: 9G
US-08-911-321-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 Unviersity Avenue
CITY: Toronto
STATE: Ontario
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 107, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Feline herpesvirus-1
STRAIN: 1
INDIVIDUAL ISOLATE: C-27
CELL TYPE: N/A
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: Sin
TOPOLOGY: Linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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N
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|35 FEGLTIYT 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-487-890A-107
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Gaps
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                                                                             Length 911;
                                                        Score 34; DB 2; Length 911. Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,373

FILING DATE: O'-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/337,483

FILING DATE: 08-NOV-1994

CLASSIFICATION NUMBER: US 08/37,483

PRIOR APPLICATION NUMBER: US 08/37,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION NUMBER: US 08/148,968

FILING DATE: 29-DEC-1993

PRIOR APPLICATION NUMBER: US 08/148,968

FILING DATE: US 08/148,968

FILING DATE: US 08/148,968

FILING DATE: US 08 NOV-1993

ATTONEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LOOSMOTE, Sheena
APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Soite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2; Le
Pred. No. 1.2e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE_DOCKET NUMBER: 1038-463 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                     Sequence 107, Application US/08478373
Patent No. 5922841
GENERAL INFORMATION:
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                           Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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STRANDEDNESS: sir
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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       US-08-337-483-107
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
2 IP: M5G 1R7
COMPUTER REABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
FILING DATE: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 anito Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 107, Application US/08337483
; Patent No. 5922562
; GENERAL INFORMATION:
   APPLICANT: Loosmore, Sheena
   APPLICANT: Harkness, Robin
   APPLICANT: Chong, Pele
   APPLICANT: Chong, Pele
   APPLICANT: Yang, Yan-Ping
   APPLICANT: Murdin, Andrew
   APPLICANT: Milani, Andrew
   APPLICANT: Transferrin Receptor Genes
   NUMBER OF SEQUENCES: 147
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 2; 1
Pred. No. 1.2e+02;
1; Mismatches 1;
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STREE: amino acids
TYPE: amino acids
STREEDENCE: (416) 510-1155
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Sim & McBurney
Suite 701, 330 Unviersity Avenue
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      linear
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228 FEGVAIYT 235
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                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-478-435-107
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US-08-337-483-107
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3 FEGIDIYT 10 |||: ||| 228 FEGVAIYT 235 Qy Dp

Search completed: December 6, 2001, 07:59:57 Job time: 365 sec

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dnak.type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)
N;Alternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Accession: 151344
R;Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Bloil. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o
A;Reference number: 151344
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o
A;Reference number: 151344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-278 - KOT>
A;Residues: 1-278 - KOT>
A;Residues: 1-278 - KOT>
A;Coss-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804
C;Function: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                    219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                  219241 segs, 76174552 residues
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                                                                                                     6, 2001, 07:58:27
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein • protein search, using sw model
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Maximum DB seq length: 2000000000
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A44261 A03309 PQ0138 P14588 T145474 T145474 T145474 T17598 S25585 S25585 S25585 T455132 JC7132 JC7132 A34041 T45468	ALIGNMENTS	RESULT 1.  B44261  Ghak-type molecular chaperone HSC70 - California dnak-type molecular chaperone HSC70 - California dnak-type molecular shock protein 70 homolog C; Species: Aplysia californica (California sea h. A) Alternate names: heat shock protein 70 homolog C; Date: 04-Sep-1998 #sequence_revision 04-Sep-19 C; Cacession: B44261  B; Khil, D.; Kennedy, T.E.; Barzilai, A.; Kandel, J. Cell Biol. 119, 1069-1076, 1992  A; Reference number: A44261; MUD: 93077669  A; Reference number: A44261; MUD: 93077669  A; Return: preliminary; not compared with concept A; Rediues: preliminary; not compared with concept A; Rediues: preliminary; not compared with concept A; Rediues: 1-208 extracted from NCBI backbone (NG Genetics: Cigentics: C; Function: A; Gene HSC70  C; Function: involved in protein folding and a A; Description: involved in protein folding and a C; Superfamily: heat shock protein 70  C; Keywords: ATP; molecular chaperone  Best Local Similarity 90.0%; Pred: No. 0.06  Matches 9; Conservative 0; Mismatches  Qy 1 SLFEGIDIYT 10  Db 132 SLFEGIDIYT 141	
00000000000000000		HSC Property of the control of the c	
2009 2114 372 372 467 467 6641 6641 6651 2009 630 630		ar chaperone HSC70 : heat shock prote a californica (Cali 98 #sequence_revis 64, T.E.; Barzilai / 1069-1076, 1992 m. sensitization tr. m. sensitization tr. r: A44261; MUID:93 61 mary; not compared nucleic acid -kKUH- extracted from NCB extracted from NCB at shock protein for sextracted from NCB at shock protein at shock protein at shock protein for sextracted from NCB rolled in protein at shock protein at shock protein for sextracted from NCB rolled in protein at shock protein for sextracted from NCB rolled in protein at shock protein for sextracted from NCB rolled in protein at shock protein for sextracted from NCB rolled in protein	
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444444444444444		RESULT  1. Glasser, type molecular chaperone HSC70  M.Alternate names: heat shock protein  M.Alternate names: heat shock protein  C.Species: Aplysia californica (Cali  C.Species: Aplysia californica  M.Sep-1998 #sequence_revision  M.Stwhl, D.; Kennedy, T.E.; Barzilai,  M. Cell Biol. 119, 1069-1076, 1992  A.Title: Long term sensitization tra  A.Reference number: A44261; MUID:930  A.Reference number: A44261; MUID:930  A.Residues: preliminary; not compared  A.Residues: 1-208 «KOH)  A.Residues: 1-208 «KOH)  A.Note: sequence extracted from NCBI  C.Genetics:  C.Genetics:  C.Superfamily: heat shock protein for the compared of the compare	,
		HESULT 1  B44261 Ghak Type moly MAlternate no. C; Species: App C; Date: 04-Se C; Date: Dong A; Title: Long A; Title: Long A; Reference no. A; Recession: A; Recence no. C; Genetics: C; Genetics: A; Gonetics: A; Gonetics: C; Genetics: A; Gonetics:	
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1; Indels

0; Mismatches

Score 47; DB 2; Length 278; Pred. No. 0.089;

92.2%; 90.0%;

Query Match Best Local Similarity 90.04 کمت 9; Conservative

1 SLFEGIDIYT 10

heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-467 <BOR>

A; Reference number: Z22983 A; Accession: T45477

A; Cross-references: EMBL: AF026517; PIDN: AAC05362.1

C;Genetics: A;Gene: Hsp70 C;Superfamily: heat shock protein 70

C; Accession: T45477 R; Borchiellini, C.; Le Parco, Y. submitted to the EMBL Data Library, September 1997

C; Keywords: ATP; molecular chaperone

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diaka-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum NiAlternate names: heat shock cognate protein 70 c; Species; Dictyostelium discoideum C; Species; Dictyostelium discoideum C; Date: 31-3an-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000 C; Accession: T45471 R; Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G. submitted to the EMBL Data Library, September 1997 A; Reference number: Z22980 A; Accession: T45471 A; Retrus: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated fro
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C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
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Submitted to the EMBL Data Library, September 1997
A; Reference number: 222983
A; Reference number: 222983
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-469 < BOR>
A; Cross_references: EMBL: AF026518; PIDN: AAC05363.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.2%; Score 47; DB 2; 90.0%; Pred. No. 0.16; iive 0; Mismatches
                                                                                                                   A; Reference number: 222983
A; Accession: T45476
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule, Prep: mRNA
A; Residues: 1-468 < RORS
A; Cross-references: EMBL: AF026516; PIDN: AAC05361.1
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Pred. No. 0.16;
0; Mismatches
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C;Accession: T45476
R;Borchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
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A,Note: localized to filopodias and cortex
C,Superfamily: heat shock protein 70
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C, Superfamily: heat shock protein 70
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90.0%;
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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C;Species: Eunicella cavolini
C;Species: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T454P,
R;Borchiellini, C:; Le Parco, Y.
R;Borchiellini, C:; Le EMBL Data Library, September 1997
A;Reference number: 222983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Chondrosia reniformis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
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1; Indels

Length 467;

Score 47; DB 2; Pred. No. 0.16; 0; Mismatches

92.2%; 90.0%;

Conservative

Query Match Best Local Similarity Matches 9; Conserv

1111111 || 252 SLFEGIDFYT 261

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1 SLFEGIDIYT 10

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Score 47; DB 2; Length 467; Pred. No. 0.16; 0; Mismatches 1; Indels

Query Match 92.2%; Best Local Similarity 90.0%; Matches 9; Conservative

252 SLFEGIDEYT 261

1 SLFEGIDIYT 10

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A; Cross-references: EMBL: AF026520; PIDN: AAC05364.1

A; Residues: 1-467 <BOR>

Genetics:

A; Accession: T45479

A;Gene: Hsp70 C;Superfamily: heat shock protein 70

Length 632;

DB 2; 0.22;

Score 47; Pred. No.

92.2%; 90.0%;

9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

1 SLFEGIDIYT 10

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1; Indels

Mismatches

A25646 dnaK-type molecular chaperone - chicken

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Sulvo

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Suberias: December shock protein 70

C; Species: Cercopithecus acthiops (green monkey, grivet)

C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

C; R; Sainis, I:, Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

A; Residuces: 1-638 < SAIN

A; Residuces: 1-638 < SAIN

B; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

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R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Lazaridis, I:

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R; Sainis, I:; Angelidis, C:; Pagoulatos, G:; Laz
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N.Alternate names: heat shock protein 701V; hsp701V protein
C.Species: Paracentrotus lividus (common urchin)
C.Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C.Accession: JC1391
R.Scorso, G.: Scardina, G.; Ferraro, M.G.
Gene 121, 353-358, 1992
A.Fitle: Characterization of a new member of the sea urchin Paracentrotus lividus hsp
A.Reference number: JC1391; MUID:93077053
A.Reference number: JC1391
A.Molecule type: DNA
A.Residues: 1-639 <SCO>
A.Coss-references: EMBL:X61379; NID:9312916; PIDN:CAA43653.1; PID:9312917
C.Genetics:
A.Genetics:
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Pred. No. 0.23;
0; Mismatches 1; Indels
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284 SLFEGIDFYT 293
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N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein agi
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Accession: A48872
C;Accession: A48872
J. Biol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an A;Reference number: A48872
A;Accession: A48872
A;Accession: A48872
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-636 <EDD>
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as C;Function:
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Length 634;

Score 47; DB 2; Pred. No. 0.22;

92.2%; 90.0%;

Conservative

Query Match Best Local Similarity Matches 9; Conserv

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Mismatches

Length 636;

DB 2; 0.22;

1; Indels

Mismatches Score 47; Pred. No.

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92.2%; 90.0%;

Query Match Best Local Similarity 90.0 المراقع 9; Conservative

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RESULT

1 SLFEGIDIYT 10

Page

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us-09-673-795-2.rpr

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A. Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352
A.Note: genomic clones representing six distinct members of the hsp70 gene family wer A.Note: genomic clones representing six distinct members of the hsp70 gene family wer A.Note: one of the three introns in hsp70A is in a position similar to an intron in D G. Genetics:
A.Gene: hsp70A
A.Map position: IV
A.Introns: 69/1; 331/3; 558/3
A.Map position: involved in protein folding and assembling/disassembling of protein co G. Superfamily: heat shock protein 70
C. Superfamily: heat shock; molecular chaperone; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Mag-1989 # sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: A29160; 137561; 137562
R;Hunt, C.; Morimoto, R.I.
Proc. Natl: Acad. Sci. U.S.A. 82, 6455-6459, 1985
A;Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the A;Reference number: A29160; MUID:86016721
A;Accession: A29160
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A.Residues: 1-640 < HUND
A.Residues: 1-640 < HUND
A.Crosszereferences: GB:M11717; GB:M15432; NID:g184416; PIDN:AAA52697.1; PID:g386785
A.Note: the authors mistranslated residues 463, 491, and 492
R.Drabent, B.; Genthe, A.; Benecke, B.J.
Nucleic Acids Res. 14, 8933-8948, 1986
A.Fitle: In vitro transcription of a human hsp 70 heat shock gene by extracts prepar A.Fitle: In vitro transcription of a human hsp 70 heat shock gene by extracts prepar A.Fitle: In vitro transcription of a human hsp 78 heat shock gene by extracts prepar A.Fitle: Irranslation not shown; translated from GB/EMBL/DDBJ
A.Molecule:type: DNA
A.Residues; 1-22 < RES>
A.Residues; 1-22 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: involved in protein folding and assembling/disassembling of C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A; Residues: 616-640 <RE2>
A; Crossreferences: EMBL:X04677; NID:932482; PIDN:CAA28382.1; PID:932483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X04676; NID:g32480; PIDN:CAA28381.1; PID:g32481
A;Accession: 137562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 1;
Pred. No. 0.23;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: GDB:HSPAIL; HSP70-HOM
A,Gross-references: GDB:120058; OMIM:140559
A,Map position: 6p21,3-6p21,3
A,Introns: #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dnak-type molecular chaperone HSPAIL - huma
N'Alternate names: heat shock protein, 70K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.00.
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                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S20139; MUD:8912845;
A; Accession: S20139
A; Status: translation not shown
A; Molecule type: DnA
A; Residues: 1-639 <SLA>
A; Cross references: EMBL:X12927; NID:94545; PIDN:CAA31394.1; PID:94546
A; Cross references: EMBL:X12927; NID:94545; PIDN:CAA31394.1; PID:94546
B; Goffeau, A.; Purnelle, B.
A; Recession: S64772
A; Molecule type: DNA
A; Residues: 1-639 <GOP>
A; Cross references: EMBL:Z73129; NID:91360201; PIDN:CAA97472.1; PID:91360202; MIPS:YLL02
A; Residues: 1-639 <GOP>
A; Cross references: EMBL:Z73129; NID:91360201; PIDN:CAA97472.1; PID:91360202; MIPS:YLL02
A; Experimental source: strain S288c
B; Duester hoeft, A.; Plocth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
B; Reference number: S64775
A; Recession: S64775
A; Residues: 72-639 <GOES
A; Residues: 72-639 <GOES
A; Residues: 72-639 <GOES
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A; Residues: 72-639 <AOES
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Keywords: ATP; molecular chaperone
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R;Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterizat
A;Accession: JT0285, MUID:88297155
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RESULT 12
920139
Glass and a control of the protein SSA2 - yeast (Saccharomyces cerevisiae)
N.Alternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000
C;Accession: S20139; S64772; S64775; S69383
R;Slater, M.R.; Craig, E.A.
Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-639 <PUR>
A;Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dnaK-type molecular chaperone hsp70A - Caenorhabditis elegans
N;Alternate names: heat shock protein 70 A
C;Species: Caenorhabditis elegans
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Cross-references: MIPS:YLL024c; SGD:S0003947
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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283 SLFEGIDFYT 292
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C; Function:
A; Description: involv
C; Superfamily: heat s
C; Keywords: ATP; mole
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protein co

δ Dp

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RESULT 15
S37394
Ginar-type molecular chaperone hsc70 - slime mold (Dictyostellum discoideum)
N;Alternate names: heat shock cognate protein 70
C;Species: Dictyostellum discoideum
C;Species: Ji-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: S37394
R;Haus, U; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Schl
EMBO J. 12, 3763-3771, 1993
A;Title: The heat shock cognate protein from Dictyostellum affects actin polymerization A;Accession: S37394; MUID:94008983
A;Accession: S37394
A;Molecule type: mRNA
A;Residues: 1-640 < HAU>
A;Cross-references: EMBL:X75263; NID:9433874; PIDN:CAA53039.1; PID:9433875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: hsc70
C;Function:
A.Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 2; Length 640;
Pred. No. 0.23;
0; Mismatches 1; Indels
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Gaps

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6, 2001, 07:58:27

Search completed: December Job time: 275 sec

õ q THIS PAGE BLANK (USPTO)

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 6, 2001, 08:00:51; Search time 50.21 Seconds (without alignments) 7.302 Million cell updates/sec Run on:

US-09-673-795-2 51 1 SLFEGIDIYT 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	P11503 onchocerca	Q92260 penicillium				Q06248 paracentrot	٥	P36415 dictyosteli	Q27975 bos taurus	P08107 homo sapien	P17879 mus musculu	P34930 sus scrofa	Q07439 rattus norv	P10591 saccharomyc	Q27965 bos taurus			_				P48720 blastocladi	Q9u639 manduca sex	P02826 drosophila	P22623 paracentrot	P34934 sus scrofa	P91902 ceratitis c	P29843 drosophila	P17066 homo sapien	_	Q01877 puccinia gr	55063 rattu	P34931 homo sapien
SUMMARIES		HS70_ONCVO	HS70_PENCI	HS70_CHICK	HS71_CERAE	HS72_YEAST	HS74_PARLI	HS7A_CAEEL	HS7C_DICDI	HS71_BOVIN	HS71_HUMAN	HS71_MOUSE	HS71_PIG	HS71_RAT	HS71_YEAST	HS72_BOVIN	HS74_YEAST	HS70_BRUMA	HS70_ONCTS	HS70_PLEWA	HS70_NEUCR	HS70_XENLA	HS70_BLAEM	HS7D_MANSE	HS7A_DROSI	HS72_PARLI	HS7X_PIG	HS70_CERCA	HS7A_DROME	HS76_HUMAN	HS76_PIG	HS71_PUCGR	HS73_RAT	HS7H_HUMAN
	DB	: -	П	Н	-	-			-	-		-	Н	-	П	Н	-	-	7	П	-	-	П	-	н	-	-		-	<b>,</b>	~	-	-	-
	ength	322	503	634	638	638	639	640	640	641	641	641	641	641	641	641	641	644	644	645	646	647	649	652	214	372	379	638	641	643	643	648	641	641
	Query Match	1 (1)	N	$\sim$	a	$\sim$	$\sim$	$\sim$	$^{\circ}$	a	$^{\circ}$	$^{\circ}$	~	N	$\sim$	~	3	3	~	~	~	$\sim$	$^{\circ}$	$^{\circ}$	0	0	0	0	0.2	0	0	0	φ	6.3
ď		. 6	6	6	6	6	σ	σ	6	6	σ	6	σ	6	5	σ	6	σ	σ	σ	6	σ	6	σ	6	σ	6	σ	6	σ	6	6	8	ω
		47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47				46	46	46	46	46	44	44
	Result No.	1	7	c	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30		32	33

P16627 mus musculu P53623 pichia angu	Q10265 schizosacch P53421 pichia angu	P11142 homo sapien P08109 mus musculu	P87047 paracoccidi P09435 saccharomyc	Q90473 brachydanio P19120 bos taurus	P08108 oncorhynchu
HS7T_MOUSE HS72_PICAN	HS71_SCHPO HS71_PICAN	HS7C_CHUMAN HS7C_MOUSE	HS70_PARBR HS73_YEAST	HS7C_BRARE HS7C_BOVIN	HS70_ONCMY
пп					-
641 642	643 644	646 646	649 649	649 650	651
86.3 86.3	86.3	86.3 86.3	86.3 86.3	86.3 86.3	86.3
4 4 4 4	4 4 4	† <del>†</del> † †	4 4 4 4	4 4 4 4	44
34 35	37	0 6 4 0 0 0	41 42	4 4 4	45

## ALIGNMENTS

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HS71_CERAE
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There are no restrictions on its
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01-FEB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROFEIN (HSP70).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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SEQUENCE FROM N.A.
MEDLINE-86304452; PubMed=3017985;
MOTIMOTO R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
"Organization, nucleotide sequence, and transcription of the chicken "Organization, nucleotide sequence,"
"Organization, nucleotide sequence," and transcription of the chicken "Organization," nucleotide sequence, and transcription of the chicken "Organization," nucleotide sequence, and transcription of the chicken "Organization," nucleotide sequence," and transcription of the chicken "Organization," nucleotide sequence, and the chicken "Organization," nucleotide sequence, and "Organization," nucl
                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
NCBI_TaxID=5077;
                                                                                                                                                                                                                                                                                                        ;
0
                        20-AuG-2001 (Rel. 40, Created)
20-AuG-2001 (Rel. 40, Last sequence update)
20-AuG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.2%; Score 47; DB 1;
90.0%; Pred. No. 0.093;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U64207; AAB06397.1; -.
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                      Penicillium citrinum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 SLFEGIDFYT 163
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P08106;
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                                                                                                                                           HSP70.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WEDLINE-95080396; PubMed-7988690;

REDLINE-950800396; PubMed-7988690;

REDLINE-950800396; PubMed-7988690;

Radinis I., Angelidas C., Pagoulatos G., Lazaridis I.;

Sainis I., Angelidas C., Pagoulatos G., Lazaridis I.;

Inducible member of the hsp70 gene family.";

FEBS Liett. 355:822-286(1994).

PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDLATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OFF RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STREES-INDUCED DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Burpopen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 1; Length 634; Pred. No. 0.12;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                           EMBL, J02579; AAA48825.1; -.
PIR; A25646; A25646.
HSSP; P19120; 1ATR.
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90.0%;
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289 SLFEGIDEYT 298
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Best Local Similarity
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Q28222;
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Paracentrotus
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-1- FUNCTION: SA22 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender E
Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                          shock; Multigene family; MHC III.
D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                   Length 638;
                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                   Score 47; DB 1;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   638 AA.
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Electrophoresis 15:1466-1486(1994)
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MEDLINE-97089742; Pubmed-8935650;
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                 Pfam; PF00012; HSP70; 1.
PRINTS: PR00301; HEATSHOCK70.
PROSITE: PS00291; HSP70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
PROSITE: PS01336; HSP70_3; 1.
ATP-binding; Chaperone: Heat sh SEQUENCE 638 AA; 69920 MW; I.
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                                                                                                                                                                                                                                   92.2%;
90.0%;
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norbeck J., Blomberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHOCK PROTEIN SSA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 186-195.
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284 SLFEGIDFYT 293
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                1 SLFEGIDIYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4932;
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P10592:
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SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES. SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sconzo G., Scardina G., Ferraro M.G.; "Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 gene family and its expression."; gene 121:353-358(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 1; Length 638;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; products; HSP70.

Pfam; PF00012; HSP70; 1.

PRINTS; PR00301; HEATSHCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

Heat shock; ATP-binding; Multigene family; Acetylation; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23BDDD120C194912 CRC64;
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AC 000248; DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DF 01-JUN-1994 (Rel. 29, Last sequence update)

DF 01-JUN-1994 (Rel. 29, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paracentrotus lividus (Common sea urchin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=93077053; Pubmed=1339375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69338 MW;
                                                                                                                                                                                                                                                                                                                                           EMBL; X12927; CAA31394.1; -. EMBL; Z73129; CAA97472.1; -. EMBL; X97560; CAA66167.1; -. PIR; S20139; S20139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10592; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                         PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEPD; 9800; -.
SGD; S0003947; SSA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7656;
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287 SLFEGIDFYT 296

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or send an email to license@isb-sib.ch)

EMBL; X61379; CAA43653.1; -

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RESULT CHARTC_DICDI ID P36415; TW-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-88297155; PubMed-2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                 characterization.";
Gene 64:241-255(1988).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00297; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MM; ED15409D06C500C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 10, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 1
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                 92.2%;
90.0%;
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HEAT SHOCK 70 KDA PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M18540; AAA28078.1; -. PIR; JT0285; HHKW7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P19120; 1NGI.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.2
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9, Conservative
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286 SLFEGIDFYT 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-6239;
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P09446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSP-1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
HS7A_CAEEL
HS7A_CAEEL
TO 1-MARR
DT 01-FRBH
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                                                                                                                                                                                                                                                                                               MSSIGIDLGTTYSCVGVWQNDRVEIIAND ->
IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
                                                                                                                                                                        Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F., Noegel A.A., Schleicher M.; "The heat shock cognate protein from Dictyostelium affects actin polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N -> T (IN REF. 2).

V -> A (IN REF. 2).

F -> A (IN REF. 2).

S -> A (IN REF. 2).

V -> A (IN REF. 2).

I -> L (IN REF. 2).

F -> P (IN REF. 2).

F -> P (IN REF. 2).

F -> P (IN REF. 2).
                                                                                   Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
  640 AA.
                                                                                                                                                             MEDLINE=94008983; PubMed=8404847;
                                                                                                                                                                                                                                                                                    MEDLINE-94043116; PubMed-8226849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; iX75263; CAA53039.1; --
EMBL; [122736; AAA33219.1; --
PIR; 837394. 837394.
HSSP; P19120; ING.
SWISS; 2DPAGE; P36415; DICTY.
DICTYDE; DDOOTOTS; hSPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70499 MW;
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                      EMBO J. 12:3763-3771(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01036; HSF/v_ATP-binding; Chaperone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
341
352
640 AA;
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                            NCB1_TaxID=44689;
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CONFLICT
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CONFLICT
SEQUENCE
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Gaps

; 0

92.2%; Score 47; DB 1; Length 640; 90.0%; Pred. No. 0.12; ive 0; Mismatches 1; Indels

1 SLFEGIDIYT 10

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Grosz M.D., Skow L.C., Stone R.T.;

*An Alul polymorphism at the bovine 70 kD heat-shock protein-1

(HSP70-1) locus."

Anim. Genet. 25:196.1964).

-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

REEXISTENT PROTEINS AGAINST AGREGATION AND MEDIATE THE FOLDING

OF UNGLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN

C REMICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLACATION. THEY ARE INVOLUNG A DRIVING FORCE FOR PROTEIN TRANSLACATION. THEY ARE INVOLUNG A DRIVING FORCE FOR PROTEINS TRANSLATION WHEN HSP90. THEY PARTICIPATE IN ALL THESE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE

C SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES

C DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelabs-sib.ch).
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                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Skeletal muscle;
MEDLINE-95126904; PubMed-7826329;
Gutterrez JA., Guerriero V.;
"Chemical modifications of a recombinant bovine stress-inducible 70
KDa heat-shock protein (HSp70) mimics Hsp70 isoforms from tissues.";
Biochem. J. 305:197-203(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
       DB 1; Length 640;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                          HS71_BOVIN STANDARD; PRT; 641 AA. 027975; 027964; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
       Score 47; DB 1,
Pred. No. 0.12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ANGUS;
MEDLINE-95030563; PubMed-7943958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 212-641 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRESS-INDUCED DAMAGE.
INDUCTION: BY HEAT SHOCK.
       92.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U09861; AAA73914.1; -. EMBL; U02891; AAA03450.1; -. HSSP; P19120; INGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
Query Match 92.2
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
                                                                                                                                                                                                          284 SLFEGIDFYT 293
                                                                                                                                          1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP70-1
                                                                                                                                                                                                                                                                                                              RESULT 9
H871_BOVIN
H871_BOVIN
DT 01-NOV
DE HEAT S
GN BOS ta
OC BOVIGA
OC BOVIGA
OC BOVIGA
OC BOVIGA
RR GLIEN
R
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Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P., Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.; "Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extracts
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hunt C., Morimoto R.I.; "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70."; Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.; "Human major histocompatibility complex contains genes for the major
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
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Drabbert B., Genthe A., Benecke B.-J.;
"In vitro transcription of a human hsp 70 heat shock gene by e
prepared from heat-shocked and non-heat-shocked human cells.";
                                                                Length 641;
                                                                                            Indels
                                                                                                                                                                                                                           HS71_HUMAN STANDARD; PRT; 641 AA.
P08107; P19790; O9UQMO; Q9UQL9;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 ROA PROTEIN 1 (HSP70.1) (HSP70-2).
(HSPAIA OR HSPAI) AND HSPAIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
       Chaperone; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
                                                               DB 1;
                                                               Score 47; DB 1
Pred. No. 0.12;
                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 14:8933-8949(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-91055806; Pubmed-1700760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89184548; PubMed-2538825;
                                                                92.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heat shock protein HSP70."
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
ATP-binding; Chaper.
                                                                                                                                        4111111 11
286 SLFEGIDEYT 295
                                                                Query Match
Best Local Similarity
                                                                                                                         1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                             Matches
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Hunt C., Calderwood S.;
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ID HS71_PIG
AC P34930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR001023; HSP70.
Pram; PF00012; HSP70.
PRINTS; PR00120; HSP70.1; 1.
PROSITE; PS00297; HSP70.1; 1.
PROSITE; PS0039; HSP70.2; 1.
APP-binding; Chaperone; Heat shock; Multigene family; MHC III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
N -> S (IN REF. 3; AAD21815).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS71_MOUSE STANDARD; PRT; 641 AA. P17879, 061689; P17879; 061680; Ceated) C1-NOV-1997 (Rel. 35, Last sequence update) 30-MAT-2000 (Rel. 39, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
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                                                                                                                                                                                                                                                                                                           EMBL, M59828; AAA63226.1; EMBL, M59830; AAA63227.1; EMBL, AF134726; AAD21816.1; EMBL, M17726; AAD21815.1; EMBL, M1777; AAA52697.1; EMBL, M24743; AAA59844.1; EMBL, X04676; CAA28381.1; EMBL, X04676; CAA28381.1; PIR; A29160; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70052 MW;
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Best Local Similarity 90.0
است 9; Conservative
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MIM; 603012;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            Gene 146:273-278 (1994).

Gene 146:273-278 (1994).

FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PUNCTION: IN COOPERATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYEEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OR NEWLY TRANSLATED POLYEEPTIDES IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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MEDLINE=92175874; PubMed=1339404;
Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
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EMBL; M76613; AAA57233.1; -.

EMBL; M76613; AAA57233.1; -.

EMBL; M76613; AAA57233.1; -.

HSP; JH0095; JH0095.

HSP; JH0095; JH0095.

RPGM; PF00012; HSP70-1.

RPGM; PF00012; HSP70-1; 1.

RPROSITE; PS00329; HSP70-2; 1.

RPROSITE; PS010329; HSP70-2; 1.

RPROSITE; PS010329; HSP70-3; 1.

RATP-binding; Chaperone; Heat shock; Multigene family; MHC III.

ROUNLICT 342 342 A -> R (IN REF. 1).

CONFLICT 627 PP (IN REF. 1).

SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;
"Characterization and sequence of a mouse hsp70 gene and its expression in mouse cell lines."; Gene 87:199-204(1990).
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
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                                                                                                                                                                                            TISSUE-Liver;
MEDLINE-94357449; PubMed-8076831;
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Matches 9; Conservative
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286 SLFEGIDFYT 295
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                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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P10591;
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Massa S.M., Sharp F.R.;
"CDNA cloning and expression of stress-inducible rat hsp70 in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-LEW.1W/GUN;
MEDLINE-95012453; PubMed-7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.2%; Score 47; DB 1; 90.0%; Pred. No. 0.12;
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PIR; S35718; S35718.
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InterPro; PR001023: HSP70.
Pfam; PF001021: HSP70. 1.
PRINTS; PR001301; HEATSHCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
ATP-binding; Chaperone; Heat sho SEQUENCE 641 AA; 70083 MW; F
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Bouquet Y.H.;
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HS71_RAT
AC 007439,
DC 007439,
DT 01-FEB
DT 01-NEW
DE HEAT SI
GS RATTUS
CC MAMMA1.
CO MAM
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                                                                                                                                                                                      happ'0 gene.;
Biochim. Biophys. Acta 1219:64-72(1994).
Biochim. Biophys. Acta 1219:64-72(1994).
Biochim. IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROPEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PATICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
BEDILNE-84368874; Pubmed-8086479;
Lisowska Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;
"Cloning, nucleotide sequence and expression of rat heat inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Place
InterPro; IPR001u2.,
A Figure Pro012; HSP70; 1.
A PROSITE; P800297; HSP70_1; 1.
DR PROSITE; P800297; HSP70_2; 1.
DR PROSITE; P8003036; HSP70_2; 1.
DR PROSITE; P801036; HSP70_2; 1.
DR PROSITE; P801036; HSP70_2; 1.
CONFLICT 71 72 KR -> NG (IN REF. 3).
CONFLICT 27 227 D -> H (IN REF. 3).
CONFLICT 27 227 D -> H (IN REF. 3).
CONFLICT 27 27 D -> H (IN REF. 3).
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"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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01-OCT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).
SSA1 OR YALO05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                         STRAIN=S288C / AB972;
MEDLINE-95028152; PubMed=7941740;
Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
Delanney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
the 42 kbp SP07-CENI-CDC15 region.";
Yeast 10:535-541(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-I- FUNCTION: SSAI MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSAI AND SSA2 PROTEINS IS EXPECTED. SSAI CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJINE-55203288; PubMed-7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                         Ogden R.C., Lee M.-C., Knapp G.; "Transfer RNA splicing in Saccharomyces cerevisiae: defining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
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  Nucleic Acids Res. 17:805-806(1989)
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STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 91-97 AND 325-341.
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO 207; 417 AND 421
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HSSP; P19120; 1ATR.
SWISS-2DPAGE; P10591; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEPD; 9788; -.
SGD; S0000004; SSA1.
InterPro; IPR001023; HSP70.
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                                                SEQUENCE FROM N.A
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**Rowaiski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,

**Rowaiski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,

**An den Hurk J., Babluk L.A., Zamb T.J.;

**The Heat-shock promoter-driven synthesis of secreted bovine herpesvirus

**The Heat-shock synthesis of secreted bovine herpesvirus

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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                               Length 641;
                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
Score 47; DB 1;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS72_bOVIN STANDARD; PRT; 641 AA. 027965; Q28122; 01-NOY-1997 (Rel. 35, Created) 01-NOY-1997 (Rel. 35, Last sequence update) 01-NOY-1997 (Rel. 39, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 2 (HSP70-2).
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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MEDLINE=94070117; PubMed=8249428;
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
                                                                                                                                                                                                                                                                                    92.2%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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NCBI_TaxID=9913;
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282 SLFEGIDFYT 291
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Best Local Similarity
Matches 9; Conserv
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SEOUENCE FROM N.A.
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DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_3; 1.

KW ATP-binding; Chaperone; Heat shock; Multigene family.

SQ SEQUENCE 641 AA; 70228 MW; 229C19EEBBF610DF CRC64;

Query Match

Query Match

92.2%; Score 47; DB 1; Length 641;

Best Local Similarity 90.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 1; Indels

QY 1 SLFEGIDIYT 10

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Db 286 SLFEGIDFYT 295
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ALIGNMENTS

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	AA.	Created)	sequence update)	•			Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;	dae; Littorina.				"Heat-shock genes in the heat-stressed genus Littorina.";	'DDBJ databases.						Carasssanarasan Cecki.	'toon ggorta	DB 5; Length 146;	s, 1; Indels				AA.	
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	PRT;	Created)	Last				a; Gastro	idea; Litt				at-stress	EMBL/Gen			,	 T					0; Mismatches				PRT;	
	PRELIMINARY;	(TrEMBLrel. 13,	(TremBLrel.	HEAT-SHOCK PROTEIN (FRAGMENT).		lena.	Metazoa; Mollusc	Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.	31219;	OM N.A.	Α.:	genes in the he	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.	EMBL; AF191828; AAF12787.1;	0; 1BA1.	InterPro; IPR001023; HSP70.	PS01036; HSP70_3; 1		146 146 146 AA: 16607 MW:		92.28;	'at	DIYT 10	 DFYT 88		PRELIMINARY;	
RESULT 1 090667	090667;	01-MAY-2000	01-JUN-2001	HEAT-SHOCK 1	HSC70.	Littorina plena.	Eukaryota; 1	Neotaeniogle	NCB1_TAXID=	SEGUENCE FROM N.A.	Hohenlohe P.A.;	"Heat-shock	Submitted ((	EMBL; AF191	HSSP; P19120; 1BA1.	InterPro; I		NON TER			Query Match	Matches 9;	1 SLFEGIDIYT	79 SLFEGIDFYT	RESULT 2	090670	03007
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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.2%; Score 47; DB 5; Length 158; 90.0%; Pred. No. 0.22; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                      BEQUENCE FROM N.A.

Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191830; AAF12789.1; -.
HSSP; P19120; 1BA1.
FINTERPO; IPR001023; HSP70.
FINTERPOSITE; PR00301; HEATSHCK70.
PROSITE; PR01301; HEATSHCK70.
FOR THE PROSITE; PR0130; HSP70.3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 5; Length 157;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (COT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191824; AAF12783.1;
HSSP: P19120; LBA1.
FINTES; PR0031013; HSP70.
PRINTES; PR003101; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 158 158 158 158 AA; B41E5356A24CAD2F CRC64;
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157 AA; 17834 MW; E8F743382B285EB2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9U668 PRELIMINARY; PRT; 158 AA.
09U668;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                          92.2%;
90.0%;
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Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                         Littorina plena.
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Q9U671;
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Q90668
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Q9U671
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**REALPHOLOHE P.A.;

**A Hohenlohe P.A.;

**L Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

**L Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

**REAL; AF191826; AAF12785.1; -...

**DR HSSP; P19120; 1BA1.

**DR HSSP; P19120; P1912; P19120; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Littorina scutulata.
Sukaryota: Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglosas: Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.2%; Score 47; DB 5; Length 155; 90.0%; Pred. No. 0.21; tive 0; Mismatches 1; Indels
                                                                Littorina scutulata.
Bukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglosas: Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
                                                                                                                                                            SEQUENCE FROM N.A.
Hohenlohe P.A.;
Hohenlohe P.A.;
Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAF12784.1;
HSSP; P19120; 1BA1.
InterPro; PR001023; HSP70.
PROSITE; PS01036; HSP70.]
                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%; Score 47; DB 5; Length 153; 90.0%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 153 NW; E29EE20C4CAF934D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
    01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT-SHOCK PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEAT-SHOCK PROTEIN (FRAGMENT).
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Matches 9; Conservative
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Matches 9; Conservative
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NON_TER
SEQUENCE
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090665;
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090665
ID 090
AC 091
DT 011
DT 011
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Q9U669
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Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplyaiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                      Olynov-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metzaca; Chordata; Craniata; Verfebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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"70-Kilodalton heat shock polypeptides from rainbow trout:
characterization of cDNA sequences.";
Mol. Cell. Biol. 4:1785-1791(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.2%; Score 47; DB 5; Length 220; 90.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220
24684 MW; FA8557F2BB85C37A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E4C745DE5484C17A CRC64;
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
NON_TER 1 1
NON_TER 220 SEQUENCE 220 AA; 24684 MW;
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
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HSSP; P08109; 1CKR.
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Pfam; PF00012; HSP70; 1.
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Best Local Similarity 90.0
Matches 9; Conservative
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SEQUENCE
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090520;
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                 Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
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"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191829; AAF12788.1; --
HSSP; P19120; IBAL.
InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                         "Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191827; AAF12786.1; --
HSSP; P19120; 1BA1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 5; Length 158 Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 AA; 17868 MW; D2ECE71042EC44CB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT_SHOCK PROTEIN (FRAGMENT).
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 AA.
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01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 92.2
Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
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                                                                            Littorina plena.
                                                                                                                                                                                                                            Hohenlohe P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Littorina plena
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044352
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044350
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063718;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 01, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
Rattus norveqicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
              Gaps
                                                                                                                                                                                 Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Entinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H., Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H., D'Ambrosio E., Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.

EMBL; Z27118; CAA81642.1; -.
HSSP; P08107; 1H40.
PROFIT: PF001012; HSP70.
PRAMTYS; PR001012; HSP70.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 92.2%; Score 47; DB 13; Length 367; 90.0%; Pred. No. 0.59; 1; Indels 1; Indels
               Indels
                                                                                                                                                                                                                                                                            Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: Y08578; CAA69892.1; -.
HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                  Heat shock.
NOW_TER 367 367
SEQUENCE 367 AA; 40405 MW; 8CD3DDBDF6E3C2CA CRC64;
                                                                                                                                          Last sequence update)
Last annotation update)
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    90.0%; Pred. No. 0.42;
tive 0; Mismatches
                                                                                                           367 AA
                                                                                                                               01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequ
01-UNU-2001 (TrEMBLrel. 17, Last anno
70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                              Interpro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.2
Best Local Similarity 90.0
Matches 9; Conservative
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               9; Conservative
                                                                                                            PRELIMINARY;
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     Best Local Similarity
Matches 9; Conserv
                                    1 SLFEGIDIYT 10
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Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
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                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Chondrosida; Chondrillidae; Chondrosia.
NCBI_TaxID=68574;
                                                                                                                                                                                                                                                                                                                                                                                                                                               92.2%; Score 47; DB 11; Length 455; ilarity 90.0%; Pred. No. 0.75; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Borchiellini C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026520; AAC05364.1; -.
HSSP; P08109; LCKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;
1 1
455 455
455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         044352;
01-JUN-1998 (TrEWBLrel. 06, Created)
01-JUN-1998 (TrEWBLrel. 06, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                044350;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
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Pred. No. 0.78;
0; Mismatches
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90.0%;
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Pfam; PF00012; HSP70; 1.
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Best Local Similarity 90.0°
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                                                                                            Best Local Similarity
Matches 9; Conserv
                                                                                                                                                 1 SLFEGIDIYT 10
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NCBI_TaxID=68578;
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Funiculinidae;
Funiculina.
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Bukaryota, Metazoa, Porifera, Calcarea, Calcinea, Clathrinida, Clathrinidae, Guancha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.2%; Score 47; DB 5; Length 467; 90.0%; Pred. No. 0.78; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                     92.2%; Score 47; DB 5; Length 467; 90.0%; Pred. No. 0.78; artive 0; Mismatches 1; Indels
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"Sponges paraphyly and the origin of Metazoa.";
Submitted (SEP-1999) to the EmBL/GenBank/DDBJ databases.
EMBL, PAT182195; AAF61297.1;
InterPro; IRR01023; HSP70.
PRINTS; PR00312; HSP70.1
PROSTIE; PS00329; HSP70.2; 1.
PROSTIE; PS00329; HSP70.2; 1.
PROSTIE; PS00329; HSP70.2; 1.
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Borchiellini C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AR026516; Aac05361.1; -.
HSSP; P08109; 1CKR.
InterPro; IPR001023; HSP70.
                                                                   1 1 47 47 47 467 AM; 23EB28FFD1873DA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51318 MW; F36FC06CB1DEE131 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEWBLrel. 15, Created)
01-0CT-2000 (TrEWBLrel. 15, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467 AA.
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PRINTS; PR00301; HEATSHOCK70.
                              PROSITE; PS01036; HSP70_3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.2
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                   Best_Local Similarity 90.0
Matches 9; Conservative
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252 SLFEGIDFYT 261
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SEQUENCE FROM N.A.
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                                                       NON_TER
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SEQUENCE
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09NJ92
AC 09NJ922
AC 09NJ922
DT 01-0CT-
DT 01-1JUN
DE HEAT SI
OX NUBL_TRAIN
OX NUBL_TRAIN
NA BOCCHE
RT SEQUENC

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044349
AC 044349;
DT 01-JUN-
DT 01-JUN-
DE HEAT-SE
OS FUNICULO
OS FUNICULO
OC EUKARYO
OC FUNICULO
OX NCEL_TAR
RN (1)
RP SEQUENC
RA BOTCHIE
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Appl Appli Appli Appli Appli Appli

Sequence 2

Sequence

Sequence Sequence

Sequence

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CITY: San Diego
STATE: California
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INPERMATION:
NAME: APPLICATION CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 4; Length 643; Pred. No. 2.4; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                US-08-363-010-1
US-08-911-434A-4
US-08-08-6428B-58
US-08-290-665A-58
US-08-290-665A-58
US-09-537-54
US-09-537-54
US-08-481-968A-15
US-07-912-122-4
                                                                                                                                               PCT-US93-06404-4
US-08-294-872-2
PCT-US95-09823-2
US-09-232-468A-114
US-08-686-968C-227
US-09-136-574A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ 1D NO: 3:
                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: unknown
TOPOLGGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 643 amino acids
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77.8%;
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Best Local Similarity 77.9
Matches 7; Conservative
1 SLFEGIDAY 9
RESULT
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Sequence 14, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 221, Appl
Sequence 221, Appl
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 18, Appli
Sequence 7, Appli
                                                                                               (without alignments)
2.487 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Appl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60,
                                                                                 December 6, 2001, 07:59:55; Search time 81.43 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence 8
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                                                                                                                                                                                                                                                                                                                                                                         1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTUS_COMD.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMD.pep:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-797-358B-3
US-09-457-046B-61
US-08-441-139-14
S183745-3
US-08-646-590B-32
US-09-69-225-32
US-09-69-225-32
US-09-1412-184-32
US-09-1412-184-32
US-09-1412-184-32
US-09-180-271-5
US-09-100-271-5
US-08-190-802A-221
US-08-190-802A-22
US-08-190-802A-22
US-08-190-803A-22
US-08-190-903A-22
US-08-190-903A-13
US-08-190-903A-13
US-08-100-93A-13
US-08-100-903A-13
US-08-100-903A-13
US-08-100-903A-13
US-08-100-903A-13
US-08-100-903A-13
US-08-100-903A-13
US-08-100-903A-13
US-08-100-903A-13
US-08-100-903A-100-103
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-687-865A-2
US-09-043-711-2
US-08-240-012-4
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US-08-676-841-8
                                                                                                                                                                                                                      212252 segs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          - protein search, using sw model
                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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                                                                                                                                                         1 SLFEGIDAY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                    PEP1-MOD8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match
                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                            Sequence:
                                                                                                                                                                                                                         Searched:
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Gaps

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1; Mismatches
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COMPUTER: IBM PS/4
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331400-38
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 311
TELECOMMUNICATION INFORMATION:
                                                                                                80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 66.7.
احد 6; Conservative
                                                                                                Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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CITY: ROSELAND
STATE: NEW JERSEY
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721 SIFRGIQAY 729
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286 SLYEGIDFY 294
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ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:3:
LENGTH: 800
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US-08-599-171A-32
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                                                                                                NGS-09-457-046B-61
Sequence 61, Application US/09457046B
Sequence 61, Application US/09457046B
Parant No. 6288B35
Parant No. 6288B35
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
FILE REFERENCE: 53679
CURRENT APPLICATION UNMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
TUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIPLEATION: 433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: D1619110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DCOKET NUMBER: 3646
TELECHOME: 516-742-4343
TELEPHOME: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-441-139-14
; Sequence 14, Application US/08441139
Patent No. 5773245
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.4%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: âmino acid
      11111:1 |
288 SLFEGVDFY 296
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165 SLFDGISAY 173
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Gaps
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FRESOUL;
FRESOUL;
FRATEART: DANCHIN, ANTOINE;GLASER, PHILLIPPE;KRIN, EVELYN;
FRATEICART: DANCHIN, ANTOINE;GLASER, PHILLIPPE;KRIN, EVELYN;
BAPLICART: DANCHIN, DANIEL;ULLAAN, AGNES;
TITLE OF INVENTION: ADENT CYCLASE DERIVATIVES AND THEIR
FILICAL USES
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,541
FILING DATE: 25-OCT-1989
Score 37; DB 1; Length 646; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence '32, Application US/08599171A

Patent No. 5814473

GENERAL INFORMATION:

APPLICANT: WARREN, Patrick V.

TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD
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Gaps
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Pred. No. 31;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/09412184
Patent No. 6268188
GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Warren, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: WARREN, PALTICK V.

TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,226
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                       US-09-069-226-32
; Sequence 32, Application US/09069226
; Patent No. 6013509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: HERROW, CHARLES J.
REGISTRATION 'NUMBER: 3314'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 69.6%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN
US-09-069-226-32
                                                                                                                                                                                                                                                                                                                               STREET: 6 BECKER F
CITY: ROSELAND
STATE: NEW JERSEY
                           |:|||| |
34 SIFEGIRGY 42
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      SLFEGIDAY 9
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                07068
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STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-412-184-32
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; Sequence 35, Application US/08646590B
; Patent No. 35962283
; GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Swanson, Ronald V.
TTTLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
STREET: 4225 Executive Square, Suite 1400
CITY: A Jolla
                                                                                                                                                                                                                         Score 32; DB 2; Length 303;
Pred. No. 31;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.6%; Score 32; DB 2; Length 303; 66.7%; Pred. No. 31; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,590B
FILING DATE: 08-May 1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/599,171
APPLICATION NUMBER: 08/599,171
FILING DATE: 09-FEB-1996
PRIOR APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 21-January-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D. Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REFERRENCE/DOCKET NUMBER: 09010/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619,678-5070
              TELEFAX: 201-994-1744

INFORMATION FOR SEO ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
US-08-599-171A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                             69.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acid
TYPE: amino acid
    201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66./۳
مار Gonservative 6; Conservative
                                                                                                                                                                                                                         Query Match 69.6
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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34 SIFEGIRGY 42
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ZIP: 92037
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
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US-08-646-590B-32
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Gaps
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Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REACHABLE FORPY disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,271
FILING DATE: 14-JAN-1999
PRIOR APPLICATION NUMBER: PCT/US98/03938
FILING DATE: 05-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/901,306
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/812,412
FILING DATE: 06-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
REGISTRATION NUMBER: 96,105
REGISTRATION NUMBER: 96,105
REGISTRATION NUMBER: 96,105
REGISTRATION NUMBER: 96,105
REFERENCE/DOCKET NUMBER: 96,105
REGISTRATION NUMBER: 96,105
REFERENCE/DOCKET NUMBER: 96,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Nikaido, Marmelstein, Murray & Oram 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                            NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P1615-7005
TELECOMMUNICATION: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09180271
Patent No. 6210930
GENERAL INPORMATION:
APPLICANT: FILIPPINI, Silvia
APPLICANT: LOMOVSRATA, Natalia
APPLICANT: FONSTEIN, Leonid
APPLICANT: FOLOMON, Anna L.
APPLICANT: HUTCHINSON, C. Richard
APPLICANT: OTTEN, Sharee L.
                                                                                                                                                                                TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.4%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: U.S.A.
ZIP:| 20005-5701
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-812-412-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 655 Fifte CITY: Washington
                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . |:| ||||
182 SVFRGIDA 189
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-180-271-5
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APPLICANT: LOMOVSKAYA, Natalia
APPLICANT: FONSTEIN, Leonid
APPLICANT: COLOMBO, Anna L.
APPLICANT: HUTCHINSON, C. R.
APPLICANT: HUTCHINSON, C. R.
APPLICANT: HUTCHINSON, T. N.
APPLICANT: HUTCHINSON, C. R.
APPLICANT: HUTCHINSON, C. R.
APPLICANTION: PROCESS FOR PREPARING DAUNORUBICIN AND TITLE OF INVENTION: DOXORUBICIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.6%; Score 32; DB 4; Length 303; 66.7%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
*APPLICATION NUMBER: US/08/812,412
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Nikaido, Marmelstein, Murray & Oram STREET: 655 Fifteenth Street N.W. Suite 330
                                            COMPUTER READABLE FUNCH:

MEDIUM TYPE: DISKELEL
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,184
FILING DATE:
CLASSIFICATION NUMBER: US/08/646,590
FILING DATE: 08-May-1996
APPLICATION NUMBER: 08/599,171
FILING DATE: 08-Fast-1996
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 21-January-1997
CLASSIFICATION NUMBER: 38,347
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph. D., Lisa A.
REGISTRATION INFORMATION:
TELEPHONE: 619/678-5099
INFORMATION FOR SEO ID NO: 32:
FEMATH: 303 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08812412
Patent No. 5989869
GENERAL INFORMATION:
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein
; FRACMENT TYPE: internal
US-09-412-184-32
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CORRESPONDENCE ADDRESS:
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
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34 SIFEGIRGY 42
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US-08-812-412-2
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; MOLECULE TYPE: protein US-08-225-488-2
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ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                               STATE: NY
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                                                                                                                                                                    COUNTRY:
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APPLICANT: Christensen, Tove
APPLICANT: Lehmbeck, Jan
TITLE OF INVENTION: A Fungus Wherein The area, pepC and/or
TITLE OF INVENTION: pepE Genes Have Been Inactivated
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 60134520 No. 6013452th
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.4%; Score 31; DB 3; Length 495; 83.3%; Pred. No. 88;
                                                                                                                          Score 31; DB 4; Length 403;
Pred. No. 70;
                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,415
FILING DATE: 14-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CAROL
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4657.204-US
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acid
                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                             RESULT 11
US-09-079-415-4
; Sequence 4, Application US/09079415
; Patent No. 6013452
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Patent No. 5846802
GENERAL INFORMATION:
APPLICANT: Buxton, Frank
                                                                                                                            67.48;
LENGTH: 403 amino acids
                                                                                                                          Query Match 67.4
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                  ; TYPE: amino acid
; TOPOLGY: linear
; MOLECULE TYPE: protein
US-09-180-271-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-079-415-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                           |:| ||||
182 SVFRGIDA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                    1 SLFEGIDA 8
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| 173 EGVDAY 178
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US-08-225-488-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mochly Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: W0-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPENDENCE ADDRESS:
ADDRESSE: Dellinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
APPLICANT: Visser, Jacob
TTLE OF INVENTION: No. 5846802el Fungal Protease
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 96;
1; Mismatches
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APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,214
FILING DATE: 13-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                              Ciba-Geigy Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-190-802A-221
; Sequence 221, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Spruil, W. Mirray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 4-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEPHONE: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%;
illarity 83.3%;
Conservative
                                                                                            ADDRESSEE: Ciba-Geigy Cc
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 533 amino acids
amino acid
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                                                                                                         Score 30; DB 4; Length 35; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Paerce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18 MAY-1994
CLASSIFICATION 1424
PRICE APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq. David A
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENCE/DOCKET NUMBER: 600-1-069 CIP
TELEFRAN: 201343-1684
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Pred. No. 19;
3; Mismatches
                                                                                                                                                3; Mismatches
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        ; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SOF1 rIII, Fig.
US-08-477-346-221
                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/08245511 Patent No. 5928900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITÝ: Hackensack
                                                                                                           65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 amino acids
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                           Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-245-511-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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US-08477-346-221
; Sequence 221, Application US/08477346
; Patent No. 6262033
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses;
TITLE OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 1; Length 35; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE_POCKET NUMBER: 250-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-1500
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SOF1 rill, Fig. 43
US-08-190-802A-221
                                  NAME: Fabian, Gary R.
REGIGSTRATION NUMBER: 33,875
RECEPRINCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.2%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: unknown
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ZIP: 20006-1812
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 6, 2001, 08:00:51; Search time 50.21 Seconds (without alignments) 6.572 Million cell updates/sec Run on:

PEP1-MOD8A 46 1 SLFEGIDAY 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	SUMMARIES		P115		061696	092260	P08106	Q28222 cercopi	P10592		P09446	DICDI P36415 dictyosteli	027975		SE P17879 mus m						P27541	091233		001233	P02827			SI P02826 dros		ΑE	_HUMAN P17066 homo sapien	Q04967 sus s	PUCGR Q01877 puccinia gr	902	
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P34931 homo sapien P16627 mus musculu P53623 pichia angu Q10265 schizosacch P53421 pichia angu P27322 lycopersico P26413 glychie max P19378 cricetulus P11142 homo sapien P08109 mus musculu P87047 paracoccidi O65719 arabidopsis	cida; Filarioidea;  major immunogen in demic area.";  MUNOGEN IN A ENDEMIC AREA. N 70 FAMILY.  ad through a collaboration end the EMBL outstation. en or estrictions on its s content is in no way ge by and for commercial //www.isb-sib.ch/announce/	CRC64; Length 322; ; Indels 0; Gaps 0;
.4 641 1 HS7H_HUMAN .4 641 1 HS7T_MOUSE .4 642 1 HS72_PICAN .4 644 1 HS71_PICAN .4 644 1 HS71_PICAN .4 646 1 HS72_LYCES .4 646 1 HS72_LYCES .4 646 1 HS7C_RUMAN .4 646 1 HS7C_RUMAN .4 646 1 HS7C_RUMAN .4 649 1 HS77_MOUSE .4 649 1 HS73_ARATH	ALIGNMENTS  SSULT 1  S70_ONCVO D .MS70_ONCVO D .MS70_D .MS70_ONCVO D .MS70_D .MS70_ONCVO D .MS70_D .MS70_ONCVO D .MS70_D .MS70_D .MS70_ONCVO D .MS70_D .	AA; 35614 MW; 2BA3A2E8155A7180 11y 88.9%; Score 40; DB 1; 1servative 0; Mismatches 1 51 STANDARD; PRT; 372 AA.
334 336 337 337 337 337 337 337 337 337 337	HESULT 1 HS70_ONCVO TD HS70_ONCVO TD THS70_ONCVO TD THS70_ONCVO TD THS70_SI TD THEB-1996 (Rel. 13, Last sold) TD THEB-1996 (Rel. 33, Last sold) TD THES TS TO THES STATE THE TO THE SOLD SHEPPOLS; HSPPOLS; TD THES THE THE THE SHEPPOLS; TD THES TENDING; HSPPOLS; TD THES TENDING; HSPPOLS; TD THE TON TER SPECES STATE THE NON TER STATE THE	h Simi Simi 8; FEGID FEG
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HSP70II.

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Perry M.D., Aujame L., Shtang S., Moran L.A.;
"Structure and expression of an inducible HSP70-encoding gene from
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HSSP; P19120; LATR.
MGD; MGI: 96244; HSp70-3.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PROSITE; PS00297; HSP70_1; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS01336; HSP70_3; 1.
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88.9%;
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Les 8; Conservative
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                                                            Mus musculus.";
Gene 146:273-278(1994).
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092260;
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Matches
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HS70_PENCI
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MEDLINE=91099690; PubMed=2269441;
la Rosa M., Sconzo G., Gludice G., Roccheri M.C., di Carlo M.;
"Sequence of a sea urchin hsp70 gene and its 5' flanking region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-86111900; PubMed=2868009;
MEDLINE-86111900; PubMed=2868009;
"Molecular cloning and analysis of DNA complementary to three mouse
Mr = 68,000 heat shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 96:295-300(1990).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                 Echinozoa;
                                                                                                                                                                     Paracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41347 MW; 5F8C1C590527A659 CRC64;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-UUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS73_MOUSE STANDARD; PRT; 420 AA. 061696; 061697; 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT). HSP70-3 OR HSP70A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1;
Pred. No. 0.72;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pram; Pro0012; HSP70; 1. PROSITE; PS00129; HSP70; 1. 1
PROSITE; PS001329; HSP70_1; 1. 1
PROSITE; PS010316; HSP70_1; 1. 1
PROSITE; PS01036; HSP70_3; 1. 1
ATP-binding; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X16544; CAA34544.1; -. PIR; PQ0138; PQ0138.
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 AA;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P19120; 1NGJ
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286 SLFEGIDYY 294
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                                                                                                                                                                                                                                                                       Paracentrotus
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RESULT 3
HS73\_MOUSE
HS73\_MOUSE
DC 061696,
DT 01-NOV.
DT 01-NOV.
DT 01-NOV.
DT 01-NOV.
DT 01-NOV.
DC 01697,

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FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING ON NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES EGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBERANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE. INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium
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Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
"Molecular cloning and expression of a Penicillium citrinum
allergen with sequence homology and antigenic cross-reactivity
a hsp70 human heat shock protein.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1; Length 420;
Pred. No. 0.82;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GG-2001 (Rel. 40, Created)
62-2001 (Rel. 40, Last sequence update)
76-2001 (Rel. 40, Last annotation update)
SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 V -> G.
46292 MW; 5DAlC6155C7B16B5 CRC64;
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STANDARD;
      289 SLFEGIDFY 297
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284 SLFEGIDFY 292
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                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9534;
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                                                                                                                                  HS71_CERAE
Q2822;
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                                                                                        RESULT 6
HS71_CERAE
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (HSP70).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86304452; PubMed-3017985; Morimoto R.I., Banerji S.S.; Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.; Grganization, nucleotide sequence, and transcription of the chicken HSP70 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Pred. No. 1.3;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                          Score 40; DB 1; Length 503;
Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;
                                                                                                                                                                                                                                                                            SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                          InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   634 AA.
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last seq
01-FEB-1994 (Rel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.0%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00301; HEATSHOCK70.
                                                                                      EMBL; U64207; AAB06397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J02579; AAA48825.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
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Best Local Similarity 88.۶۰
درم 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 SLFEGIDFY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A25646; A2564
HSSP; P19120; 1ATR
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SLFEGIDAY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                            HSSP; P19120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS70_CHICK
P08106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
HS70_CHICK
ID 70_CHICK
ID 70_1-AUG
DT 01-AUG
DT 01-FEB
DS Gallus
OC BURALY
OC Gallus
OX NCBLLS
OX C ALTOR
OX NCBLLS
OX NCBLS
OX NCB
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A Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;

The hsc70 gene which is slightly induced by heat is the main virus inducible member of the hsp70 gene family.";

EEBS Lett. 355:282-286(1994).

-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE OF REEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC OF NEWLY TRANSLATED POLYPEPTIDES OF PROTEINS THE NOTION THEY ARE INVOLVED IN SIGNAL TRANSDOCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES STREAMS TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

--- INDUCTION: BY HEAT SHOCK.

--- INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@illo.ch).
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                                                                                                                                                                                                                                      Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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38 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.0%; Score 40; DB 1; Length 638; 88.9%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Kidney;
MEDLINE=95080396; PubMed=7988690;
                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      638 AA; 69920 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEAM: PF00012; HSP70; 1.
PRINTS: PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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P10592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
HS72_YEAST
ID HS72_YI
AC P10592;
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1 SLFEGIDAY 9

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Gaps

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Length 638 Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=93077053; PubMed=1339375;
Scorac G., Scardina G., Ferraro M.G.;
"Characterization of a new member of the sea urchin Paracentrotus 11vidus hap70 gene family and its expression.";
Gene 121:353-358(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%; Score 40; DB 1; Length 639;
88.9%; Pred. No. 1.3;
iive 0; Mismatches 1; Indels
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;
                                                                                                                                                                                                    ACETYLATION.
23BDDD120C194912 CRC64;
                                                                                                                                                                                                                                                                                       Score 40; DB 1;
Pred. No. 1.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
11-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               639 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paracentrotus lividus (Common sea urchin).
                                                                                                                                                                                                                       638 AA; 69338 MW;
                                                                                                                                                                                                                                                                                           87.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X61379; CAA43653.1; -. PIR; JC1391; JC1391.
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InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               111111 |
282 SLFEGIDFY 290
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                                                                                                                                                                                                                                                                                                                                                                                     1 SLFEGIDAY 9
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Q06248;
                                                                                                                                                                            INIT_MET
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSP70IV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norbeck J., Blomberg A.; Protein expression during exponential growth in 0.7 M NaCl medium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (Sep-1994) to the SNISS-PROT data bank.
-!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.; "Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                      Slater M.R., Craig E.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                            Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C;
Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                  01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
AFAT SHOCK PROTEIN SSA2.
SSA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electrophoresis 15:1466-1486(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
                                                                                                                                                                                                                                                                                              MEDLINE=89128457; PubMed=2644626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95203288; PubMed=7895733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACETYLATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 91-97 AND 325-341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X12927; CAA31394.1; -. EMBL; Z73129; CAA97472.1; -. EMBL; X97560; CAA66167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 71-638 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10592; YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001023; HSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S20139; S20139.
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S0003947; SSA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEOUENCE OF 186-195
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                           NCBI_TaxID=4932;
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                                                                                       MEDLINE-94043116; PubMed-8226849;
Eddy R.J., Sauterer R.A., Condeelis J.S.;
Eddy R.J., Sauterer R.A., Condeelis J.S.;
Redinactin, an agonist-regulated F-actin capping activity is associated with an HSC70 in Diotyostelium.";
J. Biol. Chem. 268:23267-23274(1993).
-I- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROFIEIN CAP92/A4. ACTS AS A CHAPERONE BY STIMULATING THE REPOLDING OF DENATURATED CAP32 AND CAP34.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSSIGIDLGTTYSCVGVWQNDRVEIIAND -> IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
                                                                                                                                                                                                                                                                         OF THE CELL CORTEX AND CELL PROTRUSIONS.
-!- DEVELOPMENTAL STAGE: HEAT SHOOK COGNITE PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 640; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N -> T (IN REF. 2).
V -> A (IN REF. 2).
S -> A (IN REF. 2).
V -> P (IN REF. 2).
E -> P (IN REF. 2).
ZEGBDCZDB96A9F5D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X75263; CAA53039.1; -. EMBL; L22736; AAA33219.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P36415; DICTY.
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88.9%;
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Pfam; PF00012; HSP70; 1.
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Best Local Similarity 88.30,
Local 8; Conservative
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64
180
237
240
341
352
70499 N
              EMBO J. 12:3763-3771(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS01036; hsrrugarp-binding; Chaperone.
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284 SLFEGIDEY 292
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cap32/34.";
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HS71_BOVIN
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                               Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94008983; PubMed-8404847; Hartmann H., Lottspeich F., Nogel A.A., Schleicher M.: "The heat shock cognate protein from Dictyostellum affects actin polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Pred. No. 1.3;
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00229; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetczoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last annotation update)
HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
                                                                                         (Rel. 10, Created)
(Rel. 10, Last sequence update)
(Rel. 28, Last annotation update)
                                                        640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 AA.
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                                                        PRT;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88297155; PubMed-2841196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%;
88.9%;
                                                                                                                                  01-FEB-1994 (Rel. 28, Last a
HEAT SHOCK 70 KDA PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M18540; AAA28078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P19120; 1NGI.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
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                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JT0285; HHKW7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
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287 SLFEGIDFY 295
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                                                                                                                                                                                                                                                                                                                                                                               characterization.
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                                                                                                                                                                              OR HSP70A.
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                                                                                             01-MAR-1989
01-MAR-1989
                                                     HS7A_CAEEL
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P36415;
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RESULT 9
HS7A\_CAEEL
HS7A\_CAEEL
HS7A\_CAEEL
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Gaps

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Indels

RESULT 10
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1D AC P36415
DT 01-JUN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
MEDLINE-86016721; PubMed-3931075;
                                                                      SEQUENCE FROM N.A.
MEDLINE=91055806; Pubmed=1700760;
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EMBL; AF134726; AAD21816.1; -.
EMBL; AF134726; AAD21815.1; -.
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                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                      region.
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FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PROCETION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYEPPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLX AN ADDITIONAL ROLE BY PROVIDING A DENIVING FORCE FOR PROTEIN TRANSLOCATION. WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROFILES. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDOPHOBIC CHARACTER EXPOSED BY POLYBEPTIDES DURING TRANSLATION. AND MEMBRANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                               Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hep70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
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                                                                                                                                                                                                                                                               Grosz M.D., Skow L.C., Stone R.T.;
"An AluI polymorphism at the bovine 70 kD heat-shock protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRESS-INDUCED DAMAGE.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 1; Length 641; Pred. No. 1.3;
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P08107; P19790; Q9UQMO; Q9UQL9;
01-AUG-1988 (Rel. 08, Created)
01-F82=1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1/HSP70-2).
(HSPAIA OR HSPAI) AND HSPAIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shock; Multigene family.
6D548263E98780F9 CRC64;
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                                                                                                                                                                                                                          STRAIN=ANGUS;
MEDLINE=95030563; PubMed=7943958;
                                                                                                  MEDLINE=95126904; PubMed=7826329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70250 MW;
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                                                                                                                                                                                                         SEQUENCE OF 212-641 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00297; HSP70_1; 1. PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1.
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88.9%;
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Pfam; PF00012; HSP70; 1.
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                              SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
           Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641 AA;
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                             NCBI_TaxID=9913;
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ID HS71_H

AC P081107

DT 01-FEB

DT 20-AUG

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X-RAY! CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.

XA MEDLINE-9924376; PubMed=10216320;

As osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

Structure of a new crystal form of human hsp70 Arpase domain.";

Acta Crystallogr. D 55:1105-1107(1999).

COT CREATER HSP70S IN WITH OTHER CHAPERONES, HSP70S STABILIZE OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OKGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAX AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PARHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONNEATIVE OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES STRUCKE TRANSLOCATION, OR FOLLOWING STREAMS THROUGH THEIR RABILITY TO RECOGNIZE NONNATIVE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES STRUCKED PLAYER PROTEINS TRANSLOCATION, OR FOLLOWING STREAMS THROUGH THE NATIONAL TRANSLOCATION, OR FOLLOWING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING TRANSLATION THROUGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-22 nm. Second 2786141;
MEDLINE-87066768; PubMed=3786141;
Drabent B., Genthe A., Benecke B.-J.;
Drabent B., Genthe A., Benecke B.-J.;
"In vitro transcription of a human hsp 70 heat shock gene by extracts mrenared from heat-shocked and non-heat-shocked human cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).
ROWEN L., QIN S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
LOTELZ C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-36 AND 360-424 FROM N.A.
MEDLINE-89184548; PubMed-2538825;
Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
"Human major histocompatibility complex contains genes for the major heat shock protein HSP70.;
                                                                                                                                                                                                                                                                                                               Hunt C., Morimoto R.I.; "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleodide sequence of human hsp70."; Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
Miner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. | Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared from heat-shocked and non-hear
Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-22 AND 618-641 FROM N.A.
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pep1-mod8a.rsp

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EMBL; M69100; -; NOT_ANNOTATED_CDS.
PIR; S35718; S35718.
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88.9%;
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است 8; Conservative
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286 SLFEGIDFY 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS71_PIG
P34930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perry M.D., Aujame L., Shtang S., Moran L.A.;
"Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                         PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS003297; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hunt C., Calderwood S.;
"Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
Gene 87:199-204(1990).
                                                                                                                                                                                                                                                                                                  I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
W; 78F513118C96DE66 CRC64;
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Pred. No. 1.3;
0; Mismatches 1; Indels
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P17879; 061689;
01-A0G-1990 (Rel. 15, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annottation update)
HEAT SHOCK 70 AD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94357449; PubMed-8076831;
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MEDLINE-90236310; PubMed-2332169;
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                   PIR; A25773; A25773.
PDB; 1HJO; 21-OCT-98.
SWISS-2DPAGE; P08107; HUMAN.
EMBL; X04676; CAA28381.1;
EMBL; X04677; CAA28382.1;
PIR; A29160; A29160.
PIR; A45871; A45871.
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Best Local Similarity
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H871_MOUSE
H871_MOUSE
DT P1870_M
DT P17870_M
DT O1-AUG
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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REMBL; M76613; AAA57233.1; --
REMBL; M76613; AAA57233.1; --
REMBL; M76613; AAA57233.1; --
RESP; P19120; 1NGC.
RESP; P19120; 1NGC.
RESP; P19120; 1NGC.
RESP; P19203; HSP70-1.
REMINES; PR00301; HSP70, 1; 1.
REMINES; PR00302; HSP70, 1; 1.
REMINES; PS00129; HSP70_1; 1.
REMINES; PS00136; HSP70_2; 1.
REMINES; PS00136; HSP70_3; 1.
REMINES; PS
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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MEDLINE-92175874; PubMed-1339404;
Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 1.3;
0; Mismatches 1; Indels
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HATS SHOCK 70 KDA PROYEIN 1 (HSP70.1).
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BIOCHIM. Biophys. Acta 1219:64-72(1994).

-I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYEPTIDES IN THE CYTOSOL AS WELL. AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLACATION, OR FOLLOWING STRESS-INDUCED DAWAGE.

-I- INDUCTION: BY HEAT SHOCK.

-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94096443; PubMed-8271311;
Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
"cDNA cloning and expression of stress-inducible rat hsp70 in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=LEW.1W/GUN;
MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
MISDININE-84.368874; PubMed-8086479;
Lisowska 94. Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;
"Cloning, nucleotide sequence and expression of rat heat inducible
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                                                                                                                                                                                                    Score 40; DB 1; Length 641;
Pred. No. 1.3;
0; Mismatches 1; Indels
                                                                                                                              one; Heat shock; Multigene family. 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   HS71_RAT STANDARD; PRT; 641 AA. 007439; P42853; Created) 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) HSP70-1 AND HSP70-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurosci. Res. 36:325-335(1993)
                                               PRINTS; PRO0301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat sh
SEQUENCE 641 Aa; 70083 MW;
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88.9%;
             InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                        Rattus norvegicus (Rat).
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HSSP; P19120; 1NGC
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SEQUENCE FROM N.A.
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
AIP-binding; Chaperone; Heat shock; Multigene family; MHC III.
CONFLICT 71 72 KR -> NG (IN REF. 3).
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D -> H (IN REF. 2 AND 3).
G -> A (IN REF. 3).
DO2D96751C868583 CRC64;
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                                                       EMBL; L16764; AAA17441.1; --
EMBL; X77208; CAA54423.1; --
EMBL; X77207; CAA54422.1; --
EMBL; X77271; CAA52328.1; --
HSSP; P19120; 1NGC.
InterPro; IPRO1023; HSP70.
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PRINTS; PR00301; HEATSHOCK70.
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Sequence 18,
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-441-139-14
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US-08-477-046B-61
US-08-477-046B-61
US-08-878-989-18
US-08-878-989-18
US-08-860-150-7
US-09-272-796-18
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US-09-272-796-18
US-09-272-796-18
US-08-467-155A-11
US-08-67-155A-11
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US-08-201-038-11
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Gapop 10.0 , Gapext 0.5
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US-08-476-515A-84
US-08-652-877-84
US-08-652-877-86
US-08-652-877-90
US-08-652-877-90
US-08-652-877-90
US-08-652-877-90
US-08-6469-537A-7
US-08-548-468-10
US-08-548-468-10
US-08-646-590-32
US-08-646-590-32
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Pred. No. 0.15;
1; Mismatches
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US-09-412-184-32
US-08-960-756-4
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08797358B Patent No. 626847B GENERAL INFORMATION: APPLICANT: Adams, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 643 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS.
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Best Local Similarity 88.9%;
Matches 8; Conservative
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STREET: 405 Lexington Avenue CITY: New York
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                                                            ZIP: 10174
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US-09-245-041-15
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                                                                                                             Sequence 14, Application US/08441139
Fatent No. 577345
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Methods for Modifying the Production of TITLE OF INVENTION: a Polypeptide NUMBER OF SEQUENCES: 80 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 646;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,139

FILING DATE: 15-MAY 1995

CLASSIFICATION NUMBER: US/08/441,139

FILING DATE: 15-MAY 1995

ATTORNEY/AGENT INFORMATION:

NAME: D16191io, Frank S.

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION SHOWER: 16-742-4346

TELEFRA: 516-742-4366

TELEFRA: 516-742-4366

TELEFRA: 230 901 SANS UR

INFORMATION FOR SED ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 1;
Pred. No. 0.39;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 52, Application US/08928692; Patent No. 5958727; GENERAL INFORMATION: APPLICANT: Brody, Howard APPLICANT: Lamsa, Michael; APPLICANT: Hansen, Kim APPLICANT: Hansen, Kim APPLICANT: Hansen, Kim APPLICANT: Hansen, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.88;
88.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.8
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-441-139-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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286 SLYEGIDFY 294
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288 SLFEGVDFY 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                 11530
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APPLICANT: MOOSE, K.
APPLICANT: MOOSE, K.
APPLICANT: MOOSE, C.
APPLICANT: MAGIE, D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT:
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
TITLE OF INVENTION WINBER: US/09/245,041
CURRENT PAPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: 60/103,630
EARLIER FILING DATE: 1998-10-20
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: FASTESQ for Windows Version 3.0
SOFTWARE: FASTESQ for Windows Version 3.0
TYPE: PRT
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28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OFFRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 70.8%; Score 34; DB Best Local Similarity 100.0%; Pred. No. 28; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                        CLASSIFICATION: ...
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09245041 Patent No. 6274339
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 74944
REFERENCE/DOCKET NUMBER: 74124
TELECOMMUNICATION INFORMATION: 7412-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 52: SEQUENCE CHARACTERISTICS: LENGTH: 339 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
US-08-928-692-52
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US-09-245-041-15
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GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 61
LENGTH: 458
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                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION NUMBER: US/08/441,139
FILING APPLICATION DATA:

APPLICATION NUMBER: US/08/997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:

NAME: Didiglio, Frank S:

REGISTRENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:

TELERATION NUMBER: 8646
TELECOMMUNICATION INFORMATION:

TELERAT: 230 901 SANS UR

SEQUENCE CHARACTERISTICS:

LENGTH: 679 amino acids

TYPE: amino acid

STRANDEDNESS: single

TTERENCE CHARACTERISTICS:

LENGTH: AVDE: DATA

TYPE: AMINO ACID

STRANDEDNESS: Single
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Pred. No. 1.6e+02;
1; Mismatches 2;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5865803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana US-09-457-046B-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.78;
75.08;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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APPLICANT: Yaver, Deborah S.
APPLICANT: Lamasa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587270 NO. 5958727disk of No. 5958727th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Sequence 5, Application US/08441139
Patent No. 5773245
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 2;
Pred. No. 1.3e+02;
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STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                Sequence 53, Application US/08928692
Patent No. 5958727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                        STREET: 405 Lexington Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
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US-08-928-692-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 11530
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 6; Conserv
                                                                                                           GENERAL INFORMATION:
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                                          US-08-928-692-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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Gaps

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Sequence 7, Application US/09338132

Sequence 7, Application US/09338132

Sequence 7, Application US/09338132

GENERAL INFORMATION:

APPLICANT: Hemmings, Brian A.

APPLICANT: Millward, Thomas A.

TITLE OF INVENTION: UNCLEAR DEF2-Related (NDR) Kinases

FILE REFERENCE: 4-20265/A/PCT

CURRENT FILING DATE: 1999-06-22

EARLIER APPLICATION NUMBER: 08/860,150

EARLIER FILING DATE: 1997-06-19

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1994-12-22

NUMBER OF SEQ. ID NOS: 18

SOFTWARE PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ballman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Calley. Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
APPLICANT: Bhah, Purvi
TITLE OF INVENTION: DISBASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 3; I
Pred. No. 1.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                          Score 31; DB 2; I
Pred. No. 1.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
(NS-09-272-796-18
(S-09-272-796-18) Application US/09272796
(Patent No. 6207148
(GENERAL, INOFMATION:
HAPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegley, Neil C.
                                                                                                                                                                                                                                                                                                                                       G4.68;
Best Local Similarity 62.58;
Matches 5; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 465
TYPE: PRT
CRGANISM: Homo sapiens
US-09-338-132-7
                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-08-860-150-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palo Alto
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380 SFFEGVDW 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SLFEGIDF 8
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COUNTRY:
                                                                                                          SEQ ID NO 7
LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incvt-
STREF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/874,989
FILING DATE:
APPLICATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 2;
Pred. No. 1.6e+02;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
LIBRARY: GenBank
CLONE: 8541070
US-08-878-989-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.6%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 Port CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SLFEGIDF 8
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                                                                                                                                                                                                            Length 276;
                                                                                                                                                                                                           62.5%; Score 30; DB 1; Length 276
55.6%; Pred. No. 1.4e+02;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,198
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.5%; Score 30; DB 2; Le
55.6%; Pred. No. 1.4e+02;
tive 2; Mismatches 2;
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ER: 00398/100002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,155
FILLING DATE: 06-JUN-1995
CLASSIPECATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/10
TELEPHONE: 617/542-8906
                                                                                                 not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                            Query Match 62.5
Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                              TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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62 SLFNGLSFH 70
                                                                                                                                                                                                                                                                                                                        62 SLFNGLSFH 70
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       TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                       US-08-467-155A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-628-198-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC.COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/467,155A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 4; 1
Pred. No. 1.6e+02;
2; Mismatches 1.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASEED for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/878,989
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELEFRONE 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-467-155A-1; Sequence 1, Application US/08467155A; Patent No. 5736377
                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 64.6%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Band,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LIBRARY: GenBa
; CLONE: 8541070
US-09-272-796-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 |||:|:
380 SFFEGVDW 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07343
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/467,155
FILING DATE: 06-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CLARY PAULT:
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,167
TELEPRANICATION INFORMATION:
TELEPRANICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 & anino acids
TYPE: anino acids
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%;
55.6%;
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Best Local Similarity 55.6
Matches 5; *Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein PCT-US96-07343-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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62 SLFNGLSFH 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                             Sequence 1, Application US/09201038

Patent No. 6153387

GENERAL INRORMATION:
GENERAL INRORMATION:
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTY: USA
COUNTY: USA
IN MENTIN MYDER FORM:
MEDITM TYPER FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30.162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/628,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                  Gaps
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         Length 276;
Score 30; DB 5; Length 2/o
Pred. No. 1.4e+02;
                                2; Mismatches
                                                                                                                          Search completed: December 6, 2001, 07:59:57 Job time: 365 sec
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Gaps

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Sequence 1, Application PC/TUS9607343
GENERAL INFORMATION:
APPLICANT: New England Medical Center Hospitals, Inc.
APPLICANT: New England Medical Center Hospitals, Inc.
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

ZIP: 02110-2804 COMPUTER READABLE FORM:

USA

COUNTRY:

Length 276;

Score 30; DB 4; Length 276 Pred. No. 1.4e+02; 2; Mismatches 2; Indels

Query Match 62.5%; Best Local Similarity 55.6%; Matches 5; Conservative

||| |: |: 62 SLFNGLSFH 70 1 SLFEGIDFY 9

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RESULT 15 PCT-US96-07343-1

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                                                                                                                                                6, 2001, 07:59:56 ; Search time 81.43 Seconds
(without alignments)
2.487 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40,
Sequence 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                  .4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-599-171A-32
US-08-646-590B-32
US-09-6059-2632
US-08-412-184-32
US-08-441-139-14
US-08-441-139-14
US-08-441-139-14
US-08-441-139-14
US-08-441-139-14
US-08-441-139-16
US-08-441-139-16
US-08-440-103-16
US-08-440-103-16
US-08-440-103-16
US-08-440-16
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US-08-612-973-44
US-08-612-973-44
US-08-612-973-44
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US-08-612-973-44
US-08-612-973-44
US-08-612-973-44
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                                                                                                                                                                                                                                                                                                                                                                                                         212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                          1 SLFEGIDGY 9
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Match Length
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                                                                                                                                                       December
                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                             OM protein
                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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                                                                                                                                                          Run on:
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                            Sequence 2, Appli
Sequence 46, Appl
Sequence 46, Appl
Sequence 18, Appl
Sequence 36, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: WARREN, PALTICK V.
TITLE OF INVENTION:
TORRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 303;
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                                                                                                 PCT - US92 - O5374A - 2
PCT - US92 - O784 - 2
US - O8 - 927 - 346
US - O8 - 927 - 597 - 46
US - O8 - 828 - 488 - 7
US - O8 - 440 - 103 - 118
US - O8 - 210 - 118
US - O8 - 210 - 118
US - O8 - 210 - 118
US - O8 - 612 - 210 - 118
US - O8 - 612 - 973 - 36
                              US-08-050-132A-2
US-08-750-222A-2
US-08-815-652B-2
US-08-254-353A-2
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Pred. No. 4.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
FILING DATE: CONCULTENTLY
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331400-38
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/08599171A
Patent No. 5814473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 3314(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1704
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 303 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.2%;
ilarity 77.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
1 SLFEGIDGY 9
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-599-171A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-599-171A-32
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79.2%; Score 38; DB 3; Length 303; 77.8%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/09412184
Sequence 32, Application US/09412184
Datent NO. 6268188
GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Swanson, Ronald V.
ATILE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                     COMPUTER: LAW ESON CORRECT STATES OF STEMS OF ST
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09-FEB-1996
                                                                                                                                                       IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELËFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 32:
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 303 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: LINEAR;
MOLECULE TYPE: PROTEIN
US-09-069-226-32
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 08-May APPLICATION NUMBER: FILING DATE: 09-FEI
                                               E: NEW JERSEY
TRY: USA
07068
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34 SIFEGIRGY 42
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                             ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
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US-09-412-184-32
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                                                                                                                                                    Sequence 32, Application US/08646590B

Sequence 32, Application US/08646590B

Patent No. 5962283

GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Swanson, TRANSAMINASES AND AMINOTRANSFERASES
TITLE OF INFURITION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 303;
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Patent No. 6013509
GENERAL INFORMATION:
APPLICANT: WARREN
TITLE OF INVENTION: PALTICK V.
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,590B
FILING DATE: 08 May-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB;
Pred. No. 4.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFRERENCE/DOCKET NUMBER: 09010/017001
TELECOMMUNICATION INFORMATION:
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,171
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 21-January-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.28;
77.88;
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Best Local Similarity 77.5-
T. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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34 SIFEGIRGY 42
              1:|||| ||
34 SIFEGIRGY 42
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FRAGMENT TYPE:
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ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92037
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US-09-069-226-32
                                                                                                                                                          JS-08-646-590B-32
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Gaps

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RESULT 7
US-09-457-046B-61
Sequence 61, Application US/09457046B
Sequence 61, Application US/09457046B
Sequence 61, Application US/09457046B
GENERAL INFORMATION:
APPLICANT: Cordeau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REPERENCE/POCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 646 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
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Best Local Similarity 77.8
Matches 7; Conservative
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                      Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                          1||||:| |
288 SLFEGVDFY 296
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286 SLYEGIDFY 294
                                                                                                 1 SLFEGIDGY 9
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US-08-441-139-14
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COUNTRY:
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                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                     Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
ZIATE: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: <URNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
RECISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949
                                                  ATTORNEY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
RECISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: unknown
TOPOLOGY: unknown
SEQUENCE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                                                                                         Score 38;
Pred. No.
APPLICATION NUMBER: PCT/US97/01094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08797358B Patent No. 6268478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 643 amino acids TYPE: amino acid
                   21-January-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                       79.28;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                      LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77...
7, Conservative
                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
; FRACMENT TYPE: internal
US-09-412-184-32
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34 SIFEGIRGY 42
                   FILING DATE: 2 CLASSIFICATION:
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                                                                                                                                                                                                                                             Sequence 14, Application US/08441139
Patent No. 5773245
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Wittrup, Dr. Karl D.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length 646;
Pred. No. 26;
1; Mismatches 1; Indels
DB 4; Length 643;
10;
                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                               Mismatches
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, MOLECULE TYPE: peptide US-07-965-285-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 LFAGVDGH 51
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44 LFAGVDGH 51
                   2 LFEGIDGY 9
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US-08-487-231-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                               US-07-965-285-42
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 2; Length 108; Pred. No. 20; Mismatches 1; Indels
                                                                                                                                                                                                         Score 33; DB 4; Length 458;
Pred. No. 68;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR-1993
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATTORNEY AGENT INFORMATION:
NAME: MAPERS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFRENCE/POCKET NUMBER: 05286-0001-00000
TELEPHONE: 202-408-4400
CURRENT APPLICATION NUMBER: US/09/457,046B CURRENT FILING DATE: 1999-12-07 NUMBER OF SEQ ID NOS: 74 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 61 LENGTH: 458
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42, Application US/08483695 Patent No. 5866139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 42:
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Best Local Similarity 62.5%;
Matches 5; Conservative 2
                                                                                                                    TYPE: PRT; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61
                                                                                                                                                                                                              68.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 108 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                Query Match 68.8
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide US-08-483-695-42
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|165 SLFDGISAY 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-483-695-42
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Gaps

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Sequence 42, Application US/08487231
Patent No; 5919454
Batent No; 5919454
SENERATION: Christian
APPLICANT: Rremsdorf, Dina
APPLICANT: Porchon, Colectide and Peptide Sequences of a TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
                                                                          APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: None Collection and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,285
FILING DATE: 18-MAR.1993
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: FF 91 06 882
FILING DATE: 06-JUN.1991
ATTORNEY/AGENT INFORMATION:
NAME: MAYORY Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 32; DB 2;
62.5%; Pred. No. 20;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05286-0001-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 42, Application US/07965285 Patent No. 5879904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                           STREET: 1300 I Street, N.W. CIIY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 108 amino acids
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Matches 5; Conservative
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 173:
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (508)359-3885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.7
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || |:||:
44 LFAGVDGH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LFEGIDGY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Emer
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-444-818-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brechot, Christian
APPLICANT: Kremsdorf, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Forchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STREER: Dunner STREER: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
PILOR APPLICATION ATA:
APPLICATION NUMBER: US/08/487,231
FILING DATE: 18-MAR-1995
CLASSIFICATION: 435
PILING DATE: 18-MAR-1993
CLASSIFICATION: A35
PILING DATE: 18-MAR-1993
CLASSIFICATION: A35
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAYOR'S, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DATAION INFORMATION:
TELEDENOM: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 2
Pred. No. 20;
2; Mismatches
                                                                                                                                                                                          COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-201-912-42; Sequence 42, Application US/09201912; Patent No. 6710962; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 1300 I Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-487-231-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | |:||:
44 LFAGVDGH 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 173, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
                                                                                                                                                                          APPLICALLOND

PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
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US-08-231-368-16
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Sequence 16, Application US/08440103

Sequence 16, Application US/08440103

GENERAL INFORMATION:

APPLICANT: Weiner, Amy J.

APPLICANT: Houghton, Michael

TITLE OF INFORMATION:

MUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 269; 58;
                                                                                                                                                                                                                                                                                                           Score 32; DB 4; Length 139;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                    TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE: INTOLVIDIAL ISOLATE: Japanese isolate (T. Miyamura) US-08-444-818-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,103
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 1
Pred. No. 58;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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FILING DATE:

PILING DATE:

FILING DATE:

FI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Chiron Corporat
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                    66.7%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.7%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-440-103-16
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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78 LFAGVDGH 85
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Patent No. 5756312
GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Houghten, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                   GENERAL INFORMATION:

APPLICANT: Weiner, Amy J.

APPLICANT: Weiner, Amy J.

APPLICANT: Houghton, Michael

TITLE OF INFORMATION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCE: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 269;
Pred. No. 58;
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: BATCHING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/440,542
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/08/231,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33.113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 651-2708
INFORMATION FOR SEQ ID NO: 16:
Sequence 16, Application US/08440542
Patent No. 5670153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.78;
62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-440-542-16
                                                                                                                                                                          ADDRESSEE: Chiron
STREET: 4560 Hortc
CITY: Emeryville
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emeryville
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8 LFAGVDGH 15
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LFAGVDGH 15

2 LFEGIDGY 9

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEW PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/231,368
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SE-1991
ATYONEY/AGENT INFORMATION:
NAME: MCCLUNG, Barbara G.
RECISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 33,113
RELEPHONE: (510) 601-2708
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-O8-231-368-16
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### Search completed: December 6, 2001, 07:59:56 Job time: 364 sec

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0; Gaps

Query Match 66.7%; Score 32; DB 1; Length 269; Best Local Similarity 62.5%; Pred. No. 58; Matches 5; Conservative 2; Mismatches 1; Indels

2 LFEGIDGY 9 || |:||: 8 LFAGVDGH 15

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pep1-mod8g.rpr

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5.5	Compugen
version	- 2000
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

6, 2001, 07:58:26 ; Search time 88.19 Seconds
(without alignments)
7.774 Million cell updates/sec December Run on:

1 SLFEGIDGY 9 PEP1-MOD8G 48 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR\_68:\* Database

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Gaps

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Query Match 83.3%; Score 40; DB 2; Length 289; Best Local Similarity 77.8%; Pred. No. 2.2; Matches 7; Conservative 1; Mismatches 1; Indels

||||||: || 250 SLFEGLQGY 258 1 SLFEGIDGY 9

ò q RESULT B44261

	Description	hypothetical prote	$\neg$	dnaK-type molecula	dnaK-type molecula		dnaK-type molecula	heat-shock protein	heat-shock protein	heat-shock protein	heat-shock protein	ĕ	dnaK-type molecula	dnaK-type molecula	-	dnaK-type molecula	hypothetical prote	dnaK-type molecula												
		T17957	B44261	A44261	I51344	PQ0138	A26283	T45477	T45479	T45476	T45478	н96605	T45471	A25646	A48872	S31766	JC1391	S20139	HHKW7A	A29160	S37394	T21394	T43724	S53357	S35718	I54542	A45871	HHBYA1	0	B36590
	DB	5	~	~	~	7	7	~	~	7	~	~	7	~	~	7	~	~	٦	~	~	~	~	~	~	~	7	-	~	7
	Length	289	208	209	278	372	420	467	467	468	469	617	632	634	989	638	639	639	640	640	640	640	640	641	641	641	641	642	642	642
æ	Query Match	83.3	81.2	ä		81.2	÷	81.2	÷					81.2	81.2			81.2		٠					ä	ä	ä	ä	81.2	81.2
	Score	40	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
	Result No.		~	m	4	Ŋ	9	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

draktype molecular chaperone HSC70 - California sea hare (fragment)
N;Alternate names: heat shock protein 70 homolog HSC70
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999
C;Accession: B44261
R;Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119; 1069-1076; 1992
A;Title: Long-term sensitization training in Aplysia leads to an increase in the expr A;Reference number: A44261; MUID:93077669
A;Tette: Long-term sensitization training in Aplysia leads to an increase in the expr A;Reference number: A44261; MUID:93077669
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-208 <KUH3>
A;Residues: 1-208 <KUH3>
A;Residues: 1-208 <KUH3>
A;Gene: HSC70
C;Function: involved in protein folding and assembling/disassembling of protein co C;Superfamily: heat shock protein 70
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

81.2 644 2 A45635 81.2 645 2 155129 81.2 646 2 746650 81.2 647 1 HHXT/O 81.2 647 2 741121 81.2 647 2 741121 81.2 647 2 741121 81.2 647 2 741121 81.2 647 2 744530 79.2 379 2 146580 79.2 546 2 744547 79.2 547 2 744547 79.2 641 2 PC/036 79.2 641 2 PC/036 79.2 641 2 PC/036 79.2 643 2 S09036 79.2 643 2 S05586 79.2 643 2 S05586 79.2 643 2 S05586 79.2 643 2 S05586 79.2 643 2 S05936 79.2 641 2 PC/036 79.2 641 2 P	dnaK-type molecula heat shock protein heat shock protein dnaK-type molecula dnaK-type molecula heat shock protein heat shock protein dnaK-type molecula heat-shock protein heat-shock protein heat-shock protein heat-shock protein heat-shock protein heat-shock protein dnaK-type molecula heat shock protein dnaK-type molecula dnaK-type molecula dnaK-type molecula	ALIGNMENTS	a virus PBCV-1 n 15-Oct-1999 #text_change 21-Jan-2000 ay 1999 m GB/EMBL/DDBJ g4028896; PIDN:AAC96822.1 Chlorella strain NC64 hypothetical protein A454L
39 81.2 644 2 39 81.2 645 2 39 81.2 645 2 39 81.2 647 1 39 81.2 647 1 39 81.2 647 2 39 81.2 647 2 39 81.2 647 2 38 79.2 214 2 38 79.2 467 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38 79.2 641 2 38	A45635 151129 151129 1446650 HHXL70 S44168 A03309 145474 T45474 T45474 S74849 DN0668 PC7036	ALIG	rella viision 19 y, May I l from GF NID:9402 host Chlc
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	333 333 333 333 334 336 339 339 339 339 339 339 339 339 339		RESULT 1 Hypothetical prot hypothetical prot C: Species: Chlore C; Date: 15-Oct.19 C; Accession: T1/9 R: Graves, M.V.; V submitted to the A: Reference numbe A: Reference numbe A: Retaus: prelini A: Molecule type: A: Status: prelini A: Molecule type: A: Residues: 1-289 A: Residues: 1-289 A: Residues: 1-284 A: Resperimental so C: Genetics: C; Genetics: C; Superfamily: Ch

Query Match

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dark-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment N.Alternate names: heat shock protein 70 C; Species: Paracentrotus lividus (common urchin) C; Date: 23.Nov-1991 #sequence_revision 23.Nov-1991 #text_change 20-Aug-1999 C; Accession: P00138 R;Rosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D. Gafe 96, 295-300, 1990 A; Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region. A; Reference number: P00138; MUID:91099690 A; A; Accession: P00138
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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NyAlternate names: heat shock protein 68
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C;Accession: A26283
R;Lowe, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A;Title: Molecular cloning and analysis of DNA complementary to three mouse 1A;Reference number: A26283; MUID:86111900
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A; Residues: 1-372 <ROS>
A; Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001
C; Genetics:
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4.7;
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Pred. No.
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A; Introns: 68/1; 137/1; 188/3; 281/3
C; Function:
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88.9%;
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ilarity 88.9%;
Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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N;Alternate names: heat shock protein 70
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Accession: A44261
R;Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J; Cell Biol. 119, 1069-1076, 1992
A;Title: Long-term sensitization training in Aplysia leads to an increase in the express A;Reference number: A44261; MUID:93077669
A;Accession: A44261
A;Accession: A44261
A;Accession: A44261
A;Reference number: A4261
A;Reference number: A
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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N;Alternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Accession: 151344
C;Accession: 151344
C;Accession: 151344
A;Title: 70-Kilodalton heat shock polypeptides from rainbow trout: Characterization of A;Reference number: 151344; MUID:85035330
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C; Function:
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Pred. No. 2.4;
Length 208
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                                                                                 1; Indels
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A;Molecule type: mRNA
A;Residues: 1-278 <KOT>
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DB 2;
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88.9%; Pred. No. 3.4;
tive 0; Mismatches
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                                                                             Mismatches
Score 39;
Pred. No.
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88.9%;
    81.2%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                         8; Conservative
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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                                                                                                                                                                                                                      132 SLFEGIDFY 140
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Hybbus

probable heat shock protein [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C; Accession: H96605
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, Y.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Ker, M.; W., D.; Yu, G.; Fraser, C.M.; Wenter, J.C.; Davis, R.W.
A; Reference and analysis of chromosome I of the plant Arabidopsis.
A; Status: Preliminary
A; Molecule type: DNA
A; Status: Preliminary
A; Molecule type: DNA
A; Coss: references: GB:AE005173; NID:g11024845; PIDN:AAG26930.1; GSPDB:GN00141
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                                                                                                                                                  C; Species: Eunicella cavolini
C; Date: 31-3an-2000 #text_change 21-Jul-2000
C; Accession: T45478
R; Borchiellini, C.; Le Parco, Y.
Submitted to the EMBL Data Library, September 1997
A; Reference number: 222983
A; Reference number: 222983
A; Accession: T45478
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-469 < 450RA
A; Cross-references: EMBL: AF026518; PIDN: AAC05363.1
C; Genetics:
C; Superfamily: heat shock protein 70
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                                                                                RESULT 10
T45478
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
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Pred. No. 8.3;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 469
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Pred. No. 6.1;
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C; Superfamily: heat shock protein 70
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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              253 SLFEGIDFY 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
C;Accession: C; Le Parco, Y.
Submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment) heat-shock protein 70 [imported] - Funiculina quadrangularis (Species: Funiculina quadrangularis (Species: Tan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000 (SAccession: T45476 R;Borchiellini, C.; Le Parco, Y. submitted to the EMBL Data Library, September 1997
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T45479
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
                                                                                                                                                                                                                                                                       Length 467;
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A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1
C;Genetics:
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Pred. No. 6.1;
0; Mismatches
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A;Accession: T45476
A;Status: preliminary; translated from GB/EMBL/DDBJ
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88.9%; Pred. No. 6.1;
cive 0; Mismatches
                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                           A,Molecule type: mRNA
A,Residues: 1-467 <BOR>
A,Cross-references: EMBL:AF026517; PIDN:AAC05362.1
C;Genetics:
A,Gene: Hsp70
C;Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                       DB 2;
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Pred. No. 6.1;
0; Mismatches
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C;Superfamily: heat shock protein 70
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88.9%;
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88.9%;
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Best Local Similarity 86.3,
conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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A; Reference number: Z22983
A; Accession: T45477
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A; Accession: T45479
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Best Local Similarity
Matches 8; Conserv
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252 SLFEGIDFY 260
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Indels

Length 636

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A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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A; Residues: 1-588 <581.
R; Saints, I:; Angelidis, C:; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A; Title: The hsc70 gene which is slightly induced by heat is the main virus inducible
A; Reference number: 136927; MUID:95080396
A; Accession: 136927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diak-type molecular chaperone hsp70 - green monkey
N;Alternate names: heat shock protein 70
S;Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Accession: 331766; 136927
C;Accession: 331766; 136927
Submitted to the EMBL Data Library, January 1993
A;Reference number: S1766
A;Reference number: S31766
                                              A; Description: involved in protein folding and assembling/disassembling of protein co C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X70684; NID:922781; PIDN:CAA50019.1; PID:922782 A;Experimental source: kidney; cell line COS-1
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8.6;
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Pred. No. 8.6;
0; Mismatches
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Pred. No.
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Job time: 275 sec
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Best Local Similarity
Matches 8; Conserv
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                                      C; Function:
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N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein agic;Species: Dictyostellum discoideum
C;Saccis: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C;Accession: A48872
K;Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an A;Reference number: A48872; MUID:94043116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A;Note: the authors translated the codon TCG for residue 583 as Trp
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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Machine C; Accession: A25646
J. Bidl. Chem. 261, 12692-12699, 1986
A; Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene. A; Reference number: A25646; MUID: 86304452
A; Accession: A25646
A; Molecule type: DNA
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           C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000 C;Accession: T45471 R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G. submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
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                                                                                                                    A, Reference number: 222980
A, Accession: T45471
A, Status: preliminary: 'translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Residues: 1-632 - 809V-
A, Cross-references: EMBL: AF025951; PIDN: AAB81865.1
A, Experimental source: strain AX3
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8.5;
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Pred. No. 8
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dnaK-type molecular chaperone - chicken
                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: hsCi
A;Note: localized to filopodias and c
C;Superfamily: heat shock protein 70
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Best Local Similarity 88.9%;
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-636 <EDD>
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Gaps

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1; Indels

Length 638;

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 6, 2001, 08:00:51 ; Search time 50.21 Seconds (without alignments) 6.572 Million cell updates/sec Run on:

1 SLFEGIDGY 9 PEP1-MOD8G 48 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		df			SUMMARIES	
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٦	39	81.2	322	Н	HS70_ONCVO	P11503 onchocerca
7	39	81.2	372	-	HS72_PARLI	P22623 paracentrot
m	39	81.2	420	-	HS73_MOUSE	_
4	39	•	503	Н	HS70_PENCI	
Ŋ	39	•	634	-	HS70_CHICK	
9	39	81.2	638	-	HS71_CERAE	Q28222 cercopithec
7	39	•	638	-	HS72_YEAST	
80	39	81.2	639	Н	HS74_PARLI	Q06248 paracentrot
σ	39	81.2	640	-	HS7A_CAEEL	P09446 caenorhabdi
10	39	81.2	640	Н	HS7C_DICDI	P36415 dictyosteli
11		81.2	641	Н	HS71_BOVIN	
12	39	81.2	641	Н	HS71_HUMAN	P08107 homo sapien
13	39	81.2	641	-	HS71_MOUSE	_
14		81.2	641	Н	HS71_PIG	
15	39	•	641	-1	HS71_RAT	Q07439 rattus norv
16			641	Н	HS71_YEAST	P10591 saccharomyc
17	39		641	Н	HS72_BOVIN	027965 bos taurus
18	39	٠	641	-4	HS74_YEAST	
19	39	٠	644	#4	HS70_BRUMA	P27541 brugia mala
20	39		644	-	HS70_ONCTS	-
21	39		645	-	HS70_PLEWA	Q91291 pleurodeles
22	39		646	-	HS70_NEUCR	
23	39		647	~	HS70_XENLA	
24	39	ij	. 649	П	HS70_BLAEM	P48720 blastocladi
25	39		652	-	HS7D_MANSE	Q9u639 manduca sex
56	38	•	214	Н	HS7A_DROSI	P02826 drosophila
27	38	٠	379	-	HS7X_PIG	P34934 sus scrofa
28	38	٠	641	-	HS7A_DROME	P29843 drosophila
29	38	٠	643	Н	HS76_HUMAN	
30	38	6	643	Н	HS76_PIG	Q04967 sus scrofa
31	38	79.2	648	Н	HS71_PUCGR	Q01877 puccinia gr
32	36		239	-	IPT2_AGRTU	P15653 agrobacteri
33	36	75.0	641		HS73_RAT	P55063 rattus norv

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AN SE AN BBN GR AN TH	ALIGNMENT	322	upda n up RAGM	dore	, Ra	ein ilar 1989	S A A FI SHOC	It i	e. lon	emov t (S ch).					2E81	9			372
HS7H_HUMAN HS7T_MOUSE HS72_PTCAN HS71_SCHPO HS71_PTCAN HS72_LYCES HS7C_CRIGR HS7C_MOUSE HS7C_MOUSE HS7C_MOUSE HS7C_MOUSE	LIGN	: :	nce atio ) (F	roma	» در در	prot a f 236(	70 I ROM EAT	ht.	itut s as	ot r emen sib.			AL.		ваза	Score 39; Pred. No.			PRT;
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Q92260;
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SO THE BRANCH DESCRIPTION OF THE BRANCH DESC
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Lowe D.G., Moran L.A.;
"Modecular clohing and analysis of DNA complementary to three mouse "Modecular clohing and analysis of DNA complementary to three mouse M.M. = 68,000 heat shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
                                                                                                                                                                                                                                                                                                                              la Rosa M., Sconzo G., Giudice G., Roccheri M.C., di Carlo M.; "Sequence of a sea urchin hsp70 gene and its 5' flanking region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                         Gene 96:295-300(1990).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                 Paracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1; Length 372;
Pred. No. 2.6;
0; Mismatches 1; Indels
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                      01-AUG-1991 (Rel. 19, Created)
1-AUG-1991 (Rel. 19, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HE73_MOUSE STANDARD; PRT; 420 AA.

061696; 061697; Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

01-NOV-1997 (Rel. 35, Last annotation update)

HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).

HSP70-3 OR HSP70A1.
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APP-binding; Heat shock; Multigene family.
NON TER 372 372
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InterPro; IPR001023; HSP70.
Pfam: PF00012; HSP70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; PARTIAL.
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                                                                                                                                                                                                                                                                                                          MEDLINE=91099690; PubMed=2269441;
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88.9%;
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Best Local Similarity 85..
8; Conservative
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286 SLFEGIDYY 294
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                                                                                                                                                                                                        Paracentrotus
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SEQUENCE
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                                                                          MUS MUSCULUS.";
Gene 146:273-278(1994).
Gene 146:273-278(1994).
FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTEMP PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE OTYGOSOL AS WELL AS WITHIN
OFF NEWLY TRANSLATED POLYPEPTIDES IN THE THESE PROCESSES
THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
OTHER PROTEINS, THEY BIND EXTENDED PEPTIDES EGGMENTS WITH A NET
HYDOPHORIC CHARACTER EXPOSED BY POLYPEPTIDES EGGMENTS TRANSLATION
AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
INDUCTION: BY HEAT SHOCK.
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ಭ
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-: SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Pred. No. 2.9;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V -> G.
; 5DA1C6155C7B16B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:96244; HSp70-3.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70. 1.
PROSITE; PS002297; HSP70_1; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
ATP-binding; Chaperone; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M12571; AAA57234.1; -.
EMBL; M12572; AAA57235.1; -.
HSSP; P19120; 1ATR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.2%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREEXTECTION TO COURT AND AGGINGS AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELIES. THE HSP70S IN MATOCHONBIA AND THE ENDOPLASHIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROPEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

-1. INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.; "The hsc70 gene which is slightly induced by heat is the main virus inducible member of the hsp70 gene family."; FEBS Lett. 355:282-286(1994).
                                                                                                                                                                                                                                                                                                                                           Cercopithecus aethiops (Green monkey) (Grivet).

Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Chaperone; Heat shock; Multigene family; MHC III.
638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1; Length 638;
Pred. No. 4.6;
0; Mismatches 1; Indels
                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney;
MEDLINE=95080396; PubMed=7988690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATGHOCK70.
PROSITE; PS00329; HSP70_1; 1.
PROSITE; PS01039; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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88.9%;
                                                                                                                                                                                                                                                                                               HEAT SHOCK 70 KDA PROTEIN 1.
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                 STANDARD;
        111111 |
289 SLFEGIDFY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding;
SEQUENCE 6
                                                                                                                                                              HS71_CERAE
Q28222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HS72_YEAST
P10592;
                                                                                                                                        HS71_CERAE
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                                                                                                             RESULT
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to license@isb-sib.ch).
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        noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 4.6;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          81.2%; Score 39; DB 1; Length 503; 88.9%; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01306; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                                   HSSP; P19120; 3HSC.
InterPro; IPR01023; HSP70.
InterPro; IPR01023; HSP70; 1.
PRINTS; PR0301; HEATSHOCK70.
PROSITE; PS010329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 08, Last sequence update)
(Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 AA
        not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                      or send an email to license@isb-sib.ch)
modified and this statement is not rementities requires a license agreement
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88.9%;
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                                                                                                          EMBL; U64207; AAB06397.1; -
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InterPro; IPR001023; HSP70.
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Best Local Similarity 88.9،
اتع 8; Conservative
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Best Local Similarity 85...
8; Conservative
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TD HS70_CHICK
DT HS70_CHICK
DT O1-AUG-1988
DT O1-AUG-1988
DT O1-AUG-1988
DT O1-AUG-1988
DT O1-EBB-1994
DE HEAT SHOCK TO
C ENKARYOLE; MOC
C ATCHOSAUTIA;
OC GAILUS.
OC GAILUS.
OC GAILUS.
OC GAILUS.
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THE SEQUENCE FRC
RA MEDLINE-8630
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01-FEB-1994
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Gaps

4

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Gaps

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Length 638, Indels

81.2%; Score 39; DB 1; 88.9%; Pred. No. 4.6;

Mismatches

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Query Match
Best Local Similarity 88.3.
Lea 8; Conservative
PF00012; HSP70; 1.
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HS74_PARLI
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MEDLINE-97089742; PubMed-8935650;
Norbeck J., Blomberg A.;
"Protein expression during exponential growth in 0.7 M NaCl medium of Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                              Dussterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D., Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.; Submitted (SEP-1994) to the SWISS-PROT data bank.
-1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE RNOPLASMATIC RETICULUM. A FUNCTIONAL DIPFERENCE BETWEEN YEAST SRA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                          Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.; "Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                      Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                 Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
     01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSA2.
SSA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: CYTOPLASMIC-i- PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                            Electrophoresis 15:1466-1486(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95203288; PubMed=7895733;
                                                                                                                                                          MEDLINE-89128457; PubMed-2644626;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 91-97 AND 325-341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X12927; CAA31394.1; -. EMBL; Z73129; CAA97472.1; -. EMBL; X97560; CAA66167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S20139; S20139.
HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10592; YEAST.
                                                                                                                                                                                                                                                                                      SEQUENCE OF 71-638 FROM N.A.
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SGD; S0003947; SSA2.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE OF 186-195
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                                          STRAIN-S288C;
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                                                                                                                                                                                                                                                                                                                                                                                                                   database.";
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SEQUENCE FROM N.A.
SECUENCE 53077053; PubMed-1339375;
SCONZO G., Scardina G., Ferraro M.G.;
SCONZO G., SCARGINA PROFIN Paracentrotus
11vidus hsp70 gene famly and its expression.";
Gene 121:353-358(1992).
Gene 121:353-358(1992).
THE HEAT SHOCK PROFIEN 70 FAMILY.

THE PROFILE STATEMENT OF THE PROFILE OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paracehtrotus lividus (Common sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Echinidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.2%; Score 39; DB 1; Length 639;
88.9%; Pred. No. 4.6;
iive 0; Mismatches 1; Indels
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PRINTS; PR00301; HEATSHCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
ATP-binding; Heat shock; Multigene family.
                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
639 AA
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Pfam; PF00012; HSP70; 1.
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Best Local Similarity 88.9
Matches 8; Conservative
      STANDARD;
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BO J. 12:3763-3771(1993).
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ATP-binding; Chaperone.
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HS71_BOVIN
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                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snutch T.P., Heschl M.F.P., Baillie D.L., "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94008983; PubMed-8404847;
Haus U., TrommLer P., Fisher P.R., Hartmann H., Lottspeich F.,
Nogela A.A., Schleicher M.;
"The heat shock cognate protein from Dictyostelium affects actin
Polymerization through interaction with the actin-binding protein
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SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Pred. No. 4.6;
); Mismatches 1; Indels
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
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Dictyostellum discoideum (Slime mold).
Eukaryota: Mycetozoa; Dictyostellida; Dictyostellum.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 35, Last annotation update)
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HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
                                                                                       PRT;
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01-MAR-1989 (Rel. 10, Last seq
01-FEB-1994 (Rel. 28, Last ann
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InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
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88.9%;
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HEAT SHOCK 70 KDA PROTEIN A.
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                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local Similarity
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P36415;
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01-JUN-1994
                                                                                 HS7A_CAEEL
P09446;
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                                                HS7A_CAEEL
TD HS7A_CAEEL
TD HS7A_CAEEL
DT O1-MAR;
DT O1-MAR;
DT O1-MAR;
DE HEB-1 (
GN Caenor)
CC Eukabdi;
OX NCBL_T;
RA SNULLIN
RA SNOSIT
RA SROSIT
RA ATP-SI
SOUGEN
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AC P87C_D

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                                                                                    Eddy R.J., Sauterer R.A., Condealis J.S.;
Redy R.J., Sauterer R.A., Condealis J.S.;
Redynactin, an agonist-regulated F-actin capping activity is associated with an Hsc70 in Dictyostelium.";
J. Biol. Chem. 268:23267-23274 (1993).
-!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROPEIN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLING OF DENATURATED CAP32 AND CAP34.
-!- SUBCELLUAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS OF THE CALL CORFEX AND CELL PROFIESSING.
-!- DEVELOPMENTAL STRAGE: HEAT SHOCK COGNNTE PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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IHHHINGNATWVVESGPVSEVLSFN (IN REF.
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SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
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V -> A (IN REF. 2).

R -> A (IN REF. 2).

S -> A (IN REF. 2).

V -> A (IN REF. 2).

I -> L (IN REF. 2).

ZEGBDCZDB96A9F5D CRC64;
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Pred. No. 4
                                 STRAIN=AX3;
MEDLINE=94043116; PubMed=8226849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
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PS00329; HSP70_2; 1.
PS01036; HSP70_3; 1.
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88.9%;
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pep1-mod8g.rsp

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RA MEDLINE-9924376; PubMod-10216320;

RA GSIDIUK J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

RA OSIDIUK J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

R. Structure of a new crystal form of human hsp70 ArPase domain.";

RL Acta Crystallogr. D 55:1105-1107(1999).

PREMISTISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDOCTION PATHWAYS IN COOPERATION THEY ARE INVOLVED IN SIGNAL TRANSDOCTION PATHWAYS IN COOPERATION WHEN PROTEINS THEY BIND EXTENDED PEPTIDE SECHENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES CONPONENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES CHARACTER EXPOSED BY POLYPER CHARACTER EXPOSED BY POLYPEPTIDES CHARACTER EXPOSED BY POLYPER CHARACTER EXPOSED BY POL
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MEDLINE-87066768; PubMed-3786141;
Drabent B., Genthe A., Benecke B.-J.;
In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";
Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-36 AND 360-424 FROM N.A.
MEDLINE-89184548; PubMed-2538825;
Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
"Human major histocompatibility complex contains genes for the major heat shock protein HSP70.",
Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).
Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-86016721; PubMed=3931075;
Hunt C., Morimoto R.I.;
"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- INDICTION: BY HEAT SHOCK.
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                            with the nucleotide sequence of human hsp70.";
Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
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EMBL; M59830; AAA021816.1; -
EMBL; AF134726; AAD21815.1; -
EMBL; M1717; AAA52697.1; -
EMBL; M24743; AAA9844.1; -
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=91055806; PubMed=1700760;
                                                                                                                                                                                                                                                   Immunogenetics 32:242-251(1990).
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                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEATOT ACCURATION OF THE CHAPERONES, HSP70S STABILLIZE ANIM. Genet. 25:196-196(1994).

-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILLIZE PREXISERT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF UNBALY TRANSLATED FOLYEPETIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICCULM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORE PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLITY TO RECOGNIZE NOWNTIVE CONFORMATIONS OF OTHER PROFINS. THEY BIND EXTENDED PEPTIDE SECREBYS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION, OR FOLLOWING
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                                                                                                                                                                                                           Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (18970) mimics Hsp70 isoforms from tissues."; blochem. J. 305:197-203(1995).
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                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ANGUS;
MEDLINE-95030563; PubMed-7943958;
Grosz M.D., Skow L.C., Stone R.T.;
"An Alul polymorphism at the bovine 70 kD heat-shock protein-1 (HSP70-1) locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRESS-INDUCED DAMAGE.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Pred. No. 4.6;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; ....
Pfam; PP00012; HSP70; 1.
PRINTS; PR001301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS71_HUMAN STANDARD; PRT; 641 AA. P08107; P19790; Q9UQMO; Q9UQL9; 01-AUG-1988 (Rel. 08, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2). (HSPAIA OR HSPAIA AND HSPAIB.
                                                                                                                                            TISSUE-Skeletal muscle;
MEDLINE-95126904; PubMed-7826329;
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88.9%;
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Best Local Similarity 88.۶۰
انامی 8، Conservative
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                            Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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                                                                                                                SEQUENCE FROM N.A.
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HS71\_HUMAN
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AC P081.01
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Immunogenetics 35:286-289(1992).
-i- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                    Mul.;
InterPro; IPRUJL...

R PRINTS; PR0012; HSP70; 1.

R PRINTS; PR00301; HEATSHOCK70.

R PROSITE; PS003029; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_3; 1.

RW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.

ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J., Bouquet Y.H.;
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01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
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Pred. No. 4.6;
0; Mismatches
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PIR; S35718; S35718.
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EMBL, M76613; AAA57233.1; -.
PIR; JH0095, JH0095.
HSPP; P19120; INGC.
MGD; MGI:99517; HSP70-1.
InterPro; IPR001023; HSP70.
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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P34930;
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-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDITATE THE FOLDING OF NEWLY TRANSLATED POLYDEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED BEPTIDES EGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hunt C., Calderwood S.;
"Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
Gene 87:199-204(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
W, 78F513118C96DE66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.2%; Score 39; DB 1; Length 641;
88.9%; Pred. No. 4.6;
Live 0; Mismatches 1; Indels
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MEDLINE-90236310; Pubmed-2332169;
EMBL; X04676; CAA28381.1; -... EMBL; X04677; CAA28382.1; -... PIR; AA29160; A29160. PIR; A45871. PIR; AA5871. PIR; A25773; A25773. PDB; 1HJO; 21-OCT-98. SWISS-2DPAGE; P08107; HUMAN.
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
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110
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469
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469
499
4198
41 AA;
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Best Local Similarity
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SEQUENCE FROM N.A.
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286 SLFEGIDFY 294
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CONFLICT
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ID HS71_MOUSE

ID HS71_MOUSE

DT 01-AdG

DT 30-AdG

DT
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BIOCHIM. BLOPHYS. Acta 1219:64-72(1994).

-!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYEPETIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATURE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLIVEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLACTION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
—CDNA, cloning and expression of stress-inducible rat hsp70 in normal
and injured rat brain.";
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MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
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STAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
MEDLINE-94368874; PubMed-8086479,
Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;
"Cloning, nucleotide sequence and expression of rat heat inducible
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-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.2%; Score 39; DB 1; Length 641; 88.9%; Pred. No. 4.6; 1:ve 0; Mismatches 1; Indels
                                   Interpro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS0029; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-REJ-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HSP70-1 AND HSP70-2.
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    Neurosci. Res. 36:325-335(1993)

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286 SLFEGIDFY 294
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DR PRINTS: PRO0301; HEATSHOCK/0.

DR PROSTIE; PS00329; HSP70_1; 1.

DR PROSTIE; PS01036; HSP70_2; 1.

DR PROSTIE; PS01036; HSP70_3; 1.

KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.

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Copyright (c) 1993 - 2000 Compugen Ltd.
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dnaK-type molecular chaperone HSP70a - California sea hare (fragment)
N;Alternate names: heat shock protein 70
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Accession: A44261
R;Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1993
A;Title: Long-term sensitization training in Aplysia leads to an increase in the exprance number: A44261; MUID:93077669
A;Title: Long-term sensitization training in Aplysia leads to an increase in the exprancession: A44261
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-209 <KUH>
A;Note: sequence extracted from NCBI backbone (NCBIP:118951)
C;Genetics:
A;Gene: HSP70a
C;Function:

pep2-mod8a.rpr

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hat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)
hat-shock protein 70 [imported] - Funiculina quadrangularis
hat-shock protein 70 [imported] - Funiculina quadrangularis
c;species: Funiculina quadrangularis
c;species: Funiculina 2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
c;Accession: T45A F6
R;Borchiellini, C.; Le Parco, Y.
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C; Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C; Accession: T45479
R; Borchiellini, C; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A; Reference number: 222983
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heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C;Species: Chondrosia reniformis
C;Date: 31.Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45477
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A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
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0.24;
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A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
A;Cross-references: EMBL:AF026517; PIDN:AAC05362.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1997 A; Reference number: 222983 A; Accession: T45477
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Pred. No. 0
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C;Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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90.0%;
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches † 9; Conservative
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1 SLFEGIDAYT 10
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C;Species: Oncorbynchus mykiss (rainbow trout)
C;Species: Oncorphychus mykiss (rainbow trout)
C;Species: Oncorphychus mykiss (rainbow trout)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
C;Accession: I51344
R;Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of A;Reference number: 151344; MUID:85036330
A;Recession: I51344; MUID:85036330
A;Recession: I51344
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Rotcus: preliminary; translated from GB/EMBL/DDBJ
A;Rotcus: preliminary;
A;Rotcus: preliminar
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
A; Description: involved in protein folding and assembling/disassembling of protein compl
C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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N;Alternate names: heat shock protein 70
C;Species: Paracentrotus lividus (common urchin)
C;Species: Paracentrotus lividus (common urchin)
C;Accession: P00138
R;Rosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D.
Gene 96, 295-300, 1990
A;Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region.
A;Reference number: P00138; MUID:91099690
A;Accession: P00138
A;Molecule type: DNA
A;Residues: 1-372 <ROS>
A;Cross-references: EMBL:X16544; NID:910000; PIDN:CAA34544.1; PID:910001
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Pred. No. 0.19;
0; Mismatches 1; Indels
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                                                                                                                                                                                                       Score 45; DB 2; Length 209;
Pred. No. 0.097;
0; Mismatches 1; Indels
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A,Introns: 68/1; 137/1; 188/3; 281/3
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Conservative 0
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90.0%;
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Best Local Similarity 90.0°
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Length 636;

DB 2; 0.34;

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-636 <EDD>
A;Residues: 1-636 <EDD>
A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diak-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)
N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein
C;Species: Dictyostelium discoideum
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C;Accession: A48872
R;Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with
A;Reference number: A48872
A;Accession: A48872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: involved in protein folding and assembling/disassembling of protein co
C; Superfamily: heat shock protein 70
C; Reywords: ATP; molecular chaperone
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C;Superfamily: heat shock protein 70
C;Reywords: ATP; molecular chaperone
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N;Alternate names: heat shock protein 70
C;Species: Ceroopitheous aethiops (green monkey, grivet)
C;Date: 13-Jan.1995 #sequence_revision 13-Jan.1995 #text_change 20-Aug-1999
C;Accession: S31766; 136927
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
                                                                                                                                        C; Species: Gallus gallus (Chicken)
C; Species: Gallus gallus (Chicken)
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Accession: A25646; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J; Biol. Chem. 261, 12692-12699, 1986
A; Thile: Organization, nucleotide sequence, and transcription of the chicker A; Reference number: A25646; MUID:86304452
                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-634 <MOR>.
A;Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A;Note: the authors translated the codon TCG for residue 583 as Trp
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Pred. No. 0.34;
0; Mismatches
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Pred. No. 0.34;
0; Mismatches
                                                                                                 dnaK-type molecular chaperone - chicken
N;Alternate names: heat shock protein 70
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0%;
Matches 9; Conservative
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280 SLFEGIDEYT 289
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N.Alternate names: heat shock cognate protein 70
C.Species: Dictyostellum discoideum
C.Species: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
C.Accession: 745471
R.Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
submitted to the EMBL Data Library, September 1997
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A;Residues: 1-469 <BOR>
A;Cross-references: EMBL:AF026518; PIDN:AAC05363.1
A;Residues: 1-468 <BOR>
A;Cross-references: EMBL:AF026516; PIDN:AAC05361.1
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Pred. No. 0.24;
0; Mismatches
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Pred. No. 0.24;
0; Mismatches
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A;Note: localized to filopodias and cortex
C;Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: Hsp70
C;Superfamily: heat shock protein 70
                                                                     A;Gene: Hsp70
C;Superfamily: heat shock protein 70
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Best Local Similarity 90.00,
-has 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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A; Accession: T45471
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-632 <BOV>
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                                                   C; Genetics
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A. Note: genomic clones representing six distinct members of the hsp70 gene family wer A.Note: genomic clones representing six distinct members of the hsp70 gene family wer A.Note: transcripts of hsp70A are abundant in control worms and also increase two- to A.Note: one of the three introns in hsp70A is in a position similar to an intron in D A.Genetics:
A.Genetics:
A.Genetics:
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A; Cross-references: EMBL:273129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YL
A; Experimental source: strain $288C
B; Destachoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, May 1996
A; Reference number: $64775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discription molecular chaperone hsp70A - Caenorhabditis elegans
N:Alternate names: heat shock protein 70 A
C;Species: Caenorhabditis elegans
C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
C;Accession: JT0285
R;Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007
R;Slater, M.R.; Craig, E.A.
Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
A;Ference number: S20139; MUID:89128457
A;Accession: S20139
                                                                                                                                                                                     A; Status: translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-639 < SLB>
A; Cossidues: 1-639 < SLB>
A; Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546
B; Goffeau, A.; Purnelle, B.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64761
A; Accession: S64772
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Pred. No. 0.34;
0; Mismatches
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A;Map position: 12L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 72-639 <DUE>
A; Cross-references: EMBL:273129; MIPS:YLL024c
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Best Local Similarity 90.0
Matches 9; Conservative
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A; Molecule type: DNA; mRNA
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A; Accession: S69383
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                               A; Description: Nucleotide sequence of the CDNA encoding a monkey 70kd heat shock protein A; Reference number: S31766
A; Accession: S31766
A; Accession: S31766
A; Molecule type: mRNA
A; Residues: 1-638 <SAI>
FEBS Lett. 355, 282-286, 1994
A; Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me A; Recession: 115627; MUID: 95080396
A; Accession: 115627; MUID: 950801396
A; Accession: 115627
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-638 <RES>
A; Cross-references: EMBL: X70684; NID: 922781; PIDN: CAA50019.1; PID: 922782
A; Experimental source: kidney; cell line COS-1
C; Genetics: A; Genetics: A; Genetics: A; Archeir folding and accombling of protein county and accombling of
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C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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N.Alternate names: heat shock protein 701V; hsp701V protein
C; Species: Paracentrotus lividus (common urchin)
C; Date: lo.Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C; Accession: JC1391
R; Sconzo, G.; Scardina, G.; Ferraro, M.G.
Agene 121, 353-358, 1992
A; Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
A; Reference number: JC1391; MUID:93077053
A; Accession: JC1391
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dnaK-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
NyAlternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
C;Species: O7-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000
C;Accession: $20139; $64772; $64775; $69383
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A;Residues: 1-639 <SCO>
A;Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917
C;Genetics:
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Pred. No. (
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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286 SLFEGIDFYT 295
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284 SLFEGIDFYT 293
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Gaps

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A; Map position: IV
A; Introns: 69/1; 331/3; 558/3
C; Function:
A; Description: involved in protein folding and assembling/disassembling of protein completion: involved in protein 70
C; Superfamily: heat shock protein 70
C; Superfamily: heat shock; molecular chaperone; stress-induced protein
C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein completed: Dispute the shock; molecular chaperone; molecular chaperone; protein completed: Dispute the shock; molecular chaperone; molecular
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Q07439
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P22202
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P55063
P34931
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Q92260
P08106
Q28222
P10592
Q06248
P09446
P36415
Q27975
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P17066
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                      100059 seqs, 36664827 residues
                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                         HS71_CERAE
HS72_YEAST
HS74_CAREI
HS74_CAREI
HS77_DICDI
HS71_HOWAN
HS71_MOUSE
HS71_NOUSE
HS71_PIG
HS71_RST
HS71_RST
HS71_RST
HS71_RST
HS71_RST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HS7A_DROME
HS76_HUMAN
                                                                                                                                                                                                                                                                                                                                                                HS72_PARLI
HS70_PENCI
HS70_CHICK
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HS70_BRUMA
HS70_ONCTS
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HS73_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS70_NEUCR
HS70_XENLA
                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLEWA
                                                                                                                                                                                                                                                                                                                                                       HS70_ONCVO
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HS7A_DROSI
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                                   OM protein - protein search, using sw model
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                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS70_I
                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                        1 SLFEGIDAYT 10
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                                                                                                                                                                                                                                                      SwissProt_39:*
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Match Length
                                                                                        PEP2-MODBA
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                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                Perfect score:
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                                                                                         P08109 mus musculu
P87047 paracoccidi
                                                                                                                                              brachydanio
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oncorhynchu
                                               pichia angu
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               ichia angu
                                schizosacch
                                                                cricetulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89201313; PubMed-2704388;
Rothstein N.M., Higashi G., Yates J., Rajan T.V.;
Rothstein N.M., Higashi G., Yates J., Rajan T.V.;
Rochstein R.M., Higashi G., Yates J., Rajan T.V.;
Rochstein Reat shock protein 70 is a major immunogen in amicrofilaremic individuals from a filariasis-endemic area.";
Mol. Biochem. Parasitol. 33:229-236(1989).
--- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.
--- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
           P53623
Q10265
P53421
P19378
P11142
                                                                                                                          P09435
Q90473
P19120
P08108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35614 MW; 2BA3A2E8155A7180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 1;
Pred. No. 0.089;
                                                                                                                                                                                                                                                                                                                                         01-0CT-1989 (Rel. 12, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
10-FBB-1996 (Rel. 33, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 AA.
                                                                                                                                                                                                                                                                                                            322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                              ALIGNMENTS
                                            HS71_PICAN
HS7C_CRIGR
HS7C_HUMAN
HS7C_MOUSE
HS70_PARBR
                                                                                                                             HS73_YEAST
HS7C_BRARE
HS7C_BOVIN
HS70_ONCMY
             HS72_PICAN
                                HS71_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00012; HSP70; 1.
PROSITE; PS00297; HSP70_1: PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J04006; AAA29417.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Heat shock.
                                                                                                                                                                                                                                                                                                                                                                                                           Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLFEGIDAYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                          HS70_ONCVO
P11503;
 4444444444
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NON_TER
SEQUENCE
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HS70_ONCVO
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RESULT 4
HS70_CHICK
HS70_CHICK
DT HS70_CHICK
DT 01-AUG
DT 01-FEI
DE HEAT : 01-FEI
DE GAILU
OC BURL
RA MOLI
RA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus
SO DRA DRA BET SO DRA 
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBL_TaxID=5077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          la Rosa M., Sconzo G., Gludice G., Roccheri M.C., di Carlo M.; Sequence of a sea urchin hsp70 gene and its 5' flanking region."; Gene 96:295-300(1990).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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-: SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                               Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 1; Length 372;
Pred. No. 0.1;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AA; 41347 MW; 5F8C1C590527A659 CRC64;
                           1-AUG-1991 (Rel. 19, Created)
1-AUG-1991 (Rel. 19, Last sequence update)
1-JUN-1994 (Rel. 29, Last annotation update)
EAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AA.
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ATP-binding; Heat shock; Multigene family.
NON_TER 372 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                (Common sea urchin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91099690; PubMed=2269441;
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                            Paracentrotus lividus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P19120; 1NGJ.
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286 SLFEGIDYYT 295
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7656;
                                                                                                                                                                                                                                                                                                Paracentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Gonad,
                           01-AUG-1991
                                                                 01-AUG-1991
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                                                                                                                                                              HSP7011
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HS70_PENCI
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or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.; "Organization, nucleotide sequence, and transcription of the chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; JOS579; AAA48825.1; -.

EMBL; JOS5646; AZ5646.

R HSSP; P19120; 1ATR.

R InterPro; IRR01023; HSP70.

R Pfam; PF00012; HSP70; 1.

R PROSTTE; PS00297; HSP70.1; 1.

R PROSTTE; PS00329; HSP70.2; 1.

R PROSTTE; PS00329; HSP70.2; 1.

R PROSTTE; PS00329; HSP70.3; 1.

R PROSTTE; PS01036; HSP70.3; 1.

R PROSTTE; PS01036; HSP70.3; 1.

R PROSTTE; PS01036; HSP70.3; 1.

R ATP-binding; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
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Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 1;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Chaperone; Heat shock; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-EBB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (HSP70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86304452; PubMed-3017985;
                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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90.0%;
                                                                                                                                                                                                                EMBL; U64207; AAB06397.1; -. HSSP; P19120; 3HSC. InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.2%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                            Pfam; PF00012; HSP70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 SLFEGIDEYT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS70_CHICK
P08106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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STRAIN-S288C;
                                                                                                                                                                                                                                                STRAIN-S288C
                    HS72_YEAST
P10592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               database.
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Saints I., Angelidis C., Pagoulatos G., Lazaridis I.;
"The hsc70 gene which is slightly induced by heat is the main virus
inducible member of the hsp70 gene family.";

FEBS Lett. 355:282-286(1994).

-I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
OF NEMLY TEANSLAPED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
COMPORMATION THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONMATIVE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CONFORMATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   Gaps
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                                                                                                                                                                                                                                                                               Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shock; Multigene family; MHC III.
D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 638;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
 1;
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Pred. No. 0.19;
                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                           638 AA.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95080396; PubMed=7988690;
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                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRESS-INDUCED DAMAGE.
INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69920 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00297; HSP70_1; 1
PROSITE; PS00329; HSP70_2; 1
PROSITE; PS01036; HSP70_3; 1
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.2
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chaperone;
                                                                   289 SLFEGIDEYT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638 AA;
                                  1 SLFEGIDAYT 10
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                                                                                                                                                          HS71_CERAE
Q28222;
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein expression during exponential growth in 0.7 M NaCl medium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-1- FUNCTION: SA32 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SA32 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                           Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95203288; PubMed-7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender E
Volpe T., Warner J.R., McLaughlin C.S.;
"Profesin identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: CYTOPLASMIC.
PTM: PHOSPHORYLATED.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                           Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                 01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
638 AA.
                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEMS Microbiol. Lett. 137:1-8(1996).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electrophoresis 15:1466-1486(1994)
                                                                                                                                                                                                                                                        MEDLINE-89128457; PubMed-2644626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ATCC 38531 / Y41;
MEDLINE=97089742; PubMed=8935650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 91-97 AND 325-341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X12927; CAA31394.1; -. EMBL; Z73129; CAA97472.1; -. EMBL; X97560; CAA66167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 71-638 FROM N.A.
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SWISS-2DPAGE; P10592; YEAST
                                                                                       HEAT SHOCK PROTEIN SSA2.
SSA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norbeck J., Blomberg A.;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 186-195.
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                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-S288C;
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PRT;
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90.0%;
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                                                                                                STANDARD;
                                                                                                                                                                                                               Caenorhabditis elegans.
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               286 SLFEGIDFYT 295
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SLFEGIDAYT 10
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                                                                                                                                                                                                                                                                                                                                                              characterization.
                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                              HSP-1 OR HSP70A.
01-MAR-1989
                                                                                                HS7A_CAEEL
P09446;
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HS7C_DICDI
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                                                                               HS7A_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SCORD G., Scardina G., Ferraro M.G.;

"Characterization of a new member of the sea urchin Paracentrotus Ilvidus hap70 gene family and its expression.";

Gene 121:353-358(1992).

-- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               raracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinoida; Echinidae;
Paracentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 1; Length 639;
Pred. No. 0.19;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                               88.2%; Score 45; DB 1; Length 638; 90.0%; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                  1; Indels
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PROSITE; PS00129; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
   YEPD; 9800; -. SSA2.
InterPro: IPRO1023; HSP70.
Pfam; PPF00112; HSP70. 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00136; HSP70_2; 1.
PROSITE; PS00136; HSP70_2; 1.
Heat shock; ATP-binding; Multigene family; Acetylation;
                                                                                                                                                                                                 23BDDD120C194912 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                  639 AA
                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                      ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                 638 AA; 69338 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P19120; INGJ.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.2%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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282 SLFEGIDEYT 291
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                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                  1 SLFEGIDAYT 10
                                                                                                                                                  Phosphorylation.
INIT_MET 0
MOD_RES 1
SEQUENCE 638 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7656;
                                                                                                                                                                                                                                                                                                                                                                                                                                HS74_PARLI
Q06248;
                                                                                                                                                                                                                                                    Query Match
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RESULT 7 HS74\_PARLI

Matches

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                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDINE-829115; Pubmed-2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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MEDLINE=94008983; PubMed=8404847;
Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 64:241-255(1988).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1; Length 640;
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: M18540; AAA28078.1; -.
PIR; JT0285; HHKW7A.
HSSP; P19120; 1NGT.
InterPro; JF0001023; HSP70.
Pfam; PF00012; HSP70; 1
PRINTS; PR00301; HEATSHOCK70.
PROSITE: PS00329; HSP70_1; 1.
PROSITE: PS01036; HSP70_1; 1.
PROSITE: PS01036; HSP70_2; 1.
PROSITE: PS01036; HSP70_2; 1.
PROSITE: PS01036; MSP70_2; 1.
SEQUENCE 640 AA, 69823 MW; ED15409D06C500C2 CRC64;
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS7C_DICDI STANDARD; PRT; 640 AA. P36415; 01-JUN-1994 (Rel. 29, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update)
01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEAT SHOCK COGNATE PROTEIN (AGINACTIN). HSPB OR HSC70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC DAT DAT BY SEA BY S
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Anim. Genet. 25:196-196(1994).

Anim. Genet. 25:196-196(1994).

PREEXISTENT PROTEINS AGAINST AGREGATION AND MEDIATE THE FOLDING
OF WEALY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
OF UNEXT TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
OF GANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
OF RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGHAL TRANSDOCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CONFORMATIONS OF OTHER ABILITY TO RECOGNIZE NONMATIVE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CONFORMATIONS OF OTHER PROTEINS.
CITCHESS INDUCED DAMAGE.

-1: INDUCTION: BY HEAT SHOCK.
CITCHESS THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                Gutierrez J.A., Guerriero V.; Chemical modifications of a recombinant bovine stress-inducible 70 kba heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
                                                         Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                      Grosz M.D., Skow L.C., Stone R.T.;
"An AluI polymorphism at the bovine 70 kD heat-shock protein-1
(HSP70-1) locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 45; DB 1; Length 641; 90.0%; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
HS71_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9UQM0; Q9UQL9;
T 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95030563; PubMed=7943958;
                                                                                                                                                                                                 MEDLINE=95126904; PubMed=7826329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70250 MW;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 212-641 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, FINCE PSO0297; HSP70_1; 1. PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U09861; AAA73914.1; -. EMBL; U02891; AAA03450.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.2
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chaperone;
                                                                                                                                                                             TISSUE=Skeletal muscle;
                                                                                Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U02891; AAA034
HSSP; P19120; INGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLFEGIDAYT 10
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ANGUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                     Bovidae;
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
N -> T (IN REF. 2).
V -> A (IN REF. 2).
R -> A (IN REF. 2).
S -> A (IN REF. 2).
I -> L (IN REF. 2).
I -> L (IN REF. 2).
F -> P (IN REF. 2).
K -> P (IN REF. 2).
K -> P (IN REF. 2).
K -> P (IN REF. 2).
                                                                                                                                                                                                                  Eddy R.J., Sauterer R.A., Condeells J.S.;

*Aginactin, an agonist-regulated F-actin capping activity is associated with an HSC70 in Dictyostelium.";

J. Biol. Chem. 268:32367-3274(1993).

-I- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROPEIN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS OF THE CELL CORPEX AND CELL PROTRUSTONS.

-I- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL BEVELOPHENT.

-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROPEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Noegel A.A., Schleicher M.; "The heat shock cognate protein from Dictyostelium affects actin polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 45; DB 1; Length 640;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.19
0; Mismatches
                                                                                                                                                                                                 MEDLINE-94043116; PubMed-8226849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, X75263, CAA53039.1; --
EMBL, 122736, AAA33219.1; --
PIR, S37394, S37394,
HSSP, P19120, 1NGJ.
SWISS-2DPAGE; P36415, DICTY.
DictyDb, DD01078, PSPB.
InterPro, IPR001023, HSPP.
Pfam, PF00012; HSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00297; HSP70_1; 1. PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1. ATP-binding; Chaperone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.06;
                                                                                                    EMBO J. 12:3763-3771(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
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284 SLFEGIDFYT 293
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS;
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ID HS71_B

AC Q27975

DT 01-NOV

DT 01-NOV

DT 15-JUL

DE HEAT S

GN HSP70-
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Gaps

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Homo sapiens

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0; Mismatches
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MEDLINE-90236310; Pubmed-2332169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499
70052 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.2%;
nilarity 90.0%;
Conservative
                                                                                                                                                                                                                                                                    PDB; 1HJO; 21-OCT-98.
SWISS-2DPAGE; P08107; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
. M11717; AAA52697.1;
M24743; AAA59844.1;
M24744; AAA59845.1;
X04676; CAA28381.1;
X04677; CAA28382.1;
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                                                                                                                                                           A29160; A29160.
A45871; A45871.
A25773; A25773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 SLFEGIDEYT 295
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLFEGIDAYT 10
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370
469
499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                       140550;
                                                                                                                                                                                                                                                                                                                                                                  603012;
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CONFLICT
CONFLICT
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                                                                   EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                                   PIR;
                                                                                                                                                                  PIR;
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X. REAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.

X. MEDLINE-99234376; PubMed-10216320;

X. OSIPIOK J. WAISH M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

X. LILLOLUCE Of a new crystal form of human hsp70 ATPase domain.";

X. Acta Crystallogr. D 55:1105-1107(1999).

X. CACTA CRYSTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEMIX TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OF NEMIX TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OF RETICULUM PLAX AN ADDIATIONAL ROLE BY PROVIDING A DILYING FORCE FOR RETICULUM PLAX AN ADDIATIONAL ROLE BY PROVIDING A DILYING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONMATIVE

CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SECHENCY MATH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES OF THE PROTEIN PARTICIPATION OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE PROPERTY WITH A NET HYDROPHOBIC CHARA
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Drabent B., Genthe A., Benecke B.-J.;
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prepared from heat-shocked and non-heat-shocked human cells.";
Nucleic Acids Res. 14:8933-8949(1986).
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ROWEN L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89184548; PubMed-2538825;
Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
"Human major histocompatibility complex contains genes for the major heat shock protein HSP70."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hunr C., Morlmoto k.l.; "Comparison "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70."; Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                             MEDLINE-91055806; PubMed-1700760; Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
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             HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) (HSPAIA OR HSPAI) AND HSPAIB.
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Hunt C., Morimoto R.I.;
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INDUCTION: BY HEAT SHOCK.
                                                                             (Human)
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OTHER PROPERTY ON WITH OTHER CHAPERONES, HSP70S STABILIZE 1. FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PRATICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBERANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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"Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                            ;
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hunt C<sub>i</sub>, Calderwood S.; "Characterization and sequence of a mouse hsp70 gene and its expression in mouse cell lines."; Gene 87:199-204(1990).
                                       I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
W; 78F513118C96DE66 CRC64;
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286 SLFEGIDFYT 295
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                                                                HSSP; P19120; 1NGC
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Matches
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92175874; PubMed-1339404;
Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
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SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
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01-FEB-1994 (Rel. 28, Last Sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
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0; Mismatches
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InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
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Best Local Similarity 90...
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P34930;
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Biochim. Biophys. Acta 1219:64-72(1994).
Biochim. Biophys. Acta 1219 WITH OTHER CHAPERONES, HSP70S STABILIZE
-!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
- PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE POLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OF NEWLY TRANSLATED POLYPEPTIDES.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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1- INDUCTION: BY HEAT SHOCK.
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Massa S.M., Sharp F.R.;
Massa S.M., Sharp F.R.;
and sharp conting and expression of stress-inducible rat hsp70 in normal and injured rat brain.";
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Pred. No. 0.19;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shock; Multigene family.; FE77BB20A03E0A33 CRC64;
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MEDLINE-94368874; PubMed-8086479;
EMBL; M69100; -; NOT_ANNOTATED_CDS
PIR; S35718; S35718.
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MEDLINE=95012453; PubMed=7927536;
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MEDLINE=94096443; PubMed=8271311;
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SEQUENCE 641 AA; 70083 MW;
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
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90.0%;
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9; Conservative
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Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Slater M.R., Craig E.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 590-641 FROM N.A. MEDILINE-86087943; Pubmed-6096826; Ogden R.C., Lee M.-C., Knapp G.; Transfer RNA splicing in Saccharomyces cerevisiae: defining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                    PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00319; HSP70_2; 1.
APPOSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
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                                                                                                                                                                                                                                                                                                    88.2%; Score 45; DB 1; Length 641; 90.0%; Pred. No. 0.19;
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D -> H (IN REF. 2 AND 3).
G -> A (IN REF. 3).
; D02D96751C868583 CRC64;
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01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).
SSA1 OR YALOOSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     641 AA
                                                                                                                                                                                                                                                                                                                            0; Mismatches
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STRAIN-S288C / AB972;
MEDLINE-95028152; PubMed-794<u>1</u>740;
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                                                                                  EMBL; L16764; AAA1741.1; -. EMBL; X77208; CAA54423.1; -. EMBL; X77207; CAA54422.1; -. EMBL; X74211; CAA52328.1; -. HSSP; P19120; INGC.
                                                                                                                                             InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                     Query Match 88.2
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                    641 AA;
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286 SLFEGIDEYT 295
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SEQUENCE FROM N.A.
STRAIN=S288C;
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P10591;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    Norbeck J., Blomberg A.; "Protein expression during exponential growth in 0.7 M NaCl medium of Saccharomyces cerevisiae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.; Submitted (SEP-1994) to the SWISS-PROT data bank.

1- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERRNCE BETWEEN YEAST SSA1 AND SSA2 PROPERINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE ATP-DEPRNDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.

1- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                              Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Protein identifications for a Saccharomyces cerevisiae protein database.";
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BRHZ; L22015; AAC04952.1; ALT_SEQ.

PIR; S25438; HHBYA1.

PIR; S42164; S42164.

BRSP; P19120; LATR.

SWISS-ADPAGE; P10591; YEAST.

RYEDP, 97080004; SSA1.

InterPro; IPR001022; HSP70.

R PFOMINTS; PR00301; HBATSHOCK70.

R PROSITE; PS00297; HSP70.1; 1.

R PROSITE; PS00329; HSP70.1; 1.

R PROSITE; PS00329; HSP70.2; 1.

R PROSITE; PS00329; HSP70.2; 1.

R PROSITE; PS01039; HSP70.3; 1.

T MD_RES

D SEQUENCE 641 AA; 69526 MW; FA9389BAE9BID7DA CRC64;
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Pred. No. 0.19;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                           Electrophoresis 15:1466-1486(1994).
                                                                                                                                                                                                                                                                                             SEQUENCE OF 186-195.
STRAIN=ATCC 38531 / Y41;
MEDLINE=97089742; PubMed-8935650;
                                                      MEDLINE=95203288; PubMed=7895733;
SEQUENCE OF 91-97 AND 325-341.
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Matches 9; Conservative
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282 SLFEGIDFYT 291
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Q98900 fugu rubrip Q918f9 oryzias lat Q93601 caenorhabdi

OM protein

Run on:

Searched:

Database

Sequence:

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092255 arabidopsis
091ha8 arabidopsis
0919317 accophyllum
094805 trichoplusi
09x2j2 crassostrea
024952 geodia cydo
09u9b4 mytlius edu
044346 asbestoplum
044347 petrosia fi
073922 oreochromis
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073922 oreochromis
073922 oreochromis
09uvm0 rhizopus st
09uvm1 rhizopus st
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09uvm1 chizopus st
022664 spinacia ol
                       093240 paralichthy Q66256 rattus norv Q9gwj5 mus musculu 096541 setaria dig Q9njb7 wuchereria 09ngk9 wuchereria 059855 schizosaoch
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
Hohenlohe P.A.;
Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191828; AAF12787.1; -.
HSSP; P19120; 1BA1.
HISSP; P19120; 1BA1.
PROSITE; PS01036; HSP70_3; 1.
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16607 MW; C3F3556AlAF438BB CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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09U670;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                 146 AA.
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                       093240
063256
090WJ5
096541
09NJB7
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O59855
Q92S55
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073922
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Q94805
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Matches 9; Conservative
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Littorina plena.
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Query Match
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Q90669 ilttorina s
Q90665 ilttorina p
Q90671 ilttorina p
Q9066 ilttorina p
Q90666 ilttorina p
P81159 aplysia cal
Q90520 oncorhynchu
Q90520 oncorhynchu
Q90899 fugu rubrip
Q63718 rattus norv
Q4530 chondrosia
Q4452 petrobiona
Q90192 quancha lac
Q4451 euniculina
Q91941 euniculina
Q91951 fugu rubrip
Q91977 fugu rubrip
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Q9u670 littorina s
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8.592 Million cell updates/sec
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q90666
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_unclassified:*
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sp_bacteria:*
sp_fungi:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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Bukaryota, Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
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88.2%; Score 45; DB 5; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Nectaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
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"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFF191824; AAF12783.1;
HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 157;
                                                                                                                                                                                                                                               Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191830; AAF12789.1; -.
HSSP; P19120; LBA1.
InterPro; IPRO01013; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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157 AA; 17834 MW; E8F743382B285EB2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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09U668.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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88.2%; Score 45; DB 5;
Best Local Similarity 90.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches
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           HEAT-SHOCK PROTEIN (FRAGMENT).
HSC70.
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PROSITE; PS01036; HSP70_3; 1.
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85 SLFEGIDEYT 94
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                                                                                     Littorina plena.
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Q9U671
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Q90668
ID Q91
AC Q99
DT 011
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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.2%; Score 45; DB 5; Length 155; 90.0%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HohenJohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
"Submit-shock genes in the EMBL/GenBank/DDBJ databases.
EMBL; AF191826; AAF12785.1; -.
EMBL; AF191826; AAF12785.1; -.
InterPro; IPRO1032; HSP70.
PROSITE; PS01036; HSP70.3; 1.
NON_TER 155 155
SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;
                                                                                             Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoldea; Littorinidae; Littorina.
NCBI_TaxID=31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.2%; Score 45; DB 5; Length 153; 90.0%; Pred. No. 0.39; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                            Hohenlohe P.A.; "Heat-shock genus Littorina."; "heat-shock genes in the heat-stressed genus Littorina."; Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191825; AAF12784.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 153
153 Aa; 17352 MW; E29EE20C4CAF934D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
HSC70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P19120; 1BA1.
Interpro; IPR001023; HSP70.
PROSITE; PS01036; HSP70_3; 1.
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE
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RESULT 090669

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RESULT Q9U665

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Aplysia californica (California sea hare).
Eukaryota, Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysidae; Aplysia.
NCBI_TaxID=6500;
                                                              Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplyalidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                   MEDLINE=93077669; PubMed=1360013;

Ruhl D., Kennedy T., Barzilai A., Kandel E.;

Ruhl D., Kennedy T., Barzilai A., Kandel E.;

Ruhl D., Kennedy T., Barzilai A., Kandel E.;

**Long-term sensitization training in Aplysia leads to an increase in the expression of BiP, the major protein chaperon of the ER.*;

J. Cell Biol. 119:1069-1076(1992)

--- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.

--- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

EMBL; 215039; CAA78757.1;

--- INTERPO! 1281.

INTERPO: IPRO10123; HSP70.

PEAM: PF00012; HSP70:

PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to an increase in if the ER.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-93077669; PubMed-1360013;
Kuhl D., Kennedy T., Barzilai A., Kandel E.;
Kuhl D., Kennedy T., Barzilai A., Kandel E.;
Long-term sensitization training in Aplysia leads to an in the expression of BiP, the major protein chaperon of the ER J. Cell Biol. 119:1069-1076(1992).

J. Cell Biol. 119:1069-1076(1992).

-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; Z1507; CAA78755.1; -.
Interpro: IPRO0123; HSP70.
Pfam: PF00012; HSP70; I.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.2%; Score 45; DB 5; Length 220; 90.0%; Pred. No. 0.6;
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24684 MW; FA8557F2BB85C37A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P81157 PRELIMINARY; PRT; 221 AA.
P81157;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-2998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).
01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat shock; Multigene family.
NON_TER 1 220
NON_TER 220 A3; 24684 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat shock; Multigene family
NON_TER 1 21
SEQUENCE 221 AA: 24404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.2
Best Local Similarity 90.0
Matches 9; Conservative
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P81157
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0
                                                                    Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                                                                                   Hohenlohe P.A.;
Hohenlohe P.A.;
Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191807; AAF12786.1;
HSSP; P191207; IBA1
InterPro; IPR001023; HSP70.
PRINTS; PR00101; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 5; Length 158;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 5; Length 158;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191829; AAF12788.1; -.
HSSP; P19120; 1BAl.
InterPro; IPRO101033; HSP70.
PRINTS; PR00301; HEATSHOCK70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                               158 AA; 17868 MW; D2ECE71042EC44CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 AA; 17891 MW; B41E5356BCECAD2F CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                       88.2%;
90.0%;
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90.0%;
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Best Local Similarity 90.07
Local 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SLFEGIDAYT 10
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85 SLFEGIDFYT 94
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                                                          Littorina plena.
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SEQUENCE
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P81159 P81159; œ

RESULT P81159 ID P8 AC P8 DT 01

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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SLFEGIDAYT 10
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                                                                                                                                                                                      367
                                                                                                                                               Heat shock.
NON_TER
SEQUENCE
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SEQUENCE
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044350
DQ 44350
AC 044350
DT 01-JUN
DT 01-JUN
DT 01-JUN
DT 01-JUN
DC 01-JUN

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Q63718;
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                                                                                   Gaps
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Cheraryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-85036330; PubMed-6092938; Kothary R.K., Jones D., Candido E.P.M.; Kothary R.K., Jones D., Candido E.P.M.; "70-Kilodatton heat shock polypeptides from rainbow trout: characterization of cDNA sequences."; wall Cell. Biol. 4:1785-1791(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 278
Score 45; DB 5; Length 221;
Pred. No. 0.6;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30327 MW; E4C745DE5484C17A CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
170 KDA HEAT SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
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Pred. No. 0.79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.2%;
90.0%;
       88.2%;
90.0%;
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                                                                                       9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SLFEGIDAYT 10
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   Query Match
Best Local Similarity
                                                                                                                                                              1 SLFEGIDAYT 10
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SEQUENCE
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Q90520
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                                                                                   Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Bukaryota, Metazoa; Porifera; Demospongiae; Tetractinomorpha; Cohondrosida; Chondrillidae; Chondrosia.
NCBI_TaxID=68574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 11; Length 455; Pred. No. 1.4;
                                                                                                                                                                                  Score 45; DB 13; Length 367, Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angeletti B., Passarelli F., Orru D., Pascale E., Butler I D'Ambrosio E.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
HSBL; AST118; CAA81642.1; --
HSSP; P08107; 1HJO.
InterPro; IPR01023; HSP70.
Prim; PR00012; HSP70; 1.
PRNTS; PR00301; HEATSHOCK70.
PROSITE; PS001036; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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50404 MW; 0F45F12CBA1E2971 CRC64;
                                                                                                                         367 AA; 40405 MW; 8CD3DD8DF6E3C2CA CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                         455 AA
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Borchiellini C., Le Parco Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.2%;
90.0%;
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE: PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                      88.2%;
90.0%;
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Best Local Similarity 90...
Best Local 9; Conservative
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268 SLFEGIDEYT 277
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Petrobiona massiliana.
Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
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Clathrinidae; Guancha.
NCBI_TaxID-115120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Borchiellini C., Le Parco Y.;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF026520; AAC05364.1; -.

HSSP; P08109; 1CKR.

InterPro; IPR00102; HSP70.

PROSTIE; PF00101; HEATSHOCK70.

PROSTIE; PS01036; HSP70.3; 1.

NON_TER 467 467

SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 5; Length 467;
Pred. No. 1.5;
0; Mismatches 1; Indels
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF025517; AAC05362.1; -.
HSSP; P08109; 1CKR.
InterPro; IFR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PROMITE; PR00329; HBATSH0CK70.
PROSITE; PS010339; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         51707 MW; ODBE6920F2E6EA96 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROFEIN HSP70 (FRAGMENT).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                          467 467
467 AA; 51
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252 SLFEGIDFYT 261
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SEQUENCE FROM N.A.
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SEQUENCE
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044352
AC 044352
AC 044352,
DT 01-JUN
DT 01-JU
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Q9NJ92
AC Q9NJ92,
DT 01-OCT-
DT 01-OCT-
DT 01-TOCT-
DT 01-TOCT-
DT 01-TOCT-
DC 0
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RA Borchiellini C., Le Parco Y.;
RT "Sponges paraphyly and the origin of Metazoa.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

BR EMBL, AFT82195; AAF61297.1; -.

DR InterPro: IPR001023; HSP70.

DR PROSITE; PS00329; HSP70.2; 1.

PT NON_TER 467 467

SQ SEQUENCE 467 AA; 51318 MW; F36FC06CBIDEE131 CRC64;

QUETY MAtch

ACCOUNTY MATCH

BR.2%; Score 45; DB 5; Length 467;

Best Local Similarity 90.0%; Pred. No.1.5;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDEYT 261

Search completed: December 6, 2001, 07:56:54

Job time: 182 sec
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pep2-mod8a.rspt

Tue Dec 11 08:45:54 2001

8, Appli 7, Appli 20, Appl 1, Appli 1, Appli 1, Appli 1, Appli

Sequence:

Run on:

Searched:

Database

Result Š.

Sequence Seq

Sequence 11,

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Sequence 3, Application US/08797358B
Patent No. 6268478
GENERAL INFORMATION:
APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Gampbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB 4; Length 643;
Pred. No. 0.032;
1; Mismatches 0; Indels
                      US-09-272-796-18

US-08-48-890A-19

US-08-478-485-19

US-08-478-713-19

US-08-474-671-19

US-08-483-577A-19

US-08-887-778-19

US-08-887-778-19

US-08-887-778-19

US-08-867-78-19

US-08-469-537A-20

US-08-469-537A-20

US-08-467-155A-1

US-08-678-198-1

US-08-678-198-1

US-08-01-038-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATONREY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNDER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 643 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.1%;
90.0%;
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Best Local Similarity
1 SLFEGIDFYT
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  RESULT
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22, Appl
24, Appl
15, Appl
84, Appl
86, Appl
86, Appl
11, Appl
11, Appl
2, Appl
2, Appl
5, Appl
                                                                                                                                                                                       ; Search time 81.43 Seconds (without alignments) 2.764 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Sequence 23, Sequence 23, Sequence 22, Sequence 24, Sequence 24, Sequence 24, Sequence 84, Sequence 84, Sequence 86, Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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Sequence 2
Sequence 2
Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgg2_6/ptcdata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/laa/PCTUS_COMB.pep:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-441-139-14
US-08-928-692-52
US-08-079-156-23
US-08-052-404-22
US-08-075-404-22
US-08-075-404-22
US-08-479-156-24
US-08-479-156-24
US-08-479-156-24
US-08-62-877-86
US-08-62-877-86
US-08-652-877-86
US-08-653-877-86
US-08-653-877-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US93-08528-56
US-08-390-000A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212252 seqs, 22503292 residues
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                                                                                                                                                                                       6, 2001, 07:59:59
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Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                       1 SLFEGIDFYT 10
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Match Length DB
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44668
4668
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309
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Gaps

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REFERENCE/DOCKET NUMBER: NIH031.001A TELECOMMUNICATION: TELEPHONE: 619-235-8550
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STREET: 405 Lexington Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: No. 5958727e
US-08-928-692-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNET/AGENT INFORMATION:
NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,
                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                             10174
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                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-052-404-23
                                         STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Д
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a Polypeptide
:: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.3%; Score 50; DB 1; Length 646; 90.0%; Pred. No. 0.078;
                                                                                                                                                                         APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                          STREET: 400 Garden City Plaza CITY: Garden City CITY: Garden City CITY: COIDMIN'S STATE. NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-UDL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52, Application US/08928692
Patent No. 5958727
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Mod
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                Sequence 14, Application US/08441139
Patent No. 5773245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 236 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 646 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 90.0
Matches 9; Conservative
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286 SLYEGIDFYT 295
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288 SLFEGVDFYT 297
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                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                11530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-928-692-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                   JS-08-441-139-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rabin, Nina
APPLICANT: Nichols, Ralph
APPLICANT: Plotz, Paul
APPLICANT: Leff, Richard
APPLICANT: Leff, Richard
TITLE OF INVENTION: Human Histidyl tRNA Synthetase
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUNESSEE: Knobbe, Martens, Olson, and Bear STREET: 620 Newport Center Dr. Sixteenth Floor CITY: Newport Beach STATE: CA
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
ATTORBY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 34,44.200-US
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                         73.6%; Score 39; DB 100.0%; Pred. No. 4.9 tive 0; Mismatches
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US-08-479-156-23
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US-08-052-404-24
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Pred. No. 50;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FALABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: PATENTION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,404
FILING DATE: 22-APR-1993
ATTONNEY/AGENT INFORMATION:
NAME: FULLER, MIChael L.
REGISTRATION NUMBER: 36,516
REGISTRATION NUMBER: 36,516
REFERENCE/POCKET UNBER: 36,516
RELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rabin, Nina
APPLICANT: Nichols, Ralph
APPLICANT: Plotz, Paul
APPLICANT: Leff, Richard
TITLE OF INVENTION: Human Histidyl tRNA Synthetase
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08479156
Patent No. 5663066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 714-760-9502 INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                    66.0%;
60.0%;
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No
                                                                                                                                                         HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGNENT TYPE: N-terminal

IMMEDIATE SOURCE:

CLONE: Hum
US-08-052-404-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal
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Best Local Similarity 60.0-
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                        || |:|:||
334 SLARGLDYYT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 1 SLFEGIDFYT 10
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
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US-08-479-156-23
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66.0%; Score 35; DB 1; Length 560; 60.0%; Pred. No. 50; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                     Sequence 22, Application US/08052404

Patent No. 5484703

GENERAL INFORMATION

APPLICANT: Rabin, Nina
APPLICANT: Nichols, Ralph

APPLICANT: Dictz, Paul

APPLICANT: Leff, Richard

TITLE OF INVENTION: Human Histidyl tRNA Synthetase

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson, and Bear

STREET: 620 Newport Center Dr. Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,404
FILING DATE: 19930422
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH031.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: FULLEr, Michael L.
REGISTATION NUMBER: 36,516
REPRENCE/DOCKET NUMBER: NIHO3
TELECOMMUNICATION INFORMATION:
TELEFAX: 714,760-5502
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 561 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
Query Match 66.0
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newport Beach
                                                                                                          334 SLARGLDYYT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || |:|:||
335 SLARGLDYYT 344
                                                                                 1 SLFEGIDFYT 10
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CLONE: Yea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
COUNTRY: USA
ZIP: 92660
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Score 35; DB 1; Length 561;
Pred. No. 50;
2; Mismatches 2; Indels
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Sequence 24, Application US/08479156

Patent No. 5663066

GENERAL INPORMATION:
APPLICANT: Rabin, Nina
APPLICANT: Nichols, Ralph
APPLICANT: Leff, Richard
TITLE OF INVENTION: Human Histidyl tRNA Synthetase
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,156
FILING DATE: J-10N-1995
CLASSIFICATION NUMBER: US 08/052,404
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael L.
REDERGENTATION NUMBER: 35,516
REFERENCE/POCKET NUMBER: 35,516
REFERENCE/POCKET NUMBER: 31,516
RELEPHONE: G19-23-8950
TELEPHONE: G19-23-8950
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
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ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/479,156
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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CLASSIFICATION: 435
PRICR, APPLICATION DATA:
APPLICATION NUMBER: US 08/052,404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 561 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.0
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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FRAGMENT TYPE:
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STATE:
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50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rabin, Nina
APPLICANT: Rabin, Nina
APPLICANT: Nichols, Ralph
APPLICANT: Plotz, Paul
APPLICANT: Leff, Richard
APPLICANT: Leff, Richard
APPLICANT: Human Histidyl tRNA Synthetase
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
  Sequence 24, Application US/08052404
Patent No. 5484703
GENERAL INPORMATION:
APPLICANT: Rabin, Mina
APPLICANT: Nichols, Ralph
APPLICANT: Laff, Richal
APPLICANT: ADDRESS:
ADDRESSER: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,404
FILING DATE: 19930422
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: FUller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: 36,516
REERENCE/DOCKET NUMBER: 36,516
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1
Pred. No. 50;
2; Mismatches
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Patent No. 5663066
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 561 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                     CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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Gaps

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Gaps

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Sequence 15, Application US/09245041

Fatent No. 6274339

GENERAL INFORMATION:
APPLICANT: Moore, K.
APPLICANT: Nagle, D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
CURRENT APPLICATION NUMBER: 05/09/245,041
CURRENT APPLICATION NUMBER: 60/093,630
EARLIER FILING DATE: 1999-07-21
EARLIER FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
LEAGTH: 2787

MANDER OF SEQ ID NOS: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-476-515A-84
; Sequence 84, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
APPLICANT: Cruhley, Gregg R.
APPLICANT: Cruhley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Human Calcium Sensor Protein,
TITLE OF INVENTION: Human Calcium Sensor Protein,
TITLE OF INVENTION: Human Calcium Sensor Protein,
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
STREFT.
STREFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2787;
                                                                                              Length 560
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Pred. No. 7.3e+02;
3; Mismatches 1; Indels
                                                                                         Score 33; DB 2; Length 560
Pred. No. 1.2e+02;
3; Mismatches 1; Indels
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55.6%;
      No. 5958727e
                                                                                              62.3%;
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COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                         Query Match 62.3
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.3
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-245-041-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collegeville
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304 SLADGIDFHS 313
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         ; MOLECULE TYPE:
US-08-928-692-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: COll
STATE: PA
                                                                                                                                                                                                                                                                                            RESULT 11
US-09-245-041-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587270 No. 5958727th P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 1; Length 561;
Pred. No. 50;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFRWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FLING DATE: 12-SEPT-1997
CLASSIFICATION: 435
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: FUller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH031.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEPAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212.867-0123
TELEFAX: 212.878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-928-692-53
; Sequence 53, Application US/08928692
: Patent No. 5958727
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 53:
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60.0%;
                                                                                                                                                                                                                          LENGTH: 561 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.0
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1| |:|:||
335 SLARGLDYYT 344
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Gaps

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APPLICANT: Akerstrom, Goran
APPLICANT: Akerstrom, Goran
APPLICANT: Akerstrom, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Rhone-Poulenc Rorer Inc. 500 Arcola Rd., 3C43
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PRIOR APPLICATION DABER: PAPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                    FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-UUNE-1995
ATTORNEY/AGENT INFORMATION:
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                                              US 08/344,836
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SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86, Application US/08652877 Patent No. 6187548 GENERAL INFORMATION:
                                                                                                                                                                                                     NAME: SAVITZKY, MARTIN
REGISTRATION NUMBER: 29,699
REFERENCE/POCKET NUMBER: A135:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 610-454-3808
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 4655 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.3%;
70.0%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
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Best Local Similarity 70.0
Matches 7; Conservative
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STREET: 500 Arcola 1
CITY: Collegeville
STATE: PA
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APPLICANT: Albanin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Crumley, Gregg R.
APPLICANT: Murray, Edward M.
APPLICANT: Hyalm, Goran
TITLE OF INVENTION: Thereof and DNA Encoding Same
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
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Pred. No. 1.3e+03;
1; Mismatches 2; Indels
OPERATING SYSTEM: WINDOWS >>> SOFTWARE: WORD 7.0 (PATENTIA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLEASFIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: SAVITARY, MARTIN
REGISTRATION NUMBER: 29,699
RELEPRANCION NUMBER: 20,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/15203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 84, Application US/08652877 Patent No. 6187548
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70.0%;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Best Local Similarity
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COUNTRY: USA
ZIP: 19426-0107
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Gaps
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Pred. No. 1.3e+03;
1; Mismatches 2; Indels
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PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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Patent No. 6187548

GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Crumley, Gregg R.
APPLICANT: Crumley, Gregg R.
APPLICANT: Hyalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Human Calcium Sensor Protein,
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
A
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NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 41355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3808
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 4655 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
FRIDRA APPLICATION DATA: 22-NOV-1995
FRIDRA APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
FRIDRA APPLICATION DATA: APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTONNEY, AGENT INFORMATION: NAME: SAVILZKY, MARTIN REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
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STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
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INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 70.0'
Matches 7; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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US-08-652-877-88
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HENGTH: 4655 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-877-88

Query Match
Best Local Similarity 70.0%; Pred: No. 1.3e+03;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps

Qy 1 SLFEGIDFYT 10

Db 608 SLFEGQVFFT 617

Search completed: December 6, 2001, 07:59:59
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                                                 6, 2001, 07:58:28; Search time 88.19 Seconds (without alignments) 8.638 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                               219241 seqs, 76174552 residues
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                                 OM protein - protein search, using sw model
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988.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 998.1 994.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 944.3 945.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3 946.3	olve
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30 52 98.1 214 2 A03309 31 52 98.1 467 2 745473 33 52 98.1 467 2 745473 33 52 98.1 467 2 745474 33 52 98.1 467 2 745474 34 52 98.1 641 2 700036 35 52 98.1 641 2 700036 36 52 98.1 641 2 700036 36 52 98.1 641 2 700036 38 52 98.1 641 2 700036 39 52 98.1 641 2 700036 41 2 50 94.3 209 2 848025 42 50 94.3 209 2 848025 43 50 94.3 209 2 848025 44 50 94.3 209 2 848025 44 50 94.3 209 2 848024 44 50 94.3 209 2 848026 44 50 94.3 372 2 700138 44 50 94.3 372 2 700138 44 50 94.3 372 2 700138 44 50 94.3 372 2 700138 44 50 94.3 372 2 700138 45 50 94.3 372 2 700138 45 50 94.3 372 2 700138 47 50 94.3 372 2 700138 48 75 70 70 70 70 70 70 70 70 70 70 70 70 70	A; Descr

A;Description: involved in protein folding and assembling/disassembling of protein coc;Superfamily: heat shock protein 70

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dnak-type molecular chaperone hsc70 [imported] – slime mold (Dictyostelium discoideum N;Alternate names: heat shock cognate protein 70
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C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45478
R;Borchiellini, C.; Le Parco, Y
submitted to the EMBL Data Library, September 1997
A;Reference number: Z22983
A;Accession: T45478
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Roctute type: mRNA
A;Residues: 1-469 <BOR>
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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
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R; Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G. submitted to the EMBL Data Library, September 1997
A; Reference number: 222980
A; Accession: T45471
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A;Molecule type: mRNA
A;Residues; 1-632 <BOV>
A;Cross-references: EMBL:AF025951; PIDN:AAB81865.1
A;Experimental source: strain AX3
C;Genelics:
A;Gene: hsc70
                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-468 <BOR>
A;Cross-references: EMBL:AF026516; PIDN:AAC05361.1
C;Genetics:
C;Accession: T45476
R;Borchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z22983
A;Accession: T45476
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C;Genetics:
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C,Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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254 SLFEGIDEYT 263
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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RESULT 5
T45476
T45476
C; Species: Funiculina duadrangularis (fragment)
C; Species: Funiculina quadrangularis
C; Species: Funiculina quadrangularis
C; Species: 31-yan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
                                                                                                                                                                                                                                                                                                                                                                                                         heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C;Species: Chondrosia reniformis
C;Species: Chondrosia reniformis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T4547
A;Borchiellini, C.; Le Parco, Y.
A;Borchiellini, C.; Le Parco, Y.
A;Reference number: 222983
A;Accession: T45477
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: manyA
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                                                                                100.0%; Score 53; DB 2; Length 278; 100.0%; Pred. No. 0.0083; Live 0; Mismatches 0; Indels
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A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
A;Cross:-references: EMBL:AF026520; PIDN:AAC05364.1
C;Genetics:
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A, Cross-references: EMBL:AF026517; PIDN:AAC05362.1
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C;Superfamily: heat shock protein 70
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A;Gene: Hsp70
C;Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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Best Local Similarity 100.

Matches 10; Conservative
                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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252 SLFEGIDFYT 261
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156 SLFEGIDFYT 165
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252 SLFEGIDFYT 261
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10; Conservative

Best Local Similarity Matches 10; Conserv

Query Match

1 SLFEGIDFYT 10

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Cypecies: Paracentrotus lividus (common urchin)
Cypecies: Scardina, G.; Scardina, G.; Ferraro, M.G.
Gene 121, 353-358, 1992
A.Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp
A; Mcession: JC1391
A; Mcesion: JC1391
A; Mcession: JC1391
A; Mcession: JC1391
A; Mcession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Molecule type: MRNA
A; Residues: 1-638 <SAI>
B; Saints, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A; Title: The hsc70 gene which is slightly induced by heat is the main virus inducible A; Reference number: 136927; MUID: 95080396
A; Accession: 136927; MUID: 95080396
A; Accession: 136927
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-638 <RES>
A; Cross-references: EMBL; X70684; NID: 922781; PIDN: CAA50019.1; PID: 922782
A; Experimental source: kidney; cell line COS-1
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                                 dnaK-type molecular chaperone hsp70 - green monkey
N;Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 **sequence_revision 13-Jan-1995 **text_change 20-Aug-1999
C;Accession: S31766; 136927
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock prot A;Reference number: S31766
A;Accession: S31766
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C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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284 SLFEGIDEYT 293
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N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein agi
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Accession: A48872
R;Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J;Biol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-requiated F-actin capping activity is associated with an A;Reference number: A48872; MUID:94043116
A;Recession: A48872
A;Reference number: A48872
A;Rolecule type: mRNA
A;Residues: Preliminary
A;Molecule type: mRNA
A;Residues: 1-636 < Cabb.
A;Cross-references: GB:L22736; NID:9433179; PIDN:AAA33219.1; PID:9433180
A;Cross-references: GB:L22736; NID:9433179; PIDN:AAA33219.1; PID:9433180
A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Vd
C;Function:
A;Description: Involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Reywords: ATP; molecular chaperone
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A. Residues: 1-634 < MOR>
A. Residues: 1-634 < MOR>
A. Residues: 1-634 < MOR>
A. Stronger of the codon TCG for residue 583 as Trp
C. Function:
A. Note: the authors translated the codon TCG for residue 583 as Trp
C. Function:
A. Description: involved in protein folding and assembling/disassembling of protein compl
C. Superfamily: heat shock protein 70
C. Keywords: ATP; molecular chaperone
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Nalternate names: heat takok protein 70
C; Alternate names: heat takok protein 70
C; Species: Gallus gallus (chicken)
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
R; Accession: 261, 12692-12699, 1986
A; Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.
A; Reference number: A25646; MUID:86304452
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100.0%; Score 53; DB 2; Length 632; 100.0%; Pred. No. 0.02;
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Mismatches

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Conservative

Query Match Best Local Similarity Matches 10; Conserv

1 SLFEGIDFYT 10

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Best Local Similarity 100.

280 SLFEGIDEYT 289

RESULT

1 SLFEGIDFYT 10

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A; Cross-references: GB:M18540; NID:9156351; PIDN:AAA28078.1; PID:9156352
A; Note: genomic clones representing six distinct members of the hsp70 gene family wer A; Note: transcripts of hsp70A are abundant in control worms and also increase two. to A; Note: one of the three introns in hsp70A is in a position similar to an intron in D; Genetics:
A; Gene: hsp70A
A; Map position: IV
A; Introns: 69/1; 331/3; 558/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riburt, C.; Morimoto, R.I.

Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985

A.77itle: Conserved features of eukaryotic hsp70 genes revealed by comparison with the A; Reference number: A29160; MUID:86016721

A.Accession: A29160

A.Molecule type: DNA

A.Residues: 1-640 < HUN>
A.Residues: 1-640 < HUN>
A.Cross references: GB.MI1717, GB.MI5432; NID:g184416; PIDN:AAA52697.1; PID:g386785

A.Note: the authors mistranslated residues 463, 491, and 492

A.Note: the authors mistranslated residues 463, 491, and 492

A.Note: A. Genthe, A.: Benecke, B.J.

Nucleic Acids Res. 14, 8933-8948, 1986

A.Title: In vitro transcription of a human hsp.70 heat shock gene by extracts prepare A.Recence in which is a number: 137561; MUID:87066768
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                                                                                                                                                                                                                                                                                                                                                 A; Description: involved in protein folding and assembling/disassembling of protein co c; Superfamily: heat shock protein 70 C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: A29160; 137561; 137562
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A, Status: translation not shown; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-22 < RES>
A, Cross-references: EMBL: X04676; NID: 932480; PIDN: CAA28381.1; PID: 932481
A, Accession: 137562
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A.Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483
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A;Cross-references: GDB:120058; OMIM:140559
A;Map position: 6p21.3-6p21.3
A;Introns: #status absent
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286 SLFEGIDFYT 295
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287 SLFEGIDEYT 296
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A.Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterizat
A.Faference number: JT0285, MUID:88297155
A.Accession: JT0285
A.Molecule type: DNA; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-639 <SLA>
A; Residues: 1-639 <SLA>
A; Residues: 1-639 <SLA>
A; Residues: 1-639 <SLA>
A; Cross-references: EMBL:X12927; NID:94545; PIDN:CAA31394.1; PID:94546
B; Goffeau, A : Purnelle, B
submitted to the Protein Sequence Database, May 1996
A; Reference number: $64761
A; Reference number: $64702
A; Residues: 1-639 <GOF>
A; Residues: 1-639 <GOF>
A; Residues: 1-639 <GOF>
A; Residues: 1-639 <GOF>
A; Reperimented source: strain $288C
A; Experimented source: strain $288C
B; Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
Submitted to the Protein Sequence Database, May 1996
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A; Accession: $64775
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 272-639 vDUE>
A; Cross references: EMBL: 273129; MIPS: YLL024c
A; Experimental source: strain $288C
B; Parnelle, B; Goffeau, A
B; Experimental source: strain $288C
B; Parnelle, B; Goffeau, A
B; Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
A; Reference number: $69380
A; Reference number: $69380
A; Accession: $69383
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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                                                                                            dnaK-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
N.Alternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S20139; Seq1772; S64775; S69383
R;Slater, M.R.; Craig, E.A.
Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
A;Reference number: S20139; WuID:89128457
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N;Alternate names: heat shock protein 70 A
C;Species: Caenorhabditis elegans
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
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A; Residues: 1-639 <PUR>
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R; Snutch, T.P.; Hesc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 12L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: SGD:SSA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
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dnak-type molecular chaperone hsc70 - slime mold (Dictyostelium discoideum)
N;Alternate names: heat shock cognate protein 70
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Accession: S37394
E;Haus, U; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Schl
EMBO J. 12, 3763-3771, 1993
A;Tile: The heat shock cognate protein from Dictyostellum affects actin polymerization
A;Reference number: S37394; MUID:94008983
A;Accession: S37394
A;Residues: 1-640 <AHJO
A;Residues: 1-640 <AHJO
A;Cross-references: EMBL:X75263; NID:9433874; PIDN:CAA53039.1; PID:9433875
C;Genetics:
A;Genetics:
A
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C; Superfamily: heat shock protein 70
C; Keywords: ATP; molecular chaperone
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0; Gaps

Query Match 100.0%; Score 53; DB 2; Length 640; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 10; Conservative 0; Mismatches 0; Indels

1 SLFEGIDFYT 10 ||||||||||||| 284 SLFEGIDFYT 293

g ç

Search completed: December 6, 2001, 07:58:28 Job time: 276 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 6, 2001, 08:00:53 ; Search time 50.21 Seconds (without alignments) 7.302 Million cell updates/sec Run on:

PEP2-MOD8F 53 1 SLFEGIDFYT 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1		COSTOS GALLUS GALL				P36415 dictyosteli			Snw	P34930 sus scrofa	Q07439 rattus norv		Q27965 bos taurus			_	Q91291 pleurodeles	Q01233 neurospora	.,	P48720 blastocladi	-	-		P29843 drosophila	P17066 homo sapien		Q01877 puccinia gr	paracentr	P55063 rattus norv	P34931 homo sapien	P16627 mus musculu
SUMMARIES	HS70_ONCVO	HS70_PENCI	HS71 CERAE	HS72_YEAST	HS74_PARLI	HS7A_CAEEL	- 1	- 1	HS71_HUMAN	- 1	HS71_PIG	HS71_RAT	HS71_YEAST	HS72_BOVIN	HS74_YEAST	HS70_BRUMA	HS70_ONCTS	HS70_PLEWA	HS70_NEUCR	HS70_XENLA	HS70_BLAEM	HS7D_MANSE		HS7X_PIG	HS7A_DROME	HS76_HUMAN	HS76_PIG	HS71_PUCGR	HS72_PARLI	HS73_RAT	HS7H_HUMAN	HS7T_MOUSE
DB	ί			-	Н	-1	-	н,	⊣ .	<b>~</b>		-	-	~	<del>, -1</del>		~	-	-	-				-	-	~	Н	H	Н	Н	-	П
% Query Match Length	322	503	638	638	639	640	640	641	641	641	641	641	641	641	641	644	644	645	646	647	649	652	214	379	641	643	643	648	372	64:1	641	641
% Query Match	100.0	100.0	100.0	100.0			100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0			100.0	100.0	100.0	100.0	98.1	98.1	98.1	œ	œ	98.1	₹	94.3	94.3	94.3
Score	53		, K	23	23	53	53	23	53	53	23	53	53	53	53	23	23	23	53	53	23	53	25	52	52	52	52	52	20	20	20	20
Result No.	(	7 6	) <del>4</del>	Ŋ	9	7	<b>œ</b>	σ,	010	Π:	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33

P53623 pichia angu Q10265 schizosacch P53421 pichia angu P19378 cricetulus P11142 homo sapien P08109 mus musculu P87047 paracoccidi P09435 saccharomyc Q90473 brachydanio P19120 bos taurus P08108 oncorhynchu Q05944 hydra magni		T 1  ONCYO  STANDARD; PRT; 322 AA.  P1502.  O1-OCT-1989 (Rel. 12, Created)  O1-FEB-1996 (Rel. 33, Last sequence update)  O1-FEB-1996 (Rel. 34, Last sequence update)  SEQUENCE FROM N.A.  NCBL_TAXID=6282;  (1)  SEQUENCE FROM N.A.  MCBLINE-PS201313; PubMed-2704388;  Rochocarca volvulus heat shock protein 70 is a major immunogen in amortofilaremic individuals from a filariasis-endemic area. ";  MOLD BIOCHEM. PARABLIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.  -1 DISBASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOSEN IN A MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.  -1 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FRAMILY.  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swisz Institute of Bioinformatics and the EMBL outstation. Let be European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way moddified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).  HSSD: J04006; AAA29417.1;  HSSD: J04006; AAA29417.1;  HSSD: J04006; AAA29417.1;  HSSP: J19120; JATR.  HSSP: J19120; JATR.  HSSP: J19120; JATR.	CRC64; Length 322;	o; Indets o; caps
3 642 1 HS72_PICAN 643 1 HS71_SCHPO 644 1 HS71_PICAN 3 646 1 HS7C_RUGR 3 646 1 HS7C_RUGR 3 646 1 HS7C_RUGR 3 649 1 HS70_PARBR 649 1 HS70_PARBR 649 1 HS70_BARBR 649 1 HS7C_BRARB 650 1 HS7C_BOVIN 3 651 1 HS70_ONCMY 654 1 HS70_ONCMY	ALIGNMENTS	### 1  ONCYO  HS7D_ONCYO  STANDARD; PRT; 322 AA.  P11503;  P11503;  O1-PEB-1996 (Rel. 12, Created)  O1-PEB-1996 (Rel. 33, Last sequence update)  O1-PEB-1996 (Rel. 33, Last annotation update)  EAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).  Onchocerca volvulus.  Onchocercidae; Onchocerca.  NCBI_TAXID=6282;  [1]  NCBI_TAXID=6282;  [2]  NCBI_TAXID=6282;  [3]  NCBI_TAXID=6282;  [4]  NCBI_TAXID=6282;  [5]  NCBI_TAXID=6282;  [6]  NCBI_TAXID=6329;  [7]  NCBI_TAXID=6329;  NCBI_TAXID=6329;  NCBI_TAXID=6329;  NCBI_TAXID=89201313; PubMed=2704388;  NCBI_TAXID=89201313; PubMed=270498;  NCBI_TAXID=80201313; PubMed=2704171;  NCBI_TAXID=80201313; PubMed=2704171;  NCBI_TAXID=80201313; PubMed=2704171;  NCBI_TAXID=80201313; PubMed=2704171;  NCBI_TAXID=80201313; PubMed=2704171;  NCBI_TAXID=80201314 PubMed=2704171;  NCBI_TAXID=80201314 PubMed=2704171;  NCBI_TAXID=802014 PubMed=2704171;  NCBI_TAXID=802014 PubMed=2704171;  NCBI_TAXID=802014 PubMed=27041718;  NCBI_TAXID=802014 PubMed=2704181718;  NCBI_TAXID=802014 PubMed=2704181718;  NCBI_TAXID=8020	1, PARTI 2, PARTI 2, PARTI 14 MW; 2	Servative 10 52 STANDARD;
34 35 36 36 37 37 39 39 40 40 40 40 40 40 40 40 40 40 40 40 40		30L -0	Pfam; PF0001 PROSITE; PSG PROSITE; PSG ATP-Dinding; NON_TER NON_TER SEQUENCE 3	Marcnes 10;  1 SLFEGIE 43 SLFEGIE SULT 2 70_PENCI HS70_PENCI
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EMBL; X70684; CAA50019.1; -.
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Q28222;
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                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDIA BLANCE FROM N.A. MEDIATE-86304452; PubMed=3017985; Morimoto R.I., Bunt C., Huang S.-Y., Berg K.L., Banerji S.S.; Morimoto R.I., nucleotide sequence, and transcription of the chicken "Organization, nucleotide sequence, and transcription of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                          Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.; "Molecular cloning and expression of a Penicillium citrinum allergen with sequence homology and antigenic cross-reactivity a hsp70 human heat shock protein."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases:
-- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 261:12692-12699(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 53; DB 1; Length 503; 100.0%; Pred. No. 0.0059; Dred. No. 0.0059; Live 0; Mismatches 0; Indels
             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HATS SHOCK 70 KDA PROTEIN (HSP70).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HSP70; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                            EMBL; U64207; AAB06397.1; -. HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                Penicillium citrinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 SLFEGIDFYT 163
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SLFEGIDFYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                      NCBI_TaxID=5077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSP70 gene.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS70_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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MEDLINE-51080936; pubMed=7988690;

MEDLINE-51080396; pubMed=7988690;

MEDLINE-1. Angelidis C., Pagoulatos G., Lazaridis I.;

Tinducible member of the hsp70 gene family.";

Tinducible member of the hsp70 gene family.";

PRESISTENT PROPERINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEMIX TRANSLAYED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULM PLAX AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROPISES THE MASSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDOCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE COMPONANTINE CONFORMATIONS OF OTHER PROPISEINS. THEY BIND EXTENDED PEPTIDE SEMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES OF THE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 53; DB 1; Length 634; 100.0%; Pred. No. 0.0076;
                                                                                                                                                                                                                           PIR; A25646; A27.

HSSP, P9120: 1ATR.

InterPro; IR001023; HSP70.

Pfam; PF00012; HSP70; 1.

PRINTS; P800301; HSATSHCK70.

PROSITE; P800329; HSP70_1; 1.

PROSITE; P801036; HSP70_2; 1.

PROSITE; P801036; HSP70_3; 1.

PROSITE; P801036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                      EMBL; J02579; AAA48825.1;
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Best Local Similarity 100.
Matches 10; Conservative
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HSP70IV
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Protein expression during exponential growth in 0.7 M NaCl medium of Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                   Gaps
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Submitted (SEP-1994) to the SWISS-PROT data bank.
-1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.; "Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 71-638 FROM N.A. Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                 shock; Multigene family; MHC III.
D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                           Query Match 100.0%; Score 53; DB 1; Length 638; Best Local Similarity 100.0%; Pred. No. 0.0077; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-07U-1989 (Rel. 11, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       638 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89128457; PubMed-2644626;
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MEDLINE-97089742; PubMed-8935650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLATION, AND PHOSPHORYLATION.
                    Pfam; PF00012; HSP70; 1.
PRINTS: PR003014; HBAF8HOK70.
PROSITE: PS00129; HSP70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
ATP-binding: Chaperone; Heat sht SEQUENCE 638 AA; 69920 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 91-97 AND 325-341.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHOCK PROTEIN SSA2.
                                                                                                                                                                                                                                                                                                                                                                          111111111
284 SLFEGIDFYT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 186-195
                                                                                                                                                                                                                                                                                                                                              1 SLFEGIDFYT 10
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS72_YEAST
P10592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         database.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93077053; PubMed=1339375; Sconzo G., Scardina G., Ferraro M.G.; Sconzo G., Scardina G., Ferraro M.G.; "Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 gene family and its expression."; Gene 121:353-358(1992).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                          -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinosea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 1; Length 63/
Pred. No. 0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IRO01023; HSP70.

Pfam; PR00102; HSP70; 1.

PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00329; HSP70_1; 1.

PROSITE; PS003039; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

Heat shock; AFP-binding; Multigene family; Acetylation; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLATION.
23BDDD120C194912 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                           SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69338 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                     EMBL; X12927; CAA31394.1; -. EMBL; Z73129; CAA97472.1; -. EMBL; X97560; CAA66167.1; -. PIR; S20139; S20139.
                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10592; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                      PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S0003947; SSA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111111111
282 SLFEGIDFYT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLFEGIDEYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paracentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HS74_PARLI
ID HS74_PARLI
AC Q06248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INIT_MET
MOD_RES
SEQUENCE
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287 SLFEGIDEYT 296

or send an email to license@isb-sib.ch)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSSIGIDLGTTYSCVGVWQNDRVEIIAND -> IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
                                                                                                                                                                                                                                                                                                                     MEDIINE=94008983; PubMed=8404847;
Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
Noegell A.A., Schlaicher M.;
"The heat shock cognate protein from Dictyostellum affects actin
polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2E6BDC2DB96A9F5D CRC64;
                                                                                                                                                                                 Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
                                                  640 AA.
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-AX3;
MEDLINE-94043116; PubMed-8226849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X75263; CAA53039.1; --
EMBL; 122736; AAA3319.1; --
PIR; 837394; 837394.
HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P36415; DICTY.
DictyDb; D001078; hSP70.
Pfam; PP00012; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 F
70499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 12:3763-3771(1993).
                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Chaperone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32
64
180
180
237
240
341
352
640 AA;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                              HSTC_DICDI

1D HSTC_DICDI

1D HSTC_DICDI

1D 1-JUN-1994

DT 01-JUN-1994

DT DELYPOST=1

RN HSED OR HSC

DELYPOST=1

RN HSEDINE=AX3;

CC THE EUROPEE

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DR PRINTS; PRONTIC;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_FaxID=6239;
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-BR297155; PubMed-2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 53; DB 1; Length 640; 100.0%; Pred. No. 0.0077; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                       Length 639;
                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PRO0301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
                                                                                                  PRINTS; PRO0301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;
                                                                                                                                                                                                                                                                       100.0%; Score 53; DB 1; 100.0%; Pred. No. 0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN A.
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M18540; AAA28078.1; -. PIR; JT0285; HHKW7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P19120; 1NGI.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
EMBL; X61379; CAA43653.1; -. PIR; JC1391; JC1391.
                                                             InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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286 SLFEGIDFYT 295
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                                                                                                                                                                                                                                                                                                                                                               1 SLFEGIDFYT 10
                          PIR; JC1391; JC139:
HSSP; P19120; 1NGJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSP-1 OR HSP70A.
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RESULT 7 HS7A\_CAEEL

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region.
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Anim. Genet. 25:196-196 (1994).

PREAZISTENT PROTEINS AGAINST AGGREGATION AND MEDITATE THE POLDING OF UNGLISTENT PROTEINS AGAINST AGGREGATION AND MEDITATE THE POLDING OF UNGLISTENT PRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAR AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLACION. HEY ARE INOLIVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROHOBIC CHARACTER EXPOSED BY POLYPEPTIDES CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROHOBIC CHARACTER EXPOSED BY POLYPEPTIDES CONFORMATIONS OF DAMAGE.

STRESS-INDUCED DAMAGE.

-1-INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 Kba heat-shock protein (18970) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grosz M.D., Skow L.C., Stone R.T.;
"An Alul polymorphism at the bovine 70 kD heat-shock protein-1
(HSP70-1) locus.";
                                                              Length 640;
                                                                                                                            Indels
                                                          Score 53; DB 1; I
Pred. No. 0.0077;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         HS71_BOVIN STANDARD; PRT; 641 AA. 027975; 027964; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Skeletal muscle;
MEDLINE=95126904; PubMed=7826329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95030563; PubMed=7943958;
                                                          100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 212-641 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U09861; AAA73914.1; -. EMBL; U02891; AAA03450.1; -. HSSP; P19120; INGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001023; HSP70.
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00012; HSP70; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                              111111111
284 SLFEGIDFYT 293
                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                           1 SLFEGIDFYT 10
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JD HS71_BOVIN

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JD 10-NOV-

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Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
Structure of a new crystal form of human hsp70 Arpase domain.";
Acta Crystallogr. D 55:1105-1107(1999).
-! FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYEPPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DINJUNG FORE FOR
PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P., Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.; Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87066768; PubMed-3786141;
Drabent B., Genthe A., Benecke B.-J.;
"In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";
                                                                                                                               Gaps
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"Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";
Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
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                                                                                   Length 641;
                                                                                                                            0; Indels
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P08107; P19790; O9UQD9;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2)
(HSPAIA OR HSPAI) AND HSPAIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
ATP-binding; Chaperone; Heat shock; Multigene family. SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                100.0%; Score 53; DB 1;
100.0%; Pred. No. 0.0077;
ive 0; Mismatches 0
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MEDLINE-91055806; PubMed-1700760;
                                                                                     Query Match 100.

Best Local Similarity 100.

Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                  286 SLFEGIDFYT 295
                                                                                                                                                                          1 SLFEGIDFYT 10
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TISSUE=Liver;
MEDLINE=94357449; PubMed=8076831;
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EMBL, M76613; AAA57233.1; -.
PIR: JH0005; JH0095.
HSSP, P19120; INGC.
MGD, MGI:99517; HSP70-1.
InterPic; IPR001023; HSP70.
Pfam; PF00102; HSP70; 1.
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                                                                                                             Gene 87:199-204(1990)
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286 SLFEGIDEYT 295
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P34930;
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HS71_PIG
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                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
INDUCTION: BY HEAT SHOCK.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pfam; PF000121; HSP70; L.
PRINTS; PR00301; HSP70.1; L.
PROSITE; PS00297; HSP70.1; 1.
PROSITE; PS01329; HSP70.2; 1.
PROSITE; PS01036; HSP70.2; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
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E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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100.0%; Pred. No. 0.0077;
Live 0; Mismatches 0
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EMBL, M59830; AAA63227.1;
EMBL, AF134726; AAD21816.1; --
EMBL, AF134726; AAD21815.1; --
EMBL, M11717; AAA52697.1;
EMBL, M24743; AAA59844.1;
EMBL, M24744; AAA59844.1;
EMBL, X04676; CAA28381.1;
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370
469
MJ
499
N
70052 MW;
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EMBL; X04677; CAA28382.1; -.
PIR; A429160, A29160,
PIR; A45871; A45871.
PIR; A55773; A25773.
PDB; 1HJO; 21-OCT-98.
SWISS-2DPAGE; P08107; HUMAN.
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Best Local Similarity 100.
Matches 10; Conservative
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641 AA;
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MIM; 603012
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HS71_MOUSE
DC PL771_M
AC PL771_M
DT 01-NOV.
DT 01-NOV.
DT 30-MAY.
DE HEAT SI
GN HSPAT SI
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                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS.";
Gene 146:273-278(1994).
Gene 146:273-278(1994).

- I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
THROUGH THEIR ABILITY TO RECCONIZE NONNATIVE CONFORMATIONS OF
OTHER PROTEINS: THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
HYDOPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
-: SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Sus.
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MEDLINE-92175874; PubMed-1339404;
Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
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PRINTS; PR00301; HEATHOCK70.

PROSITE; PS00301; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_2; 1.

ATP-Briding; Chaperone; Heat shock; Multigene family; MHC III.

CONFLICT 34 2 A -> R (IN REF. 1).

CONFLICT 627 P -> PP (IN REF. 1).

CONFLICT 627 P -> PP (IN REF. 1).
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Hunt C,, Calderwood S.;
"Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 53; DB 1; Length 641; Best Local Similarity 100.0%; Pred. No. 0.0077; Matches 10; Conservative 0; Mismatches 0; Indels
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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01-FEB-1994 (Rel. 28, Last sequence upd
01-NOV+1997 (Rel. 35, Last annotation ulear shock 70 KDA PROTEIN 1 (HSP70.1).
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Slater M.R., Craig E.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 116764; AAA17441.1; -. EMBL; X77208; CAA54423.1; -. EMBL; X77207; CAA54422.1; -. EMBL; X74211; CAA52328.1; -.
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Best Local Similarity 100.
Matches 10; Conservative
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                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C;
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P10591;
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                        Immunogenetics 35:286-289(1992).

-I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATURE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES SEGMENTS WITH A NET HYDROPHOBIC CHARACTER REVOSED BY POLLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-LEW.IW/GUN;
MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
Walter L., Rauh S., Guenther E.;
IComparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-94096443; PubMed-8271311;
Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
"CDNA cloning and expression of stress-inducible rat hsp70 in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 53; DB 1; Length 641; 100.0%; Pred. No. 0.0077; ive 0; Mismatches 0; Indels
                "Complete nucleotide sequence of a porcine HSP70 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00297; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS71_RAT STANDARD; PRT; 641 AA. 007439; P42853; Created) 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-NV-1997 (Rel. 35, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and injured rat brain.";
J. Neurosci. Res. 36:325-335(1993).
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M69100; -; NOT_ANNOTATED_CDS.
PIR; S35718; S35718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00301; HEATSHOCK70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 10; Conservative
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RESULT 13

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HS71\_RAT AC 0157 DT 01-F1 DT 01-F

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                                                                                                                                                                                                                                  AL HOPTO Gene.";

Blochim. Blophys. Acta 1219:64-72(1994).

Blochim. Blophys. Acta 1219:64-72(1994).

CC PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL. AS WITHIN CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN CC OF AND HEALTY TO RECOGNIZE NONNATIVE CONFORMATIONS OF CTARGORY THEORY PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

CC --- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

CC --- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

CC --- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
BDDLINE-94368874, PubMed-8086479;
Lisowska K., Krawczyk Z., Midak W., Wolniczek P., Wisniewski J.;
"Cloning, nucleotide sequence and expression of rat heat inducible "Cloning, nucleotide sequence."
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InterPro; IPR001u2...

A PRO312: HSP70; 1.

R PROSITE; PR00301; HSP70_1; 1.

DR PROSITE; PS00297; HSP70_2; 1.

DR PROSITE; PS00336; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_2; 1.

KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.

KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.

CONFILCT 71 72 RR -> NG (IN REF. 3).

CONFILCT 227 227 D -> H (IN REF. 3).

CONFILCT 227 227 G -> A (IN REF. 3).

CONFILCT 227 227 G -> A (IN REF. 3).

CONFILCT 227 227 G -> A (IN REF. 3).

CONFILCT 227 227 G -> A (IN REF. 3).

CONFILCT 227 227 G -> A (IN REF. 3).

CONFILCT 227 227 D -> H (IN REF. 3).

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CONFILCT 227 227 D -> H (IN REF. 3).

CONFILCT 227 227 D -> H (IN REF. 3).

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CONFILCT 227 227 D -> H (IN REF. 3).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-OCT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).
SSA1 OR YALOOSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 53; DB 1; 100.0%; Pred. No. 0.0077;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Norbeck J., Blomberg A.; Protein expression during exponential growth in 0.7 M NaCl medium of
                                                      Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B., Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.; "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 42 kbp SPO7-CENI-CDC15 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                              Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.; Protein identifications for a Saccharomyces cerevisiae protein darabase ".
                                                                                                                                                                Ogden R.C., Lee M.-C., Knapp G.;
"Transfer RNA splicing in Saccharomyces cerevisiae: defining the
                                                                                                                                                                                                                                                 Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                     Nucleic Acids Res. 12:9367-9382(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEMS Microbiol. Lett. 137:1-8(1996)
 Nucleic Acids Res. 17:805-806(1989)
                                                                                                                                                                                                                                                                                                                                                                   Electrophoresis 15:1466-1486(1994).
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EMBL; L22015; AAC04952.1; ALT_SEQ
                       SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE-95028152; PubMed-7941740;
                                                                                                                                       SEQUENCE OF 590-641 FROM N.A. MEDLINE-85087943; PubMed=6096826;
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
                                                                                                                                                                                                                                                                                                     MEDLINE-95203288; PubMed-7895733;
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                                                                                                                                                                                                                             REVISIONS TO 207; 417 AND 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEGAN, PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PR051TE; PS00297; HSP70_1; 1.
PR051TE; PS00129; HSP70_2; 1.
PR051TE; PS01036; HSP70_3; 1.
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SWISS-2DPAGE; P10591; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEPD; 9788; -.
SGD; S0000004; SSA1.
InterPro; IPR001023; HSP70.
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PIR; S42164; S42164.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 186-195
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                                                                                                                                                                                                                                                                                           STRAIN-S288C
                                                                                                                                                                                                                                            Slater M.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kowalski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S., van den Hurk J., Babiuk L.A., Zamb T.J.; teletan den Hurk J., Babiuk L.A., Zamb T.J.; persetan promoter-driven synthesis of secreted bovine herpesvirus glycoproteins in transfected cells."; Vaccine 11:1100-1107(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                             Length 641;
                                                                                                                                                                                    100.0%; Score 53; DB 1; Length 64
100.0%; Pred. No. 0.0077;
v*cmatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grosz M.D., Skow L.C.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
Heat shock; ATP-binding; Multigene family; Acetylation.
INIT_MET 0 0 0 MOD_RES 1 1 ACETYLATION.
SEQUENCE 641 Aa; 69526 MW; FA9389BAE9BID7DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS72_BOVIN STANDARD; PRT; 641 AA. 027965; 028122; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 39, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 2 (HSP70-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
MEDLINE=94070117; PubMed=8249428;
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
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SEQUENCE OF 1-28 FROM N.A.
                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 10; Conservative
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282 SLFEGIDEYT 291
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HS72_BOVIN
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PROSITE; PS00329; HSP70\_2; 1.
PROSITE; PS01036; HSP70\_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 641 AA; 70228 MW; 229C19EEBBF610DF CRC64; DR WW SO

Gaps ö Query Match 100.0%; Score 53; DB 1; Length 641; Best Local Similarity 100.0%; Pred. No. 0.0077; Matches 10; Conservative 0; Mismatches 0; Indels

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1 SLFEGIDEYT 10 ||||||||||||| 286 SLFEGIDEYT 295 q

Search completed: December 6, 2001, 08:00:53 Job time: 421 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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<sup>1</sup> SLFEGIDFYT 10 PEP2-MOD8F 53 Perfect score: Sequence: Title:

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### SPTREMBL\_17:\* Database :

sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_invertebrate:\*
sp\_mammal:\*
sp\_mammal:\*
sp\_organelle:\*
sp\_organelle:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O9u667 littorina p	Q9u670 littorina s	Q9u669 littorina s	Q9u665 littorina p	Q9u671 littorina s	Q9u668 littorina p	Q9u666 littorina p	P81159 aplysia cal	Q90520 oncorhynchu	Q98899 fugu rubrip	Q63718 rattus norv	044350 chondrosia	044352 petrobiona	Q9nj92 guancha lac	044349 funiculina	044351 eunicella c	Q98897 fuqu rubrip	015766 dictyosteli	Q98900 fugu rubrip
SUMMARIES	DB ID	5 Q90667	5 Q9U670	5 Q90669	5 Q90665	5 090671	5 090668	5 Q90666	5 P81159	13 Q90520	13 Q98899	11 Q63718	5 044350	5 044352	5 Q9NJ92	5 044349	5 044351	13 Q98897	5 015766	13 Q98900
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AC 090670;
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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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#### ALIGNMENTS

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RESULT I	ID Q9U667 PRELIMINARY; PRT; 146 AA.	AC 090667;	DT 01-MAY-2000 (TrEMBLrel. 13, Created)	DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	OT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	DE HEAT-SHOCK PROTEIN (FRAGMENT).	GN HSC70.	OS Littorina plena.	OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;	OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.	OX NCBI_TaxID=31219;	RN [1]	RP SEQUENCE FROM N.A.	RA Hohenlohe P.A.;	RT "Heat-shock genes in the heat-stressed genus Littorina.";	DR EMBL; AF191828; AAF12787.1;	DR InterPro; IPR001023; HSP70.	DR PROSITE; PS01036; HSP70_3; 1.	NON_TER	NON_TER	SQ SEQUENCE 146 AA; 16607 MW; C3F3556AlAF438BB CRC64;	Query Match 100.0%; Score 53; DB 5; Length 146;	0%; Pred. No. 0.013;	Matches 10; Conservative 0; Mismatches 0; Indels
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

<sup>473505</sup> seqs, 146272329 residues Searched:

<sup>473505</sup> Total number of hits satisfying chosen parameters:

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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
                                                     Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Nectaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
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Hohenion P.A.;
Hat.shock genes in the heat-stressed genus Littorina.";
Submitted (Oct. 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191824: AAF12783.1;
HNSP; P19120; LBAL.
Interpro; PR00301; HBATSHOCK70.
PROSITE; PS010301; HBATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
NON_TER
1 1 1
NON_TER 158 158
SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;
                                                                                                                                                      Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (Oct.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191830; AAF12789.1;
HSSP; P19120; LBAI.
HTGFPO; PPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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HEAT-SHOCK PROTEIN (FRAGMENT).
HSC70.
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Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE FROM N.A.
                                               Littorina plena.
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SEQUENCE
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31221;
                                                            Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Hohenlohe P.A.;
Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191826; AAF12785.1; -.
HSSP; P19120; 1BA1.
                                                                                                                                                                              Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAF12784.1; -.
HSSP; P19120; 1BA1.
InterPro; IPR01023; HSP70.
PROSITE; PS01036; HSP70.3; 1.
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SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;
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NON_TER 153 153
SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
             01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT-SHOCK PROTEIN (FRAGMENT).
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PROSITE; PS01036; HSP70_3; 1.
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Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE FROM N.A.
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RESULT Q9U669

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RESULT 4 Q9U665 ID Q9U665 AC Q9U665 DT 01-MAY DT 01-MAY

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Aplysia californica (California sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                             MEDLINE-93077669; PubMed-1360013;
MEDLINE-93077669; PubMed-1360013;
Kuhl D., Kennedy T., Barzilai A., Kandel E.;
"Long-term sensitization training in Aplysia leads to an increase in the expression of BLP, the major protein chaperon of the ER.";
J. Cell Biol. 119:1069-1076(1992).
--- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
--- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
BENBL: 215039; CAAA78757.1; ---
HSSP; P19120; LBA1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
BALNADOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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MEDLINE-85036330; PubMed-6092938;
Kothary R.K., Jones D., Candido E.P.M.;
"TO'Kilodalton heat shock polypeptides from rainbow trout:
"haracterization of cDNA sequences.";
Mol. Cell. Biol. 4:1785-1791(1984).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
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PROSITE: PS00329; HSP70_2; 1.
PROSITE: PS01036; HSP70_3; 1.
Heat shock; Multigene family.
NON_TER 1 1
NON_TER 278
SEQUENCE 278 AA; 30327 MW;
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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NON_TER 1 20
NON_TER 220 A3; 24684 MW;
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Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 53; DB 5; Length 158; 100.0%; Pred. No. 0.015;
                                                                 Eukaryota: Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hohenlohe P.A.; Heat-shock genus Littorina."; Submitted (Oct-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191829; AAF12788.1; EMBL, AF191829; BAR12788.1; Interpro: IPROJ01033; HSP70. PRINTS; PROJ0301; HEATSHOCK70. PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                               Hohenlohe P.A.; "Heat-shock genes in the heat-stressed genus Littorina."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191827; AAF12786.1; -. HSSP; P19120; IBAL. InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                              158 158 158 158 MW; D2ECE71042EC44CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 AA; 17891 MW; B41E5356BCECAD2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                          PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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                                                        Littorina plena.
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RESULT P81159 ID P8 AC P8 DT 01

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SEQUENCE FROM N.A.

BOTCHIGHLINI C., Le Parco Y.;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF026520; AAC05364.1; -.

HSSP; P08109; LOKR.

InterPro; IFR001023; HSP70.
            1 1
455 455
455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;
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                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches '10; Conservative
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254 SLFEGIDFYT 263
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252 SLFEGIDEYT 261
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                             Gaps
                                                                                                                                                                                                                                                            Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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Submitted (MOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, 227118; CAA81642.1; -.
HSSP; PO8107; 1HJO.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 367;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                   Lim E.H.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Y08578; CAA69892.1; -.
HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO! PRO01023; HSP70.
Pfam: PF00012; HSP70.
PROSITE; PS00292; HSP70_1;
PROSITE; PS01036; HSP70_1; 1.
PROSITE; PS01036; HSP70_1; 1.
Heat shock.
SOON TER 367 Aa; 40405 MW; RCD3DDBDF6E3CZCA CRC64;
                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NC KDA HEAT SHOCK PROTEIN (FRAGMENT).
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            Pred. No. 0.028;
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                             Mismatches
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100.08; Pic
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PRINTS: PR00301; HSP70; 1.
PROSITE; PS00329; HSP70_2; 1.
Heat shock.
             Best Local Similarity 100.
Matches 10; Conservative
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268 SLFEGIDFYT 277
                                                                        156 SLFEGIDFYT 165
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                                                       1 SLFEGIDFYT 10
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Petrobiona.
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Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Chondrosida; Chondrillidae; Chondrosia.
NCBI_TaxID=68574;
              Length 455;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
100.0%; Score 53; DB 11;
100.0%; Pred. No. 0.05;
tive 0; Mismatches 0;
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100.0%; Score 53; DB 5; Length 468; 100.0%; Pred. No. 0.052; tive 0; Mismatches 0; Indels
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS010329; HSP70_2; 1.
NON_TER 1 1 1
NON_TER 468 468
SEQUENCE 468 AA; 51533 MW; EDED2B46
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Matches 10; Conservative
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Funiculinidae;
Funiculina.
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Bukaryota; Metazoa; Porifera; Calcarea; Calcinea; Clathrinida;
Clathrinidae; Guancha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borchtellini C., Le Parco Y.;
"Sponges paraphyly and the origin of Metazoa.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF182195; AAF61297.1;
InterPro; IPR001023; HSP70.;
Pfam; PF00012; HSP70.1.
PROSITE; PS00329; HSP70.2; 1.
PROSITE; PS01036; HSP70.2; 1.
PROSITE; PS01036; HSP70.2; 1.
NON_TER 467 467
SEQUENCE 467 AA; 51318 MM; F36FC06CBIDEE131 CRC64;
                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 53; DB 5; Length 467; Best Local Similarity 100.0%; Pred. No. 0.052; Matches 10; Conservative 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
BOTCHISHIS (2, Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026516; AAC05361.1; -.
HSSP; P08109; ICKR.
InterPro; IPR001023; HSP70.
                                                                                                                           467 467
467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;
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467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
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    PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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252 SLFEGIDEYT 261
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252 SLFEGIDFYT 261
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                                                                                     NON_TER
NON_TER
SEQUENCE
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09NJ92
AC 09NJ92;
DT 01-0CT--
DT 01-0CT--
DT 01-0CT--
DE HEAT SHC
OS GUARATON
OC CLATALIO
OC CLATALIO
OC NOBLTAN
IN [1]
RP SEQUENCI
RA BOLCHICL
RA BOLCHICL
RA SECUENCI
RA SECUE
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044349
AC 044349
DT 044349
DT 01-JUN
DT 01-JUN
DE HEAT-Si
GN HSPP10.
CC FUNICU
CC FUNI
                 SHERS
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Appli Appli Appli Appli Appli Appli Appli

2, 2, 46,

seduence Sequence Seq

46, 118, 118, 118, 136, 48,

Sequence Sequence

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APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
CONTRY: United States
COUNTRY: United States
ZIE: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: <Unknown>
US-08-325-630-9
US-08-50-132A-2
US-08-150-132A-2
US-08-15-52B-2
US-08-24-353A-2
PCT-US95-07374A-2
PCT-US95-07374A-2
PCT-US95-07374A-2
US-08-612-973-46
US-08-440-103-18
US-08-440-103-18
US-08-440-210-18
US-08-440-210-18
US-08-421-368-118
US-08-210-368-118
US-08-210-368-118
US-08-210-368-118
US-08-210-388-118
US-08-210-388-118
US-08-210-388-118
US-08-210-388-118
US-08-210-388-118
US-08-210-373-48
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FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-927-597-48
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Pred. No. 2.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08797358B Patent No. 6268478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 643 amino acids
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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        US-08-797-358B-3
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                                                                                                                                                                                  ; Search time 81.43 Seconds (without alignments) 2.764 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14,
Sequence 32,
Sequence 32,
Sequence 32,
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Sequence 40,
Sequence 40,
Sequence 2, A
Sequence 9, A
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/FB_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/FCTUS_COMB.pep:*
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-441-139-14
US-08-59-171A-32
US-08-646-590B-32
US-09-069-226-32
US-09-012-184-32
US-09-412-184-32
US-08-477-231-42
US-08-477-231-42
US-08-440-103-16
US-08-440-103-16
US-08-231-366-16
US-08-231-366-16
US-08-241-366-16
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US-08-612-973-42
US-08-927-597-42
US-08-612-973-44
US-08-927-597-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-325-630-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                        6, 2001, 07:59:59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                            1 SLFEGIDGYT 10
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Match Length DB
                                                                                                                                                                                                                                                                                           PEP2-MOD8G
                                                                                                                                                                                        December
                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
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                                                                                                                                    OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                     Run on:
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Indels

DB 4; Length 643; 2.2;

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Sequence 32, Application US/08646590B

GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Warnen, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREËT: La Jolla

CITT: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 2; Length 303;
Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 08-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
FILING DATE: CONCULTENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 08-MAY 1996
CLASSIFICATION: 435
PRIOR APPLICATION 1935
PRIOR APPLICATION DATE: 08/599,171
FILING DATE: 09-FEB-1996
PRIOR APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 21-January-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                  331400-38
                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 3314(
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 71.7%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 303 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                           FILING DATE: CONCULTE
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-599-171A-32
                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 SIFEGIRGY 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SLFEGIDGY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA
US
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Sequence 32, Application US/08599171A

Patent No. 5814473

GENERAL INFORMATION:

APPLICANT: WARREN, PALTICK V.

TITLE OF INVERTION:

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

CITY: NOSELAND

STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.4%; Score 41; DB 1; Length 646;
80.0%; Pred. No. 5.3;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                             APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
RAPPLICATION NUMBER: US 08/089,997
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEBRAX: 516-742-4346
TELEERAX: 516-742-4366
TELEERAX: 516-742-4366
TELEERAX: 516-742-4366
TELEERAX: 516-742-4366
TELEERAX: 516-742-4366
TELEERAX: 516-742-6436
TELEMENT FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 646 amino acids
TURD THE TOWN TOWER: US OF TOWN TOWN.
                                                                                                                                                                                                                                                                      STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           Sequence 14, Application US/08441139
Patent No. 5773245
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.4
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-441-139-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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286 SLYEGIDFYT 295
11111:1 11
288 SLFEGVDFYT 297
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                                                                                                                                Sequence 32, Application US/09412184
Patent No. 6268188
GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Warnen, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 8.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-509
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,590
FILING DATE: 08-May-1996
APPLICATION NUMBER: 08/599,171
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 21-January-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42, Application US/08483695; Sequence 42, Application US/08483695; Patent No. 5866139; GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Porchon, Colette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.78;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 303 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.07
Fra 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-412-184-32
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34 SIFEGIRGY 42
                                          34 SIFEGIRGY 42
        1 SLFEGIDGY 9
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                                                                                                                                                                                                                                                                                                                                                    STATE: CA
COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                      US-09-412-184-32
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                                                                                                                                                                                                                                                                                                                 71.7%; Score 38; DB 2; Length 303; 77.8%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 3; Length 303;
Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: WARREN, PALTICK V.
TILLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SECUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                          09010/017001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/09069226
Patent No. 6013509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: HERENON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFRENCE/POCKET NUMBER: 3314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
REGISTRATION UNDRER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELERONE: 019/678-5070
TELERAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.78;
77.88;
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LENGTH: 303 AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.7
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                 MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: PROTEIN US-09-069-226-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEW JERSEY
: USA
                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6 BECKEI
CITY: ROSELAND
STATE: NEW JERSE
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     1:1111 11
34 SIFEGIRGY 42
                                                                                                                                                                                                                                                                                                                                                                                                 1 SLFEGIDGY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                          US-08-646-590B-32
                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-09-069-226-32
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 1300 I Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS: LENGTH: 108 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meyers, Kenneth J
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-07-965-285-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LFEGIDGYT 10
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STATE:
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APPLICANT: Brechot, Dina
APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 2; Length 108; Pred. No. 4;
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                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/483,695
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05286-0001-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
IPLING DATE: 18-MAR-1993
APPLICATION NUMBER: FR 91 06 882
FILING DATE: 06-UNI-1991
ATTORNEY AGENT INFORMATION:
NAME: MEGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 05286-0001-
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-965-285-42; Sequence 42, Application US/07965285; Patent No. 5879904; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 1300 I Street, N.W
Washington
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INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 69.8
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-08-483-695-42
                                                                                                                                                                             Washington
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                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LFEGIDGYT 10
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44 LFAGVDGHT 52
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GENERAL INFORMATION:
APPLICANT: Brechot, Christian
APPLICANT: Kremscorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER.OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.8%; Score 37; DB 2; Length 108; 66.7%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRÉSSEE: Finnegan, Henderson, Farabow, Garrett & ADDRÉSSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,231
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,285
FILING DATE: 18-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION UNBER: FR 91 06 882
FILING DATE: 06-JUN-1991
ATTORNEY/AGENT INFORMATION:
SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/07/965,285 FILING DATE: 18-MAR-1993
                                                                                                                                                                                                                                                                                                                              05286-0001-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                               FILING DATE: 18-MAR-1993
CLASSIFICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATE: 891 06 882
FILING DATE: 06-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001
TELEPHONE: 202-408-4000
TELEPHONE: 202-408-4000
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APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
WUMBER OF SEQÜENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 4; Length 139;
Pred. No. 5.3;
       Indels
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US-08-444-818-173
                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: MANBY Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/444,818
         1;
         2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PROR APPLICATION DATA:
APPLICATION UNBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: HARDIN, Allsa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           Sequence 173, Application US/08444818 Patent No. 6150087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08440103
Patent No. 5670152
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 173: SEQUENCE CHARACTERISTICS: LENGTH: 139 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (508)359-3876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (508)359-3885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 66.7.
مار، مارید
کارید وزیر Conservative
         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                   11 |:||:|
44 LFAGVDGHT 52
                                             2 LFEGIDGYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                            US-08-444-818-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-440-103-16
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         Matches
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APPLICANT: Brechot, Christian
APPLICANT: KremsGorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                          Score 37; DB 2; Length 108;
                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,912
25,146
PP: 05286-0001-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE-POCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                Pred. No
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Application US/09201912
Patent No. 6210962
 REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 0528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPKX: 202-408-4400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 42:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        : 108 amino acids
amino acid
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LENGTH: 108 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-487-231-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-09-201-912-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                 2 LFEGIDGYT 10
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44 LFAGVDGHT 52
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US-09-201-912-42
                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                        Query Match
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Sequence 16, Application US/08231368

Sequence 16, Application US/08231368

Patent No: 5756312

GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSES: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 269;
Pred. No. 11;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
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PRIORA APPLICATION DATA:
APPLICATION NUMBER: US 07/759,575

FILING DATE: 13-SEP-1991
ATTORREY/AGENT INFORMATION:
NAME: MCCLUNG, BArbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/COCKET NUMBER: 025.001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYRE: amino acid
TYRE: amino acid
                 US 07/759,575
                                                                             NAME: MCCLUNG, BARDATA G. REGISTRATION NUMBER: 33,113 REFERENCE/DOCKET NUMBER: 02(TELECOMMUNICATION INFORMATION:
                                                                                                                                                                 TELEPHONE: (510) 601-2708
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                           69.8%;
66.7%;
FILING DATE:
APPLICATION NUMBER: US 0
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 66.7'
...-hes 6; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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8 LFAGVDGHT 16
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Sequence 16, Application US/08440542
Patent No. 5670153
GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Length 269;
Pred. No. 11;
2; Mismatches 1; Indels
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COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,542
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
PRIOR ADDITATION: 424
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,103
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
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APPLICATION NUMBER: US/08/231,368
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOORET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          US 07/759,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
           Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (510) 601-2708
TELEFAX: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                            4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: US 0
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 269 amino acids TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 6; Conserv
                                                  Emeryville
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        ADDRESSEE:
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                                                                                            COUNTRY:
                                                     CITY:
STATE:
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Gaps



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SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-210-16
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AEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/440,210
FILING DATE: 12-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE: 13-MAY-1995
PRIOR APPLICATION NUMBER: US/08/231,368
FILING DATE: 13-SEP-1991
APPLICATION NUMBER: US/07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNg, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE (MARACTED FILE)
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US-08-40-210-16
; Sequence 16, Application US/08440210
; Patent No. 5766845
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Search completed: December 6, Job time: 367 sec
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Matches 6; Conserv
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Best Local Similarity 66.
Matches 6; Conservative
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APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Chiron Corporation STREET: 4560 Horton Street CITY: Emeryville STATE: CA
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8 LFAGVDGHT 16
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66.7%;
                 2001, 07:59:59
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched
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score
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seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                length: 2000000000
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Match
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pir2:*
pir3:*
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GenCore version (c) 1993 - 2000
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A48872
S31766
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dnak-type molecular chaperone HSP70a - California sea hare (fragment)
N;Alternate names: heat shock protein 70
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999
C;Accession: A44261
R;Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1992
A;Title: Long-term sensitization training in Aplysia leads to an increase in the A;Reference number: A44261; MUID:93077669
A;Reference number: A44261; MUID:93077669
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-209 <KUH>
A;Note: sequence extracted from NCBI backbone (NCBIP:118951)
C;Genetics:
A;Gene: HSP70a
C;Function: dnak type molecular chaperone HSC70 - California sea hare (fragment)
N;Alternate names: heat shock protein 70 homolog HSC70
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999
C;Accession: B44261
R;Kinli, D;Kennedy, T.E;Barzilai, A.;Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1992
A;Title: Long-term sensitization training in Aplysia leads to an increase in the A;Reference number: A44261; MUID:93077669
A;Rocession: B44261
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-208 <KUH>
A;Residues: 1-208 <KUH>
A;Residues: 1-208 <KUH>
A;Gene: HSC70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of prote
C;Superfamily: heat shock protein 70
C;Keywords: Affp; molecular chaperone Š 밁 A44261 Matches Query Match Best Local : 132 SLFEGIDFYT 141 Local Similarity les 9; Conserv 1 SLFEGIDGYT 10 Conservative 90.0%; 0; Score 44; Pred. No. ALIGNMENTS Mismatches in Aplysia leads to an increase in DB 2; 0.42; assembling/disassembling of protein co 1; Length 208; Indels to an increase in the expr 0 Gaps the expr 0

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A;Description: involved in protein folding and assembling/disassembling of protein C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: Ibisa
R;Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
Mol. Cell. Biol. 4, 1785-1791, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dnaK-type molecular chaperone (clone pTHS70.7) - ra
N;Alternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
                                                                                                                                                                                                                                                           R;Rosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D. Gene 96, 295-300, 1990
A;Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region.
A;Reference number: PQ0138; MUID:91099690
A;Accession: PQ0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: involved in protein folding and assembling/disassembling of protein compl C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804 C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polypeptides
A;Reference number: 151344; MUID:85036330
A;Accession: 151344
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                                                                                A;Description: involved in protein folding and assembling/disassembling of protein complC;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                C;Genetics:
A;Gene: hsp70 II
A;Introns: 68/1; 137/1; 188/3; 281/3
                                                                                                                                                                                                                                                                                                                                                                                   dnaK-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment)
N;Alternate names: heat shock protein 70
C;Species: Paracentrotus lividus (common urchin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-278 < KOT>
                                                                                                                                                                                                                                                                                                                                                 C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 20-Aug-1999 C;Accession: PQ0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              よ
                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-372 <ROS>
A;Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 9
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Best Local
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            Query Match
Best Local
Matches
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nes 9; Conserv
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9; Conserv
similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                  Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D.
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90.0%;
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Pred. No.
                  Score 44; I
Pred. No. 0.
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 Mismatches
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No.
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0.59;
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0.43;
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                    .82;
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                                  2;
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                              Length 372;
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submitted to the EMBL Data Library, September 1997
A; Reference number: Z22983
A; Accession: T45477
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-467 <BOR>
A; Residues: 1-467 <BORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heat-shock protein 70 [imported] - Chondrosia reniformis (fragment) C;Species: Chondrosia reniformis C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
R;Borchiellini, C:; Le Parco, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, September A; Reference number: Z22983 A; Accession: T45479
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C; Superfamily:
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R; Borchiellini, C.; Le Parco, Y.
                                                                                       heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment) C;Species: Funiculina quadrangularis C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45476 R;Borchiellini, C.; Le Parco, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1
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                              submitted to the EMBL Data A; Reference number: Z22983 A; Accession: T45476
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A; Molecule
              A;Status:
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Best Local :
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                                                                                                                                                                                                                                                                           SLFEGIDFYT 261
                  preliminary;
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                    similarity
9; Conserv
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                  translated
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90.0%;
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Pred. No. 1.1;
0; Mismatches
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Pred. No. 1
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                    from GB/EMBL/DDBJ
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A; Residues: 1-468 <BOR>
A; Cross references: EMBL: AF026516;
C; Genetics:
A; Gene: Hsp70
C; Superfamily: heat shock protein
                                            Query Match
Best Local Similarity
""" 9; Conserv
                                                                                                                                                                                                                                                                                                                                 C;Species: Dictyostelium discoideum
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: Hsp7U
C;Superfamily: heat shock protein
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A;Molecule type: mRNA
A;Residues: 1-469 <BOR>
A;Cross-references: EMBL:AF026518; PIDN:AAC05363.1
C;Genetics:
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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45478
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T45478
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                                                                                                                            A; Note: localized to filopodias and cortex C; Superfamily: heat shock protein 70
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A; Residues: 1-632 <BOV>
                                                                                                                                                                                                                                                                                                                    C; Accession: T45471
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N;Alternate names: heat shock cognate protein 70
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C;Genetics:
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A; Accession: T45471
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A; Accession: T45478
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Best Local
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 SLFEGIDFYT 294
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9; Conserv
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9; Conserv
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                                                        Conservative
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90.0%;
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Pred. No.
                                                                      Score 44; DB
Pred. No. 1.5;
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September 1997
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                                                       Mismatches
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R;Sainis,
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dnaK-type molecular chaperone hsp70 - green monkey
N;Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S31766; 136927
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: \bar{1}^-636 <EDD> A;Residues: \bar{1}^-636 <EDD> A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180 A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with A;Reference number: A48872; MUID:94043116
A;Accession: A48872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dnaK-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)
N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein
C;Species: Dictyostelium discoideum
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C;Accession: A48872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 261, 120
A;Title: Organization,
A;Reference number: A25
A;Accession: A25646
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N;Alternate names: heat shock protein 70
C;Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
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A; Residues: 1-634 <MOR>
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I.; Angelidis, C.; Pagoulatos, G.; Lazaridis,
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261, 12692-12699, 1986
zation, nucleotide sequence,
nber: A25646; MUID:86304452
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Pred. No.
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A; Molecule type: mRNA
A; Residues: 1-638 <SAI>
R; Sainis, I; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
R; Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
R; Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
R; Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
R; Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
R; Sainis, I.; Angelidis, I.; Pagoulatos, I.; Pittle: The hsc70 gene which is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the saint is slightly induced by heat is the national section of the nat
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A;Description: Nucleo
A;Reference number: S
A;Accession: S31766
dnaK-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: heat shock protein YG102; protein L0971; protein Y
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Ju
C;Accession: S20139; S64772; S64775; S69383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: JC1391
R;Sconzo, G.; Scardina, G.; Ferraro, M.G.
Gene 121, 353-358, 1992
A;Title: Characterization of a new member
A;Reference number: JC1391; MUID:93077053
A;Accession: JC1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
N;Alternate names: heat shock protein 70IV; hsp70IV protein
C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
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C;Genetics:
A;Gene: hsp70IV
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C; Function:
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A; Residues: 1-639 <SCO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description: involved in protein folding and assembling/disassembling of Superfamily: heat shock protein 70 (Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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9; Conserv
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Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein
Decr: S31766
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90.0%;
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                                    A; Note:
C; Geneti
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N;Alternate names: heat shock protein
C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                               A; Reference number: A; Accession: JT0285
                                                                                                                                                                                                                                                                                                      Gene 64, 241-255, 1988
A; Title: The Caenorhabditis
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submitted to the EMBL Data Library, April 1996 A;Description: The sequence of 32 kb on the left mily and a new ABC transporter homologous to the A;Reference number: $69380 A;Recession: $69383
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R; Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, submitted to the Protein Sequence Database, May 1996

A; Reference number: $64775

A; Recession: $64775

A; Recession: $64775

A; Residues: 72-639 < DUE>
A; Residues: 72-639 < DUE>
A; Cross-references: EMBL: Z73129; MIPS:YLL024c
A; Experimental source: strain $288C
R; Purnelle, B.; Goffeau, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Goffeau, A.; Purnelle, B.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64761
A;Recession: S64772
A;Molecule type: DNA
A;Residues: 1-639 <GOF>
A;Cross references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YL
A;Cross references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YL
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A;Residues: 1-639 <SLA>
A;Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546
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Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of 1
A;Reference number: S20139; MUID:891:
A;Accession: S20139
A;Status: translation not shown
                                                                                                                                                                                                                                A; Description: involved in protein to C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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A; Map position: 12L
C; Function:
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A; Residues: 1-639 < PUR>
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A;Molecule type: DNA; mRNA A;Residues: 1-640 <SNU> A;Residues: 1-640 <SNU> A;Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352 A;Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156351; PIDN:AAA28078.1; PID:g156351; PIDN:AAA28078.1; PID:g156351; PIDN:AAA28078.1; PID:g156351; PID:g156351; PID:g156351; PID:g156351; PID:g156351; PID hsp70A family wer two-'n <u>,</u> 6

Heschl, M.F.P.; Baillie, D.L.

- Caenorhabditis elegans 70 A

#text\_change 22-Jun-1999

elegans hsp70 MUID:88297155

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A;Map position: IV
A;Introns: 69/1; 331/3; 558/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comple;Superfamily: heat shock protein 70
C;Superfamily: heat shock protein 70
C;Keywords: AfP; heat shock; molecular chaperone; stress-induced protein

Query Match
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 287 SLFEGIDFYT 296

Search completed: December 6, 2001, 07:58:28

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20-AUG-2001 (Rel. 40, Last annotation update)
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01-JUN-1994 (Rel. 29, Last annotation updat
HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FR
                           Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.; Molecular cloning and expression of a Penicillium citrinum allergen with sequence homology and antigenic cross-reactivity a hsp70 human heat shock protein."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               PENCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                Penicillium citrinum.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; PARTIAL.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paracentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSP70II.
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=5077;
                                                                                                                                                                                                                                                                                                              HS70_PENCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00012; HSP70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X16544; CAA34544.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                la Rosa M., Sconzo G., Giudice G., Roccheri M.C., di Carlo M
"Sequence of a sea urchin hsp70 gene and its 5' flanking reg
Gene 96:295-300(1990).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91099690; PubMed=2269441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                         286
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; P19120; 1NGJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                     SLFEGIDGYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372
372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41347 MW;
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Pred. No.
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II) (FRAGMENT).
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produced through a collaboration
                                                                                                                                                                                                                                   (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region.";
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HS70_CHICK
ID 70.CHICK
ID 8.CHICK
ID
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Best Local S
Matches 9
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEAT SHOCK 70 KDA PROTEIN (HSP70).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U64207; AAB06397.1; -. HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 261:12692-12699(1986).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
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9; Conservative
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83
  0.0%;
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Pred. No.
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Pred.
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  44;
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     DB 1
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0.71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Banerji S.S.
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L outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;

The hsc70 gene which is slightly induced by heat is the main virus

The hsc70 gene which is slightly induced by heat is the main virus

Tinducible member of the hsp70 gene family.";

PEBS Lett. 355:282-286(1994).

C-i- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

C-I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

C-I- FUNCTION: THE HSP70S IN THE CYTOSOL AS WELL AS WITHIN

C-I- FUNCTION AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR CORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC

C-- RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION WITH HSP90. THEY PARTICIPATE IN ALL THESE

C-- PROTEIN TRANSLOCATION WITH HSP90. THEY PARTICIPATE IN ALL THESE

C-- CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE

C-- CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES

C-- STREES-INDICED DAMAGE

C-- STREES-INDICED DAMAGE

C-- STREES-INDICED DAMAGE

C-- STREES-INDICED DAMAGE

C-- CONTRADICATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                         Matches
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15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
HEAT SHOCK 70 KDA F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01038; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS71_CERAE
Q28222;
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                                                                                                                                                                                                                                                                                                                                                        ATP-binding;
SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95080396; PubMed=7988690;
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                                                                                      284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRESS-INDUCED DAMAGE.
                                                                                   SLEEGIDEYT 293
                                                                                                                                           SLFEGIDGYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLFEGIDGYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00012;
                                                                                                                                                                                                      Similarity 90.09; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
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0012; HSP70; 1.
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                                                                                                                                                                                                                                  83.0%;
90.0%;
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                                                                                                                                                                                                   Score 44; DB 1;
Pred. No. 0.92;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                              shock; Multigene fa; D55076A0FFAB6AB3
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33 CRC64;
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P10592;
01-JUL-1989 (Rel. 11, 0
01-OCT-1994 (Rel. 30, 1
01-OCT-1996 (Rel. 34, 1
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MEDLINE-89128457; PubMed~2001.
Slater M.R., Craig E.A.;
"The SSA1 and SSA2 genes of the yeast
"The SSA1 and Res. 17:805-806(1989).
                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Volpe T., Warner J.R., McLaughlin C.S.; Submitted (SEP-1994) to the SWISS-PROT data bank.
-1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT O BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO
                                                   EMBL; X12927; CAA31394.1; -. EMBL; Z73129; CAA97472.1; -. EMBL; X97560; CAA66167.1; -. PIR; S20139; S20139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 186-195.
STRAIN=ATCC 38531 / Y41;
MEDLINE=97089742; PubMed=8935650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Volpe T., Warner J.R., Mc "Protein identifications database.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garrels J.I., Futcher B., Kobayashi R., Volpe T., Warner J.R., McLaughlin C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 71-638 FROM N.A. Duesterhoeft A., Floeth M., Submitted (MAY-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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SSA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                      between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norbeck J., Blomberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electrophoresis 15:1466-1486(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Protein expression during exponential growth in 0.7 M NaCl medium
                                                                                                                                                                                                                                                                                                                                                                                                                PTM: PHOSPHORYLATED. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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APR-1996)
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EMBL/GenBank/DDBJ
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HSSP; P19120; 1NGJ. SWISS-2DPAGE; P10592;

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SGD; S0003947; SSA2.

Interpro; IPR001023; HSP70.

Pfam; PF00012; HSP70; 1.

PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS00329; HSP70_3; 1.

Heat shock; ATP-binding; Multigene family; Acetylation;
                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q06248;
Q1-JUN-1994 (Rel. 29, Created)
Q1-JUN-1994 (Rel. 29, Last sequence update)
Q1-JUN-1994 (Rel. 29, Last annotation update)
HEAT_SHOCK 70 KDA PROTEIN IV (HSP70 IV).
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                                                                                            Pfam; PF00012; HSP70; 1.

PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       sconzo G., Scardina G., Ferraro M.G.;
"Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 gene family and its expression.";
Gene 121:353-358(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                            PIR; JC1391; JC1391.
HSSP; P19120; 1NGJ.
                                                                                                                                                                                                                                        EMBL; X61379; CAA43653.1; -.
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1 SLFEGIDGYT 10
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Pred. No.
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; 23BDDD120C194912
                           Score 44; DB 1;
Pred. No. 0.92;
0; Mismatches
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RESULT 8
HS7A_CAEEL
ID HS7A_CAEEL
AC P09446;
DT 01-MAR-1989
DT 01-FEB-1994
DE HEAT SHOCK
GN HSP-1 OR HS7
OC ENKARYOTA;
OC ENKARYOTA;
OC Rhabditidae
OX NUTL' TAXID-
RP SEQUENCE FR
RX MEDLINE-882
RA SNUTCH T.P.
RT "The Caenor
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RT Characteriz
RL Gene 64:241
CC -!-SIMILAR
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DR HSSP; P191:
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01-MAR-1989 (Rel.
01-FEB-1994 (Rel.
HEAT SHOCK 70 KDA
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                                                                                                                                                                                                                                                                                                             DICDI STANDARD; PRT; 640 AA P36415; O1-JUN-1994 (Rel. 29, Created) O1-JUN-1994 (Rel. 29, Last sequence update) O1-WV-1997 (Rel. 35, Last annotation update) HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
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PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
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Gene 64:241-255(1988).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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"The Caenorhabditis elegans hsp70 ge
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                                                                                                                                                                                                               Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JT0285; HHKW7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M18540; AAA28078.1; -.
MEDLINE=94008983; Haus U., Trommler
                                                                        STRAIN-AX3;
                                                                                                                                                                                                                                                                                HSPB OR HSC70.
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286 SLFEGIDFYT
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=44689;
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9; Conservative
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Peloderinae; Caenorhabditis.
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A PROTEIN A.
   PubMed=8404847;
P., Fisher P.R.,
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90.0%;
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Pred. No. 0.92
0; Mismatches
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          H., Lottspeich
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HS71_BOVIN STAN
ID HS71_BOVIN STAN
AC 027975; 027964;
DT 01-NOV-1997 (Rel. 3
DT 01-NOV-1997 (Rel. 3
DT 15-JUL-1999 (Rel. 3
DE HEAT SHOCK 70 KDA P
GN HSP70-1.
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                                                                                                                                                                                                                    RESULT 10
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DictyDb; DD01078; hspB.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
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SWISS-2DPAGE; P36415; DICTY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Biol. Chem. 268:23267-23274(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Noegel A.A., Schleicher "The heat shock cognate polymerization through i cap32/34.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S37394; S37394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94043116; PubMed=8226849
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                                                                                                                                                                                                                                                                                                284
                                                                                                                                                                                                                                                                                                                                              1 SLFEGIDGYT 10
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FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-IBINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.

SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS OF THE CELL CORTEX AND CELL PROTRUSIONS.

DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
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                                                                                                                                                                                                                                                                                                SLFEGIDFYT 293
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                STANDARD;
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35, Last sequence update)
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PROTEIN 1 (HSP70-1).
                                                                                                                                                                                                                                                                                                                                                                                                                           83.0%;
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HS71_HUMAN STANDARD; PI
PO8107; P19790; Q9UQMO; Q9UQLO;
O1-AUG-1988 (Rel. 08, Created)
O1-FEB-1994 (Rel. 28, Last seque
20-AUG-2001 (Rel. 40, Last annoi
                                                                                              HUMAN
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PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE COMFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
                                                                                                                                                                                                                                                                                                                                          Pfam; pF00012; HSP70; 1.

PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS00329; HSP70_3; 1.

ATP-binding; Chaperone; Heat shock; Multigene family.

SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U09861; AAA73914.1; -. EMBL; U02891; AAA03450.1; -. HSSP; P19120; INGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An AluI polymorphism at the bovine 70 (HSP70-1) Locus.";
Anim Genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=95126904; PubMed=7826329; Gutierrez J.A., Guerriero V.; Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."; Blochem. J. 305:197-203(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ANGUS;
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                                                                                                                                                                            286
                                                                                                                                                                                                             1 SLFEGIDGYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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9; Conserv
                                                                                                                                                                                                                                                  Conservative
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Pred. No. 0.
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Last sequence update)
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RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.

RX MEDLINE-99234376, PubMed-10216320;

RO Sipluk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

RT "Structure of a new crystal form of human hsp70 ATPase domain.";

LA cta Crystallogr. D 55:1105-1107(1999)

C :-!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

C PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING

C OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN

C C RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION

PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE MONNATIVE COMPONENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDE DURING TRANSLATION AND MFMHDDAND CONTRACTED BY POLYPEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDE DURING TRANSLATION AND MFMHDDAND CONTRACTER EXPOSED BY POLYPEPTIDE CONTRACTER EXPOSED BY POLYPEPTIDE CONTRACTE
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Mammalia; Eutheria;
                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "In vitro transcription of a human hsp 70 heat shock gene by prepared from heat-shocked and non-heat-shocked human cells." Nucleic Acids Res. 14:8933-8949(1986).
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Rowen L., Qin S., Madan A., Dickhoff R., Dorortz C., Ratcliffe A., Abbasi N., Shaffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milner C.M., Ca
"Structure and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drabent B., Genthe A., Benecke B.-J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-36 AND 360-424 FROM N.A. MEDLINE-89184548; PubMed-2538825;
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"Conserved features of eukaryotic hsp70 genes revealed with the nucleotide sequence of human hsp70.";
Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=86016721; PubMed=3931075;
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                                                                                                                                                                                                                                                                                                              INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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                      M59828; AAA63226.1; -. M59830; AAA63227.1; -. AF134726; AAD21816.1;
                                                                                                                                                                                                non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MAR-1999) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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SWISS-2DPAGE; P08107; HUMAN.
                                                                                                                                                                                                                                                                                                                "Characterization and sequence of a expression in mouse cell lines."; Gene 87:199-204(1990).
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Pfam; PF00012; HSP70; 1.
                                                                                                                                                                  Gene
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"Structure and expression
                                                                                                                                                                                                                                                    MEDLINE=94357449; PubMed=8076831;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                Hunt C., Calderwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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, M24743; AAA59944.1;
, M24744; AAA59845.1;
, X04676; CAA28381.1;
, X04677; CAA28382.1;
                 OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZATE. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
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1HJO; 2
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FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING PROTEINS AGAINST AG WITH AG WI
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A25773.
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90.0%;
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E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
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N -> S (IN REF. 3; AAD21815).
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HEAT SHOCK 70 KDA F
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P34930;
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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                                                                                                                                                                                                                                                                                       Peelman L.J., de Weghe A.R., Bouquet Y.H.;
                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
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MGD; MGI:99517; Hsp70-1
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                                                                                                                                                                                                                                                         "Complete nucleotide sequence c
Immunogenetics 35:286-289(1992)
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92175874; PubMed=1339404;
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
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    -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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                                                                                                              FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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28, Last sequence update)
35, Last annotation update)
PROTEIN 1 (HSP70.1).
                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69994 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.0%;
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                                                                                                                                                                                                                                                                                                   Coppieters W.R., van Zeveren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44;
Pred. No.
                                                                                                                                                                                                                                                                     of a porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41475360F6749F2F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 AA
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                                                       There are no
                                                                                                                                                                                                                                                                       HSP70 gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 641;
                                                                      and the
                                                                                     through
                                                       he EMBL outst
                                                                                                                                                                                                                                                                                                     A.J.,
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                                                                          collaboration - Loutstation -
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Best Local
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                          BIOCHIM. BIOCHYS. ACTA 1219:64-72(1994).

BIOCHIM. BIOCHYS. ACTA 1219:64-72(1994).

FINANCISCON TRANSLATED POLYPERTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZATED POLYPERTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZATED. FOLYPERTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZATES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PROTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

-! INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS71_RAT STANDARD; PRT; 641 AA (0.07439; P42853; 0.07439; P42853; 0.01-FEB-1995 (Rel. 31, Created) 0.01-FEB-1995 (Rel. 31, Last sequence update) 0.01-NOV-1997 (Rel. 35, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC66
                                                                                                                                                                                                                                                                                                                                                                                                                                           Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J., Massa S.M., Sharp F.R.; massa S.M., Sharp expression of stress-inducible rat hsp70 in normal and injured rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE-94096443; PubMed-8271311;
MEDLINE-94096443; PubMed-8271311;
                                                                                                                                                                                                                                            MEDLINE-94368874; PubMed-8086479;
                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                   Walter L., Rauh F., Guenther E.; "Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat."; Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=LEW.1W/GUN;
MEDLINE=95012453; PubMed=7927536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSP70-1 AND HSP70-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001023; HSP70. Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                                                 hsp70 gene."
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

    J. Neurosci.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116
                                                                                                                                                                                                            "Cloning, nucleotide
                                                                                                                                                                                                                           Lisowska K., Krawczyk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 SLFEGIDFYT 295
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
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                                                                                                                                                                                                                sequence
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Pred. No.
                                                                                                                                                                                                            and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on update)
).1/2).
                                                                                                                                                                                                              Wolniczek P., Wisniewski J.;
pression of rat heat inducible
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Best Local :
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EMBL; X77208;
EMBL; X77207;
EMBL; X74271;
HSSP; P19120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS71_YEAST
P10591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
REVISIONS TO Slater M.R.;
                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).
SSA1 OR YALOOSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_2; 1.
PROSITE; PS00329; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001023; HSP70.
                                                                     MEDLINE-85087943; PubMed-6096826; Ogden R.C., Lee M.-C., Knapp G.; "Transfer RNA splicing in Sacchar
                                                                                                                                                 STRAIN-S288C / AB972;
STRAIN-S288C / AB972;
MEDLINE-95028152; PubMed-7941740;
Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng
Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng
Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Buss
"Sequencing of chromosome I of Saccharomyces cerevisiae: ana
"Sequencing of chromosome I of Saccharomyces cerevisiae: ana
the 42 kbp_SP07-CENI-CDC15 region.";
                                                                                                                                                                                                                                                       Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; l
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                                                            substrates
                                                                                                                SEQUENCE OF 590-641 FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           MEDLINE-89128457; PubMed-2644626;
                                                                                                                                                                                                                                                                                                         STRAIN-S288C
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                Nucleic Acids
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286 SLFEGIDFYT 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLFEGIDGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00012; HSP70;
                                                                                                                                        10:535-541(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g; Chaperone; Heat s. 72 K
727 K
227 227 D
408 408 G
641 AA; 70163 MW;
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641 AA;
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                                                Res. 12:9367-9382(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                           Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.0%;
                                                                        Knapp G.;
in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shock; Multigene family; KR -> NG (IN REF. 3). D -> H (IN REF. 2 AND 3). G -> A (IN REF. 3).
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Pred. No. 0.
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                                                                                                                                                                                                                                                                     Saccharomyces
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0.92;
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                                                                                                                                                                                                                                                                     cerevisiae.";
                                                                          defining
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                                                                                                                                                                    analysis of
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PIR; S42164; S42164.

HSSP; P19120; 1ATR.

SWISS-2DPAGE; P10591; YEAST.

YEDD; 9788; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwende Volpe T., Warner J.R., McLaughlin C.S.; Submitted (SEP-1994) to the SWISS-PROT data bank.

Submitted (SEP-1994) to the SWISS-PROT data bank.

FUNCTION: SSAI MAY PLAY A ROLE IN THE TRANSPORT OF POLYPE BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INFO THE ENNOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN SSAI AND SA2 PROTEINS IS EXPECTED. SSAI CAN PARTICIPATE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garrels J.I., Futcher B., Kobayashi R., Latte Volpe T., Warner J.R., McLaughlin C.S.; "Protein identifications for a Saccharomyces database.";
                                                                                                                                                                                                           Heat shock;
INIT_MET
MOD_RES
SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no resture by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 38531 / Y41;
MEDLINE=97089742; PubMed=8935650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Electrophoresis 15:1466-1486(1994).
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                                                                                                                                                                                                                                                                                                     PROSITE; PS00297; HSP70_1; PROSITE; PS00329; HSP70_2; PROSITE; PS01036; HSP70_3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norbeck J., Blomberg A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 186-195
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                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001023;
Pfam; PF00012; HSP70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD; S00000004; SSA1.
  282
                                              μ
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                          SLFEGIDGYT 10
X12926; CAA31393.1;
L22015; AAC04952.1;
                                                                                            . Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JUN-1993) to
                                                                                                                                                                                                              641
                                                                                                                                                                                                                                                                               ATP-binding; Multigene family;
                                                                                              Conservative
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  291
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                                                                                                                                                                                                                69526 MW;
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                                                                                                 Score 44; DB pred. No. 0.97 0; Mismatches
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FA9389BAE9B1D7DA
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1.92;
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## ALIGNMENTS

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AC Q9

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Matches 9
Q9U670 PRELIMINARY; PRT; 153 AA. Q9U670; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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SEQUENCE
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O9U667;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Hohenlohe P.A.;

"Heat-shock genes in the heat-stressed genus Littorina.";

"Heat-shock (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF191828; AAF12787.1; -.

HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Littorina plena.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID-31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001023; HSP70.
PROSITE; PS01036; HSP70_3;
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9; Conservative
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146 AA;
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16607 MW;
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Q9U665;
Q9U665;
Q1-MAY-2000
01-MAY-2000
.01-JUN-2001
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"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAF12784.1; -.
HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
PROSITE; PS01036; HSP70_3; 1.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
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01-MAY-2000 (TIEMBLIEL 13, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
HSC70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Heat-shock genes in the heat-stressed genus Littorina.";
submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191826; AAF12785.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Hohenlohe P.A.;
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NCBI_TaxID=31221;
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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PROSITE; PS01036; HSP70_3; 1.
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nes 9; Conser
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155 AA;
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17352 MW;
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17676 MW; C191F6E5B1F346C2 CRC64;
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Pred. No.
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Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191830; AAF12789.1; -.
HSSP; P19120; 1BA1.
Q9U668;
Q9U668;
01-MAY-2000
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Q9U671;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                                                                                                                                                 Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
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                                                                                                                                                                                                                                                                                                   "Heat-shock genes in the heat-stressed genus L Submitted (OCT-1999) to the EMBL/GenBank/DDBJ EMBL, AF191824; AAF12783.1; -. HSSP; P19120; 1BA1.
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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158 AA;
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                                       PRELIMINARY;
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17834 MW;
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17887 MW;
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90.0%;
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Pred. No.
                                                                                                                                                                      Score 44; DB
Pred. No. 1.3;
                                        PRT;
                                                                                                                                                                                                                           B41E5356A24CAD2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E8F743382B285EB2 CRC64;
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  sequence update)
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Best Local :
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SEQUENCE
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SEQUENCE
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HohenLohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191827; AAF12786.1;
EMBL; P191827; BAA1.
HSSP; P19180; BBA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Littorina plena.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID-31219;
                                                                                                                                                                                                                                                                "Heat-shock genes in the heat-stressed Submitted (OCT-1999) to the EMBL/GenBar EMBL; AF191829; AAF12788.1; -.
 P81159;
01-JUN-1998
                                                                                                                                                                                                                 InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Hohenlohe P.A.;
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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HEAT-SHOCK PROTEIN (FRAGMENT).
                       P81159
                                                                                                                                                                                                                                                     HSSP; P19120; 1BA1
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                      Littorina plena.
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                                                                                                    SLFEGIDGYT 10
                                                                                SLFEGIDFYT 94
                                                                                                                                      Similarity
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158 AA;
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158 AA;
(TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                      PRELIMINARY;
                                                                                                                           Conservative
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17868 MW;
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17891 MW;
                                                                                                                                      83.0%;
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90.0%;
                                                                                                                                                                                                                                                                            rt-stressed genus Littorina.";
EMBL/GenBank/DDBJ databases.
                                                                                                                          Score 44; DB
Pred. No. 1.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D2ECE71042EC44CB CRC64;
                                                                                                                                                                                   B41E5356BCECAD2F CRC64;
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                      220
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1.3;
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Best Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                           Aplysia californica
Eukaryota; Metazoa;
Aplysiidae; Aplysia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P81157
P81157;
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MEDLINE=93077669; PubMed=1360013;
Kuhl D., Kennedy T., Barzilai A.,
"Iong-term sensitization training
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aplysia californica
Eukaryota; Metazoa;
Aplysiidae; Aplysia.
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  SEQUENCE
                                                                                                                                           InterPro; IPR001023; HSP70. Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                                 EMBL; Z15037; CAA78755.1;
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6500
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                                                                                                                          PRINTS; PR00301
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9; Conserv
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220 AA;
221 AA;
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                                                                                                                        HEATSHOCK70.
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24684 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (California sea hare)
Mollusca; Gastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mollusca;
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Mollusca; Gastropoda;
    24404 MW;
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Last annotation update)
(HSP70A) (FRAGMENT).
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Pred. No.
    853F794106E83CC9 CRC64;
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g in Aplysia leads to an
protein chaperon of the
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Q90520;
Q90520;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo galidneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
MCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q98899 PRELIMINARY; PRT; 367 AA. Q98899; 01-FEB-1997 (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
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MEDITINE-85036330; PubMed=6092938;

Kothary R.K., Jones D., Candido E.P.M.;

Kothary R.K., Jones D., Candido E.P.M.;

*70-Kilodalton heat shock polypeptides characterization of cDNA sequences.";

Mol. Cell. Biol. 4:1785-1791(1984).
                                                                                                                                                                                                                                                                                                                                                                                              Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                     Lim E.H.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ EMBL, Y08578; CAA69892.1; .. HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
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                                                                                                                                                                                                                                                                                                                       Acanthomorpha; Acanthopterygii; Tetraodontidae; Takifugu.
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=31033;
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mes 9; Conserv
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9; Conser
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278 AA;
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30327 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB Pred. No. 2.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E4C745DE5484C17A CRC64;
                                                                                                                                                                                                                                                                                                                                                             Percomorpha;
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2.6;
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                                                                                                                    databases
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RESULT 044350 ID 44350 OC 07 O
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Best Local Similarity
Matches 9; Conser
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Best Local
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Submitted (NOV-1993) to the I
Submitted (NOV-1993) to the I
EMBL; Z27118; CAA81642.1; -.
HSSP; P08107; 1HJO.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat shoc
NON_TER
NON_TER
SEQUENCE
                                                                                      Chondrosia reniformis.
Eukaryota; Metazoa; Porifer:
Chondrosida; Chondrillidae;
                                                                                                                                                                           O44350;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
HEAT_SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q63718 PRELIMINARY; PRT; 455 AA.
Q63718;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00301; HEATSHOCK70. PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                           044350
  Borchiellini C.,
                         SEQUENCE FROM N.A.
                                                                  NCBI_TaxID=68574;
                                                                                                                                                           HSP70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angeletti B., Passarelli F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat shock.
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                                                                                                                                                                                                                                                                                                                                                                                                      254 SLFEGIDFYT 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shock.
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455
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367 1
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                                                                                                                                                                                                                                                                                             PRELIMINARY;
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    Le
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455
50404 MW;
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40405 MW;
    Parco Y.;
                                                                                                           Porifera; Demospongiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the
                                                                                           Chondrosia
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orru D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0F45F12CBA1E2971 CRC64;
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                                                                                                                                                                                                                                                                                               467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
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                                                                                                                                                                                                                                                                                             AA
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                                                                                                                                                                                                    update;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 14
044352
ID 044352
AC 044352
AC 044352
DT 01-JUN
RESULT 15
Q9NJ92
ID Q9NJ92
AC Q9NJ92
DT 01-OCT
DT 01-JUN
DE HEAT S
OS GUANCH
OC EUKARY
OC Clathr
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RP SEQUEN
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.0%;
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
NON_TER 467 467
                                                                                                                                                       Q9NJ92 PRELIMINARY; PRT; 467 AA. Q9NJ92; Q1-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Borchiellini C., Le Parco Y.;

Borchiellini C., Le Parco Y.;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF026520; AAC05364.1; -.

HSSP; P08109; ICKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  044352 PRELIMINARY; PRT; 467 AA. 044352; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                              Guancha lacunosa.
Eukaryota; Metazoa; Porifera; Calcarea; Calcinea; Clathrinida;
Clathrinidae; Guancha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petrobiona massiliana.
Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
Petrobiona.
  SEQUENCE FROM N.A.
                                                      NCBI_TaxID=115120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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252 SLFEGIDEYT 261
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Local Similarity 90.0%;
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SLFEGIDGYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467
467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 467
467 AA; 51707 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467
51458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 5;
Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 5; Length 467; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23EB28FFD1873DA6 CRC64;
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Best Local Similarity 90.1
Matches 9; Conservative
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SEQUENCE
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"Sponges paraphyly and the origin of Metazoa.";
"Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF182195; AAR61297.1; -.
Interpro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PFAm; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
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467 AA;
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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US-09-205-264-2
US-09-347-803-14
US-09-625-188-12
US-09-636-431-5
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2.764 Million cell updates/sec
Sequence 3, Appli
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/ Match Local Simil hes 8; (	SULT 1 1-08-797-338B-3 Sequence 3, Application US/08797358B Sequence 3, Application US/08797358B Patent No. 6268478 GENERAL INFORMATION: APPLICANT: Adams, John TITLE OF INVENTION: INTRACELLULAR NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSEE: Campbell & Flores STREET: 4370 La Jolla Village CITY: San Diego STATE: California COUNTRY: United States ZIP: 92122 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: Patentin Release #1 CURRENT APPLICATION NUMBER: US/08/797 FILING DATE: 11-Feb-1997 CLASSIFICATION: CURKNOWN> PRIOR APPLICATION NUMBER: US/08/797 FILING DATE: 12-FEB-1996 ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-CE TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001 TELEFAX: (619) 535-9001	00000000000000000000
90. Similarity 80. 8; Conservative	Application US/ Siz68478 WFORMATION: ICANT: Adams, JC E OF INVENTION: ER OF SEQUENCES: ER OF SEQUENCES: ER OF SEQUENCES ER OF	888877777777777777
90.2 80.0 7ative	Application US/08797358B 26847B 26847B CANT: Adams, John COF INVENTION: INTRACELLULA R OF SEQUENCES: 9 SPONDENCE ADDRESS: R OF SEQUENCES: 9 SPONDENCE ADDRESS: ROF SEQUENCES: 9 STATE: California COUNTRY: United States ZIP: 92122 THER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: PATENTION LOTA: APPLICATION NUMBER: US/08/7 FILING DATE: 11-Feb-199 TILING DATE: 11-Feb-199 TILING DATE: 12-FEB-199 FILING DATE: 12-FEB-1996 INEY/AGENT INFORMATION: NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: 9- TOMMUNICATION INFORMATION: TELEPHONE: (619) 535-8949 N FOR SEQ ID NO: 3: TRANDEDNESS: unknown TOPOLOGY: unknown TOPOLOGY: unknown ULE TYPE: protein NNCE DESCRIPTION: SEQ ID NO:	711 911 911 911 911 913 913 913 913 913 9
28;	US/0879735  John N: INTRACE ES: 9 ES: 9 ES: 9 Ornia Led States ted States ted States tentIn Rei ON DATA: NUMBER: US 11-Feb-19 ON: <unknown 12-feb-19="" data:="" informat<="" information:="" number:="" td="" us=""><td>44αααωα44αα 2222222222222222222222222222</td></unknown>	44αααωα44αα 2222222222222222222222222222
Score Pred.	n US/08797358B  s, John ION: INTRACELLULAR NCES: 9 ADDRESS: Campbell & Flores Campbell & Flores ifornia nited States LE FORM: E: Floppy disk EE: Floppy disk ES: Floppy disk IM PC compatible SYSTEM: PC-DOS/MS-D PATENTIN Release #1 TION DATA: N NUMBER: US/08/797 TION: <unknown> ON DATA: N NUMBER: US 60/011 E: 12-FEB-1996 INFORMATION: bell, Cathryn A. ON NUMBER: 31,815 DOCKET NUMBER: P-CE ON INFORMATION: (619) 535-904 ID NO: 3: TERISTICS: 3 amino acids o acid sis: unknown profein profein profein SEQ ID NO: 3</unknown>	US-08-4 US-08-4 US-08-4 US-08-4 US-08-4 US-08-6 US-08-
ore 46; DB ed. No. 0.29 Mismatches	TLAR VITA  FOR THE LIP  Lage Dri  10  17797,358  17797,358  115  P-CE 316	09-340-479 08-487-890 08-37-478-35 08-478-373 08-478-373 08-487-890 08-487-438 08-478-373 08-478-373 08-478-373 08-478-373 08-897-438 08-679-006 08-679-006 08-637-763 08-637-763
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 646 amino acids
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APPLICANT: Wittrup,
APPLICANT: Robinson,
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 52, Application US/08928692
                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
"ADDRESSEE: No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
                                                                                            NUMBER OF SEQUENCES:
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STATE: NY
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06-JUL-1993
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METHODS FOR INCREASING SECRETION
RECOMBINANTLY EXPRESSED PROTEINS
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Pred. No. 0.71;
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                                                                                                            ; ORGANISM: Bacillus licheniformis US-09-198-956-6
                                                                                                                                                          SEQ ID NO 6
LENGTH: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09198956 Patent No. 6165769
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Best Local :
                                Matches
                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                 APPLICANT: Schulein, Martin
APPLICANT: Lange, Niels Erik K.
APPLICANT: Bjonrvad, Mads E.
APPLICANT: Schnorr, Kirk
TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
FILE REFERENCE: 5377.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 212-867-01:
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/198,956
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: 1344/97
EARLIER FILING DATE: 1997-11-24
EARLIER APPLICATION NUMBER: 60/067,240
EARLIER FILING DATE: 1997-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Andersen, Lene N.
                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 26
                                                                                                                                             TYPE: PRT
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NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
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OPERATING SYSTEM:
SOFTWARE: FastSE(
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CITY: N
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nes 6; Conserv
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3 FEGIDLY 9
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                                Similarity 5; Conserv
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85.7%;
                                               64.78;
71.48;
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                                  Mismatches
                                               Score 33; DB 4;
Pred. No. 65;
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Pred. No.
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APPLICANT:

Schryvers, Anthony

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US-08-478-435-19
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Best Local Similarity
Thes 5; Conserve
                                                                                                       RESULT
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                                                  Sequence 19, Application US/08478435 Patent No. 5922323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/487,890A FILING DATE: 07-JUN-1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/175,116 FILING DATE: 29-DEC-1993 PRIOR APPLICATION DATA: APPLICATION UMBER: US 08/148,968 FILING DATE: 08-NOV-1993 ATTORNEY,AGENT INFORMATION:
                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19
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 APPLICANT:
APPLICANT:
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopby disk
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I REGISTRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                      28 FEGVAIYT 35
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                                                                                                                                                                                     3 FEGIDLYT 10
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Loosmore, Sheena
Harkness, Robin
                                                                                                                                                                                                                    Conservative
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Klein, Michel
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Harkness, Robin
Schryvers, Anthony
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Pred. No. 6.
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RESULT 7
US-08-337-483-19
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Best Local Similarity 62:
Matches 5; Conservative
                                                                                                GENERAL INFORMATION:
APPLICANT: LOOSMOTO
APPLICANT: Harkness
APPLICANT: Schryvei
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Patent No. 5922562
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PRIOR APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
115 OB 1/148 068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                    APPLICANT:
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                                   APPLICANT:
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CITY: Toronto
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28 FEGVAIYT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 36 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: M5G 1R7
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INVENTION: Transferrin Receptor Genes
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Suite 701, 330 University Avenue
            Gray-Owen, Scott
Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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Gray-Owen, Scot
Yang, Yan-Ping
                                                                                  Chong, Pele
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Klein, Michel
                                                                                                Schryvers,
                                                                                                                    Harkness, Robin
                                                                                                                                Loosmore, Sheena
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62.5%;
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                                                                                                    Anthony
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US-08-478-373-19
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                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/0:
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
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OPERATING SYSTEM:
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                                                                                                                                                                                      CITY: Toronto
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les 5; Conserv
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                                                                                                                                        TE: Ontario
WTRY: Canada
M5G 1R7
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Suite 701, 330 University Avenue
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Suite 701, 330 Unviersity Avenue
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Klein, Michel
VEMTION: Transferrin Receptor Genes
EQUENCES: 147
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Yang, Yan-Ping
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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62.5%;
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Pred. No.
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6.6;
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Best Local Similarity
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                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING APSTEM: PC-DOS/MS-DOS

OPERATING APSTEM: PA-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,671

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                           APPLICATION NUMBER: US 0 FILING DATE: 08-NOV-1994 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            FITLE OF INVENTION:
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                                                                                                                                                                                                                                               STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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CITY: Toronto
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APPLICATION NUMBER: US 08/175,116 FILING DATE: 29-DEC-1993
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Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
                                                                                                                                                                                                                                                                                                              Suite 701, 330 University Avenue
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Harkness, Robin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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147
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28: 1038-463 MIS:vg
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Pred. No.
2; Mismatc
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US-08-483-577A-19
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,577A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/337,483

FILING DATE: 08-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/37,483

FILING DATE: 08-NOV-1994

PRIOR APPLICATION NUMBER: US 08/175,116

EPILING DATE: 29-DEC-1993
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
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CITY: Toronto
STATE: Ontario
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ELECOMMUNICATION INFORMATION:
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: Can
ZIP: M5G 1R7
                                  NAME: Stewart, Michael REGISTRATION NUMBER: 24
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nes 5; Conserv
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Klein, Michel
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Yang, Yan-Ping
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Harkness, Robin
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62.5%;
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                  1038-511
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Pred. No. 6.
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Best Local Similarity oz...
Thes 5; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
                                                                                              APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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LENGTH: 36 amino acids
                                                                REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Toronto
STATE: Ontario
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                                                TELEPHONE:
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M5G 1R7
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Murdin, Andrew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harkness, Robin
                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         loosmore, Sheena
                                                  (416) 595-1155
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                                                                                  1038-720
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Pred. No. 6.6;
2; Mismatches
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6.6;
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; TYPE: amino acid
; STRANDEDNESS: sir
; TOPOLOGY: linear
US-08-897-438-19
                                               Query Match
Best Local Similarity
Fighter 5; Conserve
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US-08-817-811-55
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Best Local Similarity 62..
"^+^hes 5; Conservative
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                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO 96/11944

FILING DATE: 25-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: FBRC:005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                             TELEFAX: 512/474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
APPLICANT: Good, Michael F.
APPLICANT: Saul, Allan J.
TITLE OF INVENTION: COMPRISING SAME
TITLE OF INVENTION: COMPRISING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/817.811 FILING DATE: 14 APR-1997 CLASSIFICATION: 424 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 512/418-3000
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CITY: Houston
STATE: Texas
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ZIP: 77210
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                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
20 SILEGLNLYS 29
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                              1 SLFEGIDLYT 10
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                                                                Conservative
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                                                                 4; Mismatches
                                                                                Score 32; DB Pred. No. 16;
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RESULT 13 US-09~205-264-2

Query Match

62.7%;

Score 32;

DB 5;

Length 301;

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-264-2
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; MOLECULE TYPE: PCT-US95-13975-72
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Best Local Similarity bu...
Conservative
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EARLIER FILING DATE: 1997-12-05
NUMBER: SEQ ID NOS: 9
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 2
LENGTH: 161
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Olsen, et al.
TITLE OF INVENTION: Synferon
FILE REFERENCE: PF404
CURRENT APPLICATION NUMBER: US/09/205,264
CURRENT FILING DATE: 1998-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09205264
Patent No. 6114145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 72, Application PC/TUS9513975
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
                                                                                                       TELEFAX: (212)391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13975
FILING DATE: 26-OCT-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: McDonell, Michael W.
TITLE OF INVENTION: Recombinant Feline Herpes virus
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39118-PCT
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/3 FILING DATE: 26-OCT-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM 330 OPERATING SYSTEM:
                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                      TOPOLOGY:
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                                    I: 301 amino acids
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OGY: linear
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IBM 330 466 DX2
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66.7%;
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Pred. No.
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Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1FEGLTYT 8

RESULT 15
US-09-347-803-14
Sequence 14, Application US/09347803
Patent No. 6274379
Sequence 14, Application US/09347803
Patent No. First Sequence 18, 111
Applicant: Since 1 No. 111
Applicant: Since 1 No. 120
Patent No. 12
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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T45468	A34041	S48025	S48024	JC7132	T45517	S09036	S25585	PC7036	JN0668	T45474	T45473	I46588	PQ0138	A03309	T0755U
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## ALIGNMENTS

RESULT

dnaK-type molecular chaperone HSC70 - California sea hare (fragment)
%;Alternate names: heat shock protein 70 homolog HSC70
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999
C;Accession: B44261

A;Title: Long-term sensitization training in Aplysia leads A;Reference number: A44261; MUID:93077669 A;Accession: B44261

to an increase in the expr

R;Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R. J. Cell Biol. 119, 1069-1076, 1992

A;Description: involved in protein for C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone A; Reference number: I51344; A; Accession: I51344 A; Status: preliminary; trans A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-208 <KUH> A:Description: involved in protein folding C;Superfamily: heat shock protein 70 A;Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804 C;Function: A; Molecule type: mRNA A; Residues: 1-278 <KOT> R; Kothary, R.K.; Jones, D.; Candido, E.P.M. Mol. Cell. Biol. 4, 1785-1791, 1984 dnaK-type molecular chaperone (clone pTHS70.7) - ra N;Alternate names: 70K heat shock protein C;Species: Oncorhynchus mykiss (rainbow trout) C;Date: 21-Feb\_1997 #sequence\_revision 21-Feb-1997 밁 Q A; Title: 70-kilodalton heat shock C; Accession: I51344 C; Function: A; Gene: HSC70 C; Genetics: A; Note: sequence extracted from Matches 132 SLFEGIDFYT 141 Local Similarity nes 9; Conserv 1 SLFEGIDLYT 10 Conservative translated from GB/EMBL/DDBJ 92.2%; shock polypeptides MUID:85036330 NCBI backbone (NCBIP:118950) 0; Score 47; DB 2; Pred. No. 0.061; folding Mismatches and assembling/disassembling of protein and assembling/disassembling of protein from rainbow trout (fragment) 1; #text\_change rainbow trout: Characterization Length 208 Indels 20-Aug-1999 ç Gaps 0 8 0

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heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C;Species: Chondrosia reniformis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45477
R;Borchiellini, C:; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z22983
A;Accession: T45477
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Gene: Hsp70
C;Superfamily: heat shock
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment) C;Species: Funiculina quadrangularis C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
                                                      RESULT
T45476
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A; Residues: 1-467 <BOR>
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A; Residues: 1-467 <BOR>
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A; Accession: T45479
                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1
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Best Local S
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Best Local Similarity 90.0
"^+^hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                        252
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nes 9; Conserv
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                                                                                                                                            SLFEGIDLYT 10
                                                                                                                        SLFEGIDFYT 261
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                C.; Le Parco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecular chaperone
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90.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No.
                                                                                                                                                                                           0,;
                                                                                                                                                                                                           Score 47; DB 2; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                September 1997
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0.15;
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0.085;
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C;Accession: T45476
R;Borchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library,
A;Reference number: Z22983
A;Accession: T45476
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A;Molecule type: mRNA
A;Residues: 1-468 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heat-shock protein 70 [imported] - Eunicella cavolini (iragment) C;Species: Eunicella cavolini C;Species: Eunicella cavolini C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45478
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T45478
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C;Superfamily: heat shock protein
                                                                                                                                                                                                                                                                                                                              RESULT
T45471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Borchiellini, C.; Le Paro
submitted to the EMBL Data
A; Reference number: Z22983
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                                                                                                                                                                                        C; Date: J. C; Accession: T45471
C; Accession: T45471
R; Boves, H.; Mintert, U.; Dittrich,
R; Boves, H.; Mintert, Data Library,
                                                                                                                                                                                                                                                                   dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum N;Alternate names: heat shock cognate protein 70 C;Species: Dictyostelium discoideum
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C;Superfamily: heat shock protein
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A; Residues: 1-469 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated
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A;Gene: hsc70
A;Note: localized to filopodias and cortex
C;Superfamily: heat shock protein 70
                                                                                                                                                            A; Reference number: Z22980
A; Accession: T45471
                                                      C; Genetics:
                                                                     A; Experimental
                                                                                    A; Molecule type: mRNA
A; Residues: 1-632 <BOV>
A; Cross-references: EMB
                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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Eunicella cavolini
                                                                   nces: EMBL:AF025951;
source: strain AX3
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAC05363.1
                                                                                        PIDN: AAB81865.1
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                                                                                                                                                                                                 W.; Faix, J.; Gerisch,
September 1997
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C;Accession: A25646
R;MorImoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 12692-12699, 1986
A;Title: Organization, nucleotide sequence, and transcription of the A;Reference number: A25646; MUID:86304452
A;Accession: A25646
A;Molecule type: DNA
A;Residues: 1-634 <MOR>
A;Rote: the authors translated the codon TCG for residue 583 as Translate
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status, parama
A;Nolecule type: mRNA
A;Residues: 1-636 <EDD>
A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Eddy, R.J.; Sauterer, R.A.; Condeells, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with A;Reference number: A48872; MUID:94043116
A;Accession: A48872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dnaK-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)
N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein C;Species: Dictyostelium discoideum
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C;Accession: A48872
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RESULT
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Best Local S
Matches 9
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Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
Accession: A25646
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Best Local
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Best Local
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                                                                                       SLFEGIDFYT 289
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9; Conserv
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9; Conserv
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Pred. No.
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0.21;
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A; Gene: hsp70IV
A; Introns: 61/2
C; Function:
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A; Residues: 1-638 <SAI>
R; Sainis, I; Angelidis, C.; Pagoulatos, G.; Lazaridis,
R; Sainis, I; Angelidis, C. Pagoulatos, G.; Lazaridis,
R; Stitle: The hsc70 gene which is slightly induced by her
A; Title: The common gene which is slightly induced by her
A; Reference number: 136927; MUID: 95080396
A; Accession: 136927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I. submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the cDNA encoding a monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dnaK-type molecular chaperone hsp70 - green monkey
N;Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S31766; I36927
C;Accession: S31766; I36927
                                                                                                                                                                                      A;Description: involved in protein folding and assembling/disassembling C;Superfamily: heat shock protein 70 C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Sconzo, G.; Scardina, G.; Ferraro, M.G. Gene 121, 353-338, 1992
A;Title: Characterization of a new member of the A;Reference number: JC1391; MUID:93077053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dnaK-type molecular chaperone 701V - sea urchin (Paracentrotus lividus)
N;Alternate names: heat shock protein 701V; hsp701V protein
C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: involved in protein f. C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
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A;Molecule type: mRNA
A;Residues: 1-638 <RES>
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                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-639 <SCO>
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A;Experimental source: kidney; cell line COS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: S31766
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Best Local S
Matches 9
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Best Local
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90.0%;
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                                                                                 Score 47; DB Pred. No. 0.22 0; Mismatches
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A; Status: translation not shown
A; Status: translation not shown
A; Status: translation not shown
A; Residues: 1.639 < SLA>
A; Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546
A; Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546
A; Reference number: 564761
A; Accession: S64772
A; Molecule type: DNA
A; Residues: 1-639 < GOF>
A; Molecule type: DNA
A; Residues: 1-639 < GOF>
A; Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g136020
A; Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g136020
A; Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g136020
A; Reference number: S64775
A; Accession: S64775
A; Accession: S64775
A; Molecule type: DNA
A; Residues: 72-639 < ODIE>
A; Cross-references: EMBL:Z73129; MIPS:YLL024c
A; Cross-references: EMBL:Z73129; MIPS:YL024c
A; Cross-references: EMBL:Z73129; MIPS:YL024c
A; Cross-refer
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N;Alternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000
C;Accession: S20139; S64772; S64775; S69383
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Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae. A;Reference number: S20139; MUID:89128457
A;Accession: S20139
                                                                                                                                                                                                                  dnaK-type molecular chaperone hsp70A - Caenorhabdit %;Alternate names: heat shock protein 70 A C;Species: Caenorhabditis elegans C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 C;Accession: JT0285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: involved in protein folding and assembling/disassembling C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
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A: Residues: 1-639 < PUR>
                                      Gene 64, 241-255, 1988
A;TitLe: The Caenorhabditis elegans hsp70 gene
A;Reference number: JT0285; MUID:88297155
A;Accession: JT0285
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A; Molecule type: DNA; mRNA
                                                                                                                                                                                    R; Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
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Best Local
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Pred. No. 0.
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1.22;
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diaK-type molecular chaperone HSPAIL - human
N;Alternate names: heat shock protein, 70K
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: A29160; I37561; I37562
R;Hunt, C.; Morimoto, R.I.
Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985
A;Title: Conserved features of eukaryotic hsp70 genes revealed by comparison
A;Reference number: A29160; MUID:86016721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-640 <SNU>
A;Cross references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352
A;Cross references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352
A;Note: genomic clones representing six distinct members of the hsp70 gene family wer A;Note: transcripts of hsp70A are abundant in control worms and also increase two- to A;Note: one of the three introns in hsp70A is in a position similar to an intron in D C;Generitos:
A;Gene: hsp70A
A;Map position: IV
A;Introns: 69/1; 331/3; 558/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein co C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M11717; GB:M15432; NID:g184416; PIDN:AAA52697.1; PID:g386785 A;Note: the authors mistranslated residues 463, 491, and 492 R;Drabent, B.; Genthe, A.; Benecke, B.J. Nucleic Acids Res. 14, 8933-8948, 1986 A;Title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepar A;Reference number: I37561; MUID:87066768 A;Accession: I37561
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A29160
                                                                                                                            C; Keywords:
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A;Map position: 6p21.3-6p21.3
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                                                                                                                                                                                                                                                                                                                                                                               A;Status: translation not shown;
A;Molecule type: DNA
A;Residues: 616-640 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X04676; NID:g32480; PIDN:CAA28381.1; PID:g32481
A;Accession: I37562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-22 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translation not shown; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type:
A; Residues: 1-64
                                                                                                                      A;Description: involved in protein folding and assembling/disassembling C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                        C; Function
                                                                                                                                                                                                                             A; Introns: #status
                                                                                                                                                                                                                                                                                                       A; Gene: GDB: HSPA1L; HSP70-HOM
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                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X04677; NID:g32482;
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SLFEGIDFYT 295

1 SLFEGIDLYT 10

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RESULT 15
S37394
dnak-type molecular chaperone hsc70 - slime mold (Dictyostelium discoideum)
R;Alternate names: heat shock cognate protein 70
C;Species: Dictyostelium discoideum
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: S37394
R;Haus, U; frommler, P; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Schl
EMBO J. 12, 3763-3771, 1993
A;Title: The heat shock cognate protein from Dictyostelium affects actin polymerization
A;Reference number: S37394
A;Molecule type: mRNA
A;Residues: 1-640 <HAND>
A;Ccession: S37394
A;Residues: 1-640 <HAND>
A;Ccession: S37394
A;Residues: 1-640 <HAND>
A;Ccoss-references: EMBL:X75263; NID:g433874; PIDN:CAA53039.1; PID:g433875
C;Genetics:
A;Gene: hsc70
C;Function: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: AffP; molecular chaperone
Query Match
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SLFEGIDLYT 10
Db 284 SLFEGIDLYT 293
Search completed: December 6, 2001, 07:58:27
Job time: 275 sec
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Minimum DB
Maximum DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2000
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sp_unclassified:*
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 6, 2001, 07:56:52; Search time 170.25 Seconds
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Q98899
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Q44350
Q44352
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Q9NJ92
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O9u667 littorina s
O9u669 littorina s
O9u665 littorina p
O9u666 littorina p
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O9u666 littorina p
P81159 aplysia cal
P81157 aplysia cal
O90520 oncorhynchu
O98899 fugu rubrip
O63718 rattus norv
O44350 chondrosia
O44350 petrobiona
O9d92 guancha lac
O44349 funiculina
         044351 eunicella c
Q98897 fugu rubrip
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Q9c7x7 arabidopsis
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45	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21	20
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## ALIGNMENTS

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RESULT
Q9U670
ID QS
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DT 01
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Best Local Similarity
Matches 8; Conserv
Q9U670 PRELIMINARY;
Q9U670;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
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SEQUENCE
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O9U667: 01-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                    Hohenlohe P.A.; "Heat-stressed genus Littorina."; "Beat-shock genes in the heat-stressed genus Littorina."; submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191828; AAF12787.1; -. HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                    Littorina plena.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                             InterPro; IPR001023; HSP70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=31219;
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79 SLFEGIDFY 87
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146 AA;
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16607 MW;
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88.9%;
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Last sequence update)
                                                                                                                                                 Score 40; DB Pred. No. 2.3; 0; Mismatches
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Q9U665;
Q9U665;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAF12784.1; -.
HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                   O9U669; PRELIMINARY; PRT; 155 AA.
O9U669; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                 Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
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                                                                                                                                                                                                               "Heat-shock genes in the heat-stressed genus Littorina.";
submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191826; AAF12785.1; -.
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                                                                                                                                                                    SEQUENCE
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PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Hohenlohe P.A.;
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NCBI_TaxID=31221;
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8; Conservative
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153 AA;
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155 AA;
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milarity 88.9%;
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17352 MW;
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17676 MW; C191F6E5B1F346C2 CRC64;
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Last sequence update)
Last annotation update)
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01-MAY-2000
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Eukaryota; Metazoa; Meotaenioglossa; Litt
NCBI_TaxID=31219;
                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
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8; Conserv
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8; Conservative
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158 %
 (TrEMBLrel. 13, (TrEMBLrel. 13,
                             PRELIMINARY;
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Created)
Last sequence update)
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"Heat-shock genes in the heat-stressed ge Submitted (OCT-1999) to the EMBL/GenBank/EMBL, AF191830; AAF12789.1; -. HSSP; P19120; IBA1.
InterPro; IPR001023; HSP70.
PRINTE; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
NON_TER 157 157
SEQUENCE 157 AA; 17834 MW; E8F743382B
                                                                                                                                                                                                                                                                                                                                                                                                                       Q9U671 PRELIMINARY; PRT; 158 AA. Q9U671; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                            InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                      "Heat-shock genes in the heat-stressed genus Littorina.", Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191824; AAF12783.1; -.
                                                                                                                                                                                                                                                                                                                                 Littorina Scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caer
Neotaenioglossa; Littorinoidea; Littorinidae;
NCBI_TaxID-31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oa; Mollusca; Gastropoda; Cae
Littorinoidea; Littorinidae;
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17887 MW;
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               Score 40; I
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dae; Littorina.
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P81159 PRELIMINARY;
P81159;
01-JUN-1998 (TrEMBLrel. 06,
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"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191829; AAF12788.1; -.
EMBL; P19180; 1BA1.
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Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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HEAT-SHOCK PROTEIN (FRAGMENT).
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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P81157;
O1-JUN-1998 (TrEMBLrel. 06, C
01-JUN-1998 (TrEMBLrel. 06, L
01-JUN-2001 (TrEMBLrel. 17, L
HEAT SHOCK 70 KDA PROTEIN A (
                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE-93077669; PubMed-1360013;
Kuhl D., Kennedy T., Barzilai A., Kandel E.;
Kuhl D., Kennedy T., Barzilai A., Kandel E.;
"Long-term sensitization training in Aplysia leads to
"Long-term sensitization training in Aplysia leads to
                                   PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
                                                                                                            PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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"Long-term sensitization training in Aplysia leads to an increa
"Long-term sensitization training in Aplysia leads to an increa
the expression of BiP, the major protein chaperon of the ER.";
J. Cell Biol. 119:1069-1076(1992)
-i- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF
-i- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
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                                                                                                                                                                                                                                          Aplysiidae; Aplysia.
NCBI_TaxID=6500;
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Eukaryota; Metazoa;
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NCBI_TaxID=6500;
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Eukaryota; Metazoa;
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01-FEB-1997
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98899;
Q98899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90520 PRELIMINARY; PRT; 278 AA.
Q90520;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
actinopterygii; Neopterygii; Teleostei; Euteleosteti;
Control of the processor                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kothary R.K., Jones D., Candido E.P.M.;
"70-Kilodalton heat shock polypeptides from rainbow trout: characterization of cDNA sequences.";
Mol. Cell. Biol. 4:1785-1791(1984).
EMBL; K02549; AAA49562:1; -.
HSSP; P08109; 1CKR.
InterPro; IPR001023; HSP70.
                                       Submitted (OCT-1996) to the EMBL/GenBank/DDBJ EMBL; Y08578; CAA69892.1; -. HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                    Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-85036330; PubMed-6092938;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSP70-3
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NCBI_TaxID-8022;
                                                                                                                                                          Lim E.H.
                                                                                                                                                                                                                                                                     NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                Tetraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00012; HSP70;
   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
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nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PRB-1997 (TERMBLrel. 02, Created)
-FBB-1997 (TERMBLrel. 02, Last sequence update)
-JUN-2001 (TERMBLrel. 17, Last annotation update)
KDA HEAT SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLFEGIDAY 9
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       IPR001023; HSP70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278
278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                        Takifugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278
30327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%;
88.9%;
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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4.9;
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       RRN OCC OR RRN
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RESULT
Q63718
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Best Local
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Best Local
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NON_TER
SEQUENCE 3
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Q63718;
                                                                                                         044350 PRELIMINARY; PRT; 467 AA. 044350; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat. HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D'Ambrosio E.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ EMBL; 227118; CAA81642.1; -.
HSSP; P08107; 1HJO.
                                                     Chondrosia reniformis.
Eukaryota; Metazoa; Porifera; Demospongiae;
Chondrosida; Chondrillidae; Chondrosia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK ROTEIN 70 (FRAGMENT).
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PRINTS; PR00301; HEATSHOCK;
PROSITE; PS00297; HSP70_1;
PROSITE; PS01036; HSP70_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001023; HSP70. Pfam; PF00012; HSP70; 1.
Borchiellini C.,
             SEQUENCE FROM N.A.
                                         NCBI_TaxID=68574;
                                                                                                 HSP70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat shock.
                                                                                                                                                                                                                                                          254 SLFEGIDFY 262
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8; Conserv
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455
455 AA;
                                                                                                                                                                                                                                                                                                                  Conservative
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Ęe
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455
50404 MW;
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40405 MW;
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88.9%;
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88.9%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                              Score 40; 1
Pred. No. 8
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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6.8;
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3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                             11;
                                                                    Tetractinomorpha;
                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                           Length 455;
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RESULT
044352
1D 244352
AC 044
AC 044
DT 01
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Q9NJ92
RR OCC OCT DIT AC
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE
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Borchiellini C., Le Parco Y.;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF026520; AAC05564.1; -.

HSSP; P08109; 1CKR.

InterPro; IPR001023; HSP70.

Pfam; PF00012; HSP70; 1.
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044352;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
HSP70.
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EMBL; AF026517; AAC05362.1; -.
HSSP; PO8109; 1CKR.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS00329; HSP70_3; 1.
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                                                                  Eukaryota; Metazoa; Porifera; Calcarea; Calcinea; Clathrinida; Clathrinidae; Guancha.
                                                                                                                   Guancha lacunosa.
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Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
                                        NCBI_TaxID=115120;
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PROSITE; PS01036; HSP70_3; 1.
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PRINTS; PR00313; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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467 AA;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gallus gallus HSP	Human Hsp72 (heat	Human heat shock p	Heat shock protein	ES  Description							

Identifying mutant peptides from heat-shock protein 70, for treatment of cancer  $\dot{}$ 

WPI; 2000-013251/01.

Triebel F,

Gaudin C;

(INSR ) INST ROUSSY GUSTAVE

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AAR03931	AAG53605	AAG53606	AAG27768	AAW80645	AAY85808	AAB61974	AAR43002	AAB22938	AAW01638	AAB82535	AAB23651	AAB23649	AAY17408	AAY17407	AAW54364	AAR03927	AAG24331	AAG24332	AAG24333	AAG02174	AAB58386	AAW22895	AAR03928	AAB23650	AAB82534	AAB23652	AAW54349	AAR43004	AAY88411	AAY88408	AAB23653	AAW10065	AAR03929
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## ALIGNMENTS

RESULT
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XX Iden Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HIA; immune defence; immunogenicity; specificity; human leucocyte antigen. AAY44199 standard; peptide; Heat shock protein 70 amino acid residues 286-294. AAY44199; 22-APR-1999; W09954464-A1. Homo sapiens. 15-FEB-2000 22-APR-1998; 28-OCT-1999. , , (first entry) 98FR-0005033 99WO-FR00957 9 8

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This peptide corresponds to amino acid residues 286-294 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (1) amplifying hsp70 and proceed the process of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 1.
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                                                      Claim 8; Page 15; 21pp; English
                                                                                                            of heat shock
                                                                                                                                      Lymphocytes useful for treating cancer, transformed human cells with induced and
                                                                                                                                                                                                                      WPI; 2001-290909/30.
                                                                                                                                                                                                                                                                                                                                (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HSP70) peptidic fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 4.3e+05;
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                                                                                                                                         recognizes specifically d increased membrane expression
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The amino acid sequence of fragment 1 relating

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
T cell
                           This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) Cloning the amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat shock
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                                                                                                                                                                                                 Identifying mutant peptides from heat-shock protein 70,
  of cancer -
                                                                                                                                                                                                                                                 WPI;
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sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colon
                                                                                                                                                                 Claim 10; Page 6; 56pp; French
                                                                                                                                                                                                                                                                                  Triebel F,
                                                                                                                                                                                                                                                                                                               (INSR ) INST ROUSSY GUSTAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heat shock
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Pred. No. 4.3
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The amino acid sequence of fragment 2 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membranes. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic T lymphocytes in a cell culture and/or induce these cells to secrete cytotoxic factors (specifically interlexin-2, interferon-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HIA (human leucocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 15; 21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abastado JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-1999;
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nilarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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Pred. No. 0.0029;
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                                                                               The amino acid sequence of fragment 3 relating to position 286-295 of the human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccinated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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Matches 9; Conserv
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                                                              intracellular infected cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abastado JP, Bartholeyns J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat shock protein 70 (HSP70)
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Human heat shock protein SHSP70 amino acid sequence.
                                                                                                                                                                                                                                                                                  This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14922-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including
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                                                                           AAY88410 standard;
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Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
                                                                                                                                                                       This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p2l.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
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Similarity 88.9
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                  (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
                                      01-JUN-1995;
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                                                                                                                                 depression; nephrotic syndrome; SHSP70.
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                      stress and response and dia
rheumatisms, schizophrenia,
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                                                                                                                                           Disclosure; Fig 6; 11pp; Japanese.
                                                                                                                                                                                         Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its applica
                                                                                                                                                                                                                                                                                               01-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 14q22-24;
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                                                 The invention relates to a novel method of identifying compounds that conhibit proliferation of cells comprising contacting a test compound with care a cell which overexpresses Hsp72 (heat shock protein 72), and determining continually Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of complex which is detected. The invention also relates to a method of comprising compounds that inhibit Hsp72-mediated JNK phosphatase contivation, comprising contacting a test compound with a cell which care activation, comprising contacting a test compound with a cell which care determining if the compound inhibits JNK phosphatase activity. The compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity. The compound inhibitors of Hsp72 or JNK phosphatase activity. The compound identified as concers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 is used to treat a proliferative disorder such carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 function are administered to a patient conditions campound that inhibit Hsp72 function are administered to a patient conditions or activity relative to normal levels. The present sequence represents the manner of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examples;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Hsp72; heat shock protein 72; chromosome 6p21.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lllllll |
200 slfegidfy 208
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DB; AAA97541.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 16B; 77pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 624 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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RESULT 1
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   Matches
                                                                                                                                                                                                                                  According
635 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus HSP (chkhsp70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR03930 standard;
                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9002564-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hsp70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR03930
                                                                                                                                                                                   Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp?0 - AAR03922);
2. Bacillus megaterium (Bmehsp?0 - AAR03923);
3. E. coli (dnaK - AAR03924);
                                                                                                                                                                                                                                                                  Disclosure; Fig 2.1-2.14; 86pp; English
                                                                                                                                                                                                                                                                                                                   WPI; 1990-115820/15
                                                                                                                                                                                                                                                                                                                                                         (CODO-) CODON
                                                    Sequence
                                                                        Mycobacteria
                                                                                  The proteins 
vaccines and
                                                                                                                                                                                                                          including "O" (?) at position
                                                                                                                                                                                                                                                                                               Proteins homologous to heat shock proteins
                                                                                                                                                                                                                                                                                     in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 slfegidfy 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heat shock protein; Trypanosoma cruzi; vaccines; HSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conserv
1 Similarity
8; Conserv
                                                                                                                                                                                                                                  to the legend of Fig 2, the G. gallus HSP sequence acid residues, the sequence itself has only 634,
                                                                                                                                                                                                                                                                                                                                     Faulds D,
                                                                                                                                                                                                                                                                                    and diagnosis for species of eg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
    Conservative
                                                                               6. Rat rattus (rathsp/0 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapiens (humhsp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03931);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03932).
having homology to hsp's of T. cruzi can be used diagnosis involving e.g. Trypanosoma, Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                        species.
                                                      A
                                                                                                                                                                                                                                                                                                                                                                             88US-0243474
                                                                                                                                                                                                                                                                                                                                                                                                 89WO-0003955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "residue given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.3%;
                                                                                                                                                                cruzi (tc70kd - AAR03925);
cruzi (AAR03926);
             91.3%;
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Pred.
    0;
    Score 42; DB Pred. No. 1.8; 0; Mismatches
                                                                                                                                                                                                                            634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
No.
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                        DB 11;
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                                                                                                                                                                                                                                                                                               from Trypanosoma cruzi -
                                                                                                                                                                                                                                                                                     Mycoplasma or Mycobacteria,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 624;
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                       Length 634;
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slfegidfy 294

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RESULT 1
AAR03929
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Qy
                      Query Match
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                                                                                                                      6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapiens (humhsp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03932).
The proteins having homology to hsp's of T. cruzi can be used
                                                                                                                                                                                                                                                            According to the legend of Fig 2, the H. sapiens HSP sequence has 641 amino acid residues, the sequence itself has only 640, including "O" (?) at position 640.

Fig. 2 provides an alignment of heat shock proteins from a variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR03929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR03929 standard;
                                                                                                                                                                                                                                                                                                                                                                                                  Dragon E, Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-1990
                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                                                                                                                                         proteins homologous to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                        (CODO-) CODON
                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-1988;
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||||||| |
289 slfegidfy 297
                                                                              Sequence
                                                                                                    Mycobacteria species.
                                                                                                               vaccines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
 1 SLFEGIDIY 9
                                                                                                                                                                                                                                                   organisms:
                                                                                                                                                                                                                                                                                                                                                                              1990-115820/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heat shock
                       Similarity 88.9
8; Conservative
                                                                                640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSP (humhsp70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                 diagnosis involving e.g. Trypanosoma, Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                               88US-0243474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "residue given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; Trypanosoma cruzi; vaccines;
                                                                                                                                                                                                     Bacillus megaterium (Bmehsp70 - AAR03923);
E. coli (dnaK - AAR03924);
T. cruzi (tc70kd - AAR03925);
T. cruzi (AAR03926);
                                                                                                                                                                                                                                                   M.hyopneumoniae (Mhyhsp70 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 640 AA
                                   91.3%;
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                        0;
                       Score 42; DB 11;
Pred. No. 1.8;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification"
                                               Length 640;
                         Indels
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AC AAB2
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DT 05-J
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DE Huma
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KW ATPa
KW ATPa
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W W O22
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AAW10065
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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Best Local
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                             The CDNA encoding the present sequence, human heat shock protein (HSP70), is located on human chromosome 6p 21.3-22 and 14g 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained
                                                             immune response; infectious disease; malaria; cytotoxic T cell cytostatic; immunostimulant; cellular immune response inducer;
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
 WO200049041-A1
                         Homo sapiens.
                                                 protozoacide;
                                                                           ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell;
                                                                                                                Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
                                                                                                                                          05-JAN-2001
                                                                                                                                                                                           AAB23653 standard;
                                                                                                                                                                                                                                                                                                                                                                                                     stress load.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT58086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-081088/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human heat shock protein 70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW10065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW10065 standard; Protein; 640 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOKE-) HOKEN KAGAKU
                                                                                                                                                                                                                                                           |||||||| |
286 slfegidfy 294
                                                                                                                                                                                                                                                                                                            Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                   1 SLFEGIDIY 9
                                                                                                                                                                                                                                                                                                                                                                           640 AA;
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                   leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95JP-0158581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95JP-0158581.
                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                       91.3%;
88.9%;
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                                                   cancer
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Pred. No.
                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                    Length 640;
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RESULT 1
AAY8408
ID AAY88408
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer \,
   WPI; 2000-264458/23.
N-PSDB; AAA15620.
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                                                                                                                                                       01-JUN-1995;
                                                                                                                                                                                                                   01-JUN-1995;
                                                                                                                                                                                                                                                                               07-MAR-2000
                                                                                                                                                                                                                                                                                                                                        JP2000069999-A.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             depression; nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human heat shock protein HSP70 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY88408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY88408 standard; Protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 49-52; 72pp; Japanese.
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                                                                                           (HOKE-) HOKEN KAGAKU KENKYUSHO
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Search completed: December Job time: 609 sec
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                                                                                                                                                                   Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                               This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p2l.3-22 and 14Q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                           Sequence . 640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 1; 11pp; Japanese.
                                                                                          1 SLFEGIDIY 9
||||||| |
286 slfegidfy 294
                                                                                                                                                                                      91.3%;
                   6, 2001, 08:04:01
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Minimum DB
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Listing first 45 summaries
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1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSB/qcgdata/geneseq/geneseqp/AA1981.DAT:*
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SIDSB/gcgdata/geneseq/yeneseqp/AA198.DAT:

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51
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4.024 million cell updates/sec
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## SUMMARIES

Result

Query

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AAW10065	AAR03929	AAR03930	AAB23252	AAY88413	AAY88412	AAY88410	AAY88409	AAB97603	AAB97602	AAY44200	ID
Human heat shock p	Homo sapiens HSP (	Gallus gallus HSP	Human Hsp72 (heat	Human heat shock p	Heat shock protein	Heat shock protein	Heat shock protein	Description			

45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	
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AAB54038	AAR03932	AAG44949	ū	AAB61974	33	ω	AAG24333	AAW80645	AAY85808	AAR43002	AAB22938	AAW01638	AAB82535	AAB23651	AAB23649	AAY17408	AAY17407	AAW54364	AAR03927	AAG02174	AAB58386	AAW22895	AAB97601	AAY44199	AAR03928	AAB23650	AAB82534	AAB23652	AAW54349	AAR43004	AAY88411 .	4	AAB23653	
Human pancreatic c		protein	mays	$\vdash$			Arabidopsis thalia		S. pneumoniae deri	_	GFP-HSC70 fusion p		Human heat shock p	heat shock	shock	Mouse heat shock c	. Human heat shock c	Heat shock cognate		Human secreted pro	Lung cancer associ			ck prot	_	eat shock	heat	heat shock	Human heat shock 7	œ.		4	Human heat shock p	

## ALIGNMENTS

RESULT AAY44200 س

AAY44200 standard; peptide; 10 Ą

AAY44200;

15-FEB-2000 (first entry)

Heat shock protein 70 amino acid residues 286-295.

T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen. Human; heat shock protein 70; hsp70; identification; tumour; mutation;

Homo sapiens

WO9954464-A1

28-OCT-1999.

22-APR-1999; 99WO-FR00957.

22-APR-1998; 98FR-0005033.

(INSR ) INST ROUSSY GUSTAVE

Triebel F, Gaudin C;

WPI; 2000-013251/01

Identifying mutant peptides from heat-shock protein 70, for treatment of cancer -

Claim

10;

Page 6;

56pp;

French.

of the

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RESULT
AAB97602
CC heat shock protein 70 (hsp70). The invention relates to a method of CC identifying peptides, derived from hsp70 that stimulate a tumour-specific CC T cell response. Identification of the hsp70 peptides that have at least CC one mutation or alteration compared with the native sequence, and induce CC encoding DNA from one or more tumours; (i) cloning the amplified CC sequences into a vector that can be replicated in bacteria; CC (iii) sequencing fragments in each cultured bacterial colony to identify CC any hsp70 mutations, and (iv) determining the immunogenicity of the CC mutant peptides identified. The peptides, optionally formulated with an CC agent that induces cellular stress, are used for treatment of cancer, CC cancers of head and neck, particularly kidney cancer). The peptides may CC also be used to increase the proportion of tumour specific cytotoxic factors (specifically interleukin-2, interferon-gamma and CC tumour necrosis factor), particularly where the cells are used to continuogenicity and high specificity for particular HLA (human leucocyte anticen) alleles
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Best Local Similarity
Matches 10; Conserv
                                                        of heat shock protein
                                                                                                                      WPI; 2001-290909/30.
                                                                                                                                                                                                                                                                                                                                                           HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB97602 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen) alleles.
                          Claim 8; Page 15; 21pp;
                                                                        Lymphocytes transformed
                                                                                                                                                    Abastado JP,
                                                                                                                                                                                                                15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB97602
                                                                                                                                                                                  (IDMI-) IDM IMMUNO-DESIGNED MOLECULES
                                                                                                                                                                                                                                             29-SEP-2000; 2000WO-EP09530.
                                                                                                                                                                                                                                                                                                       WO200129190-A1
                                                                                                                                                                                                                                                                                                                                                                                                                            Heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                     sapiens.
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                                                                          useful for treating cancer, recognizes human cells with induced and increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corresponds to amino acid residues 286-295 rotein 70 (hsp70). The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑA;
                                                                                                                                                    Bartholeyns
                                                                                                                                                                                                                99EP-0120484.
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                                                                                                                                                                                                                                                                                                                                                                                                                         (HSP70) peptidic
                            English
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Pred. No. 0.00031;
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                                                                                     specifically
                                                                          membrane expression
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The aming acid sequence of fragment 2 relating to position 286-295

of.

epitopes

are mutated

prior to

being

The amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSPs on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the

Claim 8; Page 15; 21pp; English.

heat shock protein

Lymphocytes useful for treating cancer, recognizes transformed human cells with induced and increased of heat shock protein -

specifically membrane expression

WPI; 2001-290909/30

Abastado JP,

Bartholeyns

(IDMI-) IDM IMMUNO-DESIGNED MOLECULES

15-OCT-1999;

99EP-0120484

29-SEP-2000; 2000WO-EP09530

26-APR-2001. WO200129190-A1

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ARBSULT ARABOLT ARABOTT ARABOT
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10; Conser
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or intracellular infected cells.
                                                                                                                                                          This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including
                                                                                                                                                                                                                                                                                                  Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
                                                                                                                        Sequence
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                                                                                                                                                rheumatisms, schizophrenia, depression
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Matches 9; Conserv
                                                                                 Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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                                                                                                                                                                                                       Human heat shock protein SHSP70 amino acid sequence
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N-PSDB; AAA15622.
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Homo sapiens

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                                                                                                                                                                                                                                                                                                                     01-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP2000069999-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY88413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY88413 standard; Protein; 554 AA.
                                                                                                                                                                                                                                                               (HOKE-) HOKEN KAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 9; Conser
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                                                                                                                                                                                                                 2000-264458/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              slfegidfyt 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heat shock protein SHSP70 amino acid sequence
                                                                                                                                   continuous
                                                                                                                                   transcription of intracellular HSP70mRNA under continuous load of stress in a human being and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95JP-0158581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0257146
                                                                                                                                                                                                                                                                                                                     95JP-0158581
                                                                                                                                                                                                                                                                                                                                                                        99ЛР-0257146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred.
                                                                                                                                                                                                                                                                  X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            load in a human
                                                                                                                                                                 acute
                                                                                                                                      application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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This sequence represents the human heat shock protein SHSP70 amino acid

activity of the

Disclosure;

Fig 6; 11pp; Japanese

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RESULT
AAB23252
ID AAB2
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence. Human heat shock proteins are located on chromosomes 6p21.3-2: and 14q22-24. The invention relates to the abnormal transcription of intracellular HSF70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSF70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome.
            The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72. Optionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase activation, comprising contacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity. The compounds identified as inhibitors of Hsp72 or JNK phosphatase activity are useful for
                                                                                                                                                                                                                                                                                                     Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia, lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premallgnant condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB23252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB23252 standard;
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200054814-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Hsp72 (heat shock protein 72)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2001
                                                                                                                                                                                                                                                               Examples; Fig 16B; 77pp;
                                                                                                                                                                                                                                                                                                 1 ymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                    Volloch VZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PHYL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-2000; 2000WO-US07350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200
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                                                                                                                                                                                                                                                                                                                                                                                    2000-647056/62.
DB; AAA97541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hsp72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 90.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHYLOGENY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0125046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 2%;
                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6p21.3-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JNK phosphatase or Hsp72 is used to treat a proliferative disorder such as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention.
                                                                                                                                     According to the legend of Fig 2, the G. gallus HSP sequence 635 amino acid residues, the sequence itself has only 634, including "O" (7) at position 634.
Fig. 2 provides an alignment of heat shock proteins from a va
                                                                                                                       Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922):
                                                                                                                                                                                                        Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                                                                            WPI; 1990-115820/15
                                                                                                                                                                                                                                                                                                    Dragon E, Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                 Proteins
                                                                                                                                                                                                                                                                                                                                (CODO-) CODON
                                                                                                                                                                                                                                                                                                                                                           12-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hsp70; heat shock protein; Trypanosoma cruzi; vaccines;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR03930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR03930 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||| ||
286 slfegidfyt 295
                                                                                                                                                                                                                                    vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 9; Conserv
                                                                                                                                                                                                                                 homologous to heat shock proteins from Trypanosoma cruzi - usones and diagnosis for species of eg Mycoplasma or Mycobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                 987654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSP (chkhsp70).
                                                                                                                                                                                                                                                                                                                                                                                      89WO-0003955.
                                                                                                                                                                                                                                                                                                                                                           88US-0243474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "residue given
           Rat rattus (rathsp10 - AAR03927);

Xenopus laevis (x170 - AAR03928);

Homo sapiens (humhsp70 - AAR03929);

Gallus gallus (chkhsp70 - AAR03930);
                                                                                                         M.hyopneumoniae (Mhyhsp70 - AF
Bacillus megaterium (Bmehsp70
Zea mays (mzehsp70
                                                                    T. cruzi (AAR03926);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 634 AA
                                                                                . cruzi (tc70kd - AAR03925);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.2%;
90.0%;
                                                                                            coli (dnaK - AAR03924);
                                                                                                                                                                                                                                                                                                     Sias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as
 AAR03931);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "0" in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۳.
                                                                                                           - AAR03923);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                             has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                              used
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RESULT 1
AAR03929
99999×8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
"hes 9; Conserv
                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR03929 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11. Serratia marcescens (smahsp70 - AAR03932). The proteins having homology to hsp's of T. cruzi can be used vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma
                                                                                                                                                       of organisms:
                                                                                                                                                                                                                          Disclosure; Fig 2.1-2.14; 86pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR03929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacteria species.
                     The proteins 
vaccines and
                                                                                                                                                                o41 amino acid residues, the seque including "O" (7) at position 640. Fig. 2 provides an allorman
                                                                                                                                                                                                                                                                                                       Dragon E,
                                                                                                                                                                                                                                                                                                                                                   12-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens HSP (humhsp70).
                                                                                                                                                                                                   According
                                                                                                                                                                                                                                                 in vaccines
                                                                                                                                                                                                                                                          Proteins homologous to heat shock proteins from Trypanosoma cruzi - used
                                                                                                                                                                                                                                                                                                                             (CODO-) CODON
                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                      WO9002564-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 slfegidfyt 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                  1990-115820/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                     provides an alignment of heat shock proteins from a variety anisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922);
2. Bacillus megaterium (Bmehsp70 - AAR03923);
3. E. coli (dnaK - AAR03924);
4. T. cruzi (tc70kd - AAR03925);
5. T. cruzi (AAR03926);
6. Bat Tattin (AAR03926);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat shock protein; Trypanosoma cruzi; vaccines; HSP
                                                                                                                                                                                                   to the legend of Fig
                                                                                                                                                                                                                                                                                                       Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634 AA;
                                                                                                                                                                                                                                                and diagnosis for species of eg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                  6. Rat rattus (rathsp70 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapians (humhsp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03930);
10. Zea mays (mzehsp70 - AAR03931);
11. Serratia marcescens (smahsp70 - AAR03932).
having homology to hsp's of T. cruzi can be use diagnosis involving e.g. Trypanosoma, Mycoplasn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
           species.
                                                                                                                                                                                                                                                                                                                                                   88US-0243474.
                                                                                                                                                                                                                                                                                                                                                                          89WO-0003955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 640
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "residue given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                        Sias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .0%;
                                                                                                                                                                                      of Fig 2, the H. sapiens the sequence itself has
                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47;
Pred. No.
                                                                                                                                                                                                                          English.
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0.23;
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g
                                                                                                                                                                                                                                                Mycoplasma
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                                                                                                                                                                                         HSP sequence only 640,
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                     Mycoplasma
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Best Local Similarity
""tches 9; Conservi
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                                                                                                                         RESULT 12
AAB23653
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
"atches 9; Conserv:
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DX A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The cDNA encoding the present sequence, human heat shock protein (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW10065 standard; Protein; 640 AA.
05-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT58086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; heat shock protein 70; HSP70; primer; probe; detection;
intracellular; abnormal transcription; acute; chronic; sustained;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human heat shock protein 70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-1997
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                                                                                                AAB23653 standard; protein; 640 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOKE-) HOKEN KAGAKU KENKYUSHO KK
                                                   AAB23653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intracellular HSP70 mRNA in human acute and chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 slfegidfyt 295
                                                                                                                                                                                                                                  286 slfegidfyt 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      640 AA;
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90.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                        Score 47; DB 18;
Pred. No. 0.23;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                           Length 640;
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ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
                                                                                                                                                           Human heat shock protein Hsp70 protein sequence SEQ
                                                                                                                                                                                    ID NO:5.
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Homo sapiens

protozoacide;

leukaemia; cancer.

WO200049041-A1

24-AUG-2000

18-FEB-2000; 2000WO-JP00941

19-FEB-1999;

99JP-0041535

(SUME ) SUMITOMO ELECTRIC IND င္ပ

Shinbara N, Udono H,

WPI; 2000-543748/49.

Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer  $\,$ 

Claim 3; Page 49-52; 72pp; Japanese.

The present invention describes a fused protein (1) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (1) as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (1) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.

Sequence 640 AA;

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Query Match
Best Local Similarity
Matches 9; Conserv
  Conservative
            92.2%;
  0;
            Score 47; DB 21;
Pred. No. 0.23;
    Mismatches
                     Length 640;
    0;
    Gaps
     0
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RESULT 13 밁 Q

286

1 SLFEGIDIYT 10 slfegidfyt 295

AAY88408 standard; Protein; 640 A

AAY88408;

31-JUL-2000 (first entry)

Human heat shock protein HSP70 amino acid sequence

AAY88408
ID AAY8
XX
XX
AC AAY8
AC AAY8
AC Bum
AC Bu Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia;

depression; nephrotic syndrome

Homo sapiens

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RESULTI I ARAYBBILI ID AAYYBILI ID AAAYYBILI ID AAYYBILI ID AAYYBILI ID AAYYBILI ID AAYYBILI ID AAYYBI
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Best Local
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                                                                                                                                  Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                   Disclosure; Fig 4; 11pp; Japanese.
                                                                                                                                                                                                                       WPI; 2000-264458/23
                                                                                                                                                                                                                                                                                                                                01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human heat shock protein LHSP70 amino acid sequence
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                                                                                                                                                                                                                                                                             (HOKE-) HOKEN KAGAKU
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nephrotic syndrome; LHSP70.
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                                                                                                                                                                                                                                                                                                                                95JP-0158581.
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Pred. No.
                                                                                                                                                                                                                                                                             X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               schizophrenia;
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This sequence represents the human heat shock protein LHSP70 amino acid

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RESULT 1
ADARA 30004
ADARA 30004
ADARA 30004
ACC ADARA
AX ADARA
AX BALE
XX Sulf
XX Sulf
XX HSC7
XX HSC
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Best Local S
Matches 9
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  WPI; 1993-368422/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulphoglycolipid immobilising protein 1; sperm plasma membrane; HSC70B; mammalian; infertility; mycoplasma; HSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR43004 standard; protein; 641 AA.
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                                               Faulds DH,
                                                                                                                                                                                                           22-APR-1993;
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                                                                                                                                                                                                                                                                                                   W09321954-A
                                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                          (BERL-) BERLEX LAB INC.
(OTTA-) OTTAWA CIVIC HOSPITAL.
                                                                                                                                                                  24-APR-1992;
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286 slfegidfyt 295
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                                             Lingwood CA,
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40..115
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90.0%;
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"peptides comprising an intact domain from
the ATPase fragment of hsp70 are claimed;
the peptides are homologous to sequences
conserved between SLIP1 and 74.5kD
mycoplasma protein"
                                               Tanphaichitr N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               depression and nephrotic syndrome
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Pred.
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalian fertilisation decrease for detecting and treating infertility - using sulpho glyco lipid immobilising protein 1-sulphated-glyco moiety interfering compsn., for mycoplasma infection treatment
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                                                                                                                                                                                                                                                       Sequence
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286 slfegidfyt 295
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Matches 9
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MEDLINE=95028152; PubMed=7941740;

Clark M.W., Keng T., Storms R.K., Zhong W., F
Delaney S., Ouellette B.F.F., Barton A.B., Ka
"Sequencing of chromosome I of Saccharomyces
the 42 kbp Sp07-CENI-CDC15 region.";
Yeast 10:535-541(1994).
[3]
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P10591;
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EMBL; X77208; CAA54423.1; -.
EMBL; X77207; CAA54422.1; -.
EMBL; X74271; CAA55328.1; -.
HSSP; P19120; 1NGC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89128457; PubMed-2644626; Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUI-1989 (Rel. 11, Created)
01-CT-1994 (Rel. 30, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).
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                                                                                                                                                                                                                                                          SEQUENCE OF 590-641 FROM N.A. MEDLINE-85087943; PubMed-6096826; Ogden R.C., Lee M.-C., Knapp G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEAST
  SEQUENCE OF 91-97 AND 325-341.
STRAIN=S288C;
MEDLINE=95203288; PubMed=7895733;
                                                                                                                     REVISIONS TO Slater M.R.;
                                                                                                                                                                                        substrates.
Nucleic Aci
                                                                                                                                                                                                                               Ogden R.C., Lee M.-C., Knapp G.; "Transfer RNA splicing in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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PS00329; HSP70_2; 1.
PS01036; HSP70_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E.A.; genes of the yeast Saccharomyces cerevisiae."; 17:805-806(1989).
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ton A.B., Kaback D.B., Buss
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-i- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPE BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Volpe T., Warner J.R., McLaughlin C.S.; "Protein identifications for a Saccharomyces cerevisidatabase.";
                                                                                                                       INIT_MET
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 186-195.
STRAIN=ATCC 38531 / Y41;
MEDLINE=97089742; PubMed=8935650;
                                                                                                                                                             PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; ATP-binding; Mult
                                                                                                                                                                                                                                                                                                                               PIR;
                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACETYLATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Electrophoresis 15:1466-1486(1994).
                                                                                                                                                                                                                                                              SGD;
                                                                                                                                                                                                                                                                         YEPD;
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EMBL; L22015; AAC04952.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                    Piam;
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1 SLFEGIDLYT
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S42164; S42164.
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ATP-binding; Cim.
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ATP-binding; Cim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _PIG
HS71_PIG
P34930;
                                                                                                                                 the
                                                                                                                                                                                      "Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-289(1992).
Immunogenetics 35:286-289(1992).
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FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
THROUGH THEIR ABILITY TO RECOGNIZE MONNATIVE COMPORMATIONS OF
OTHER PROTEINS. THEY BIND EXTENDED PETIDE SEGMENTS WITH A NET
HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                          EMBL; M69100; -; NOT_ANNOTATED_CDS
PIR; S35718; S35718.
                                                                     use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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                                                                                                                                                                                                                                                                                                                                                           Bouquet Y.H.;
                                                                                                                                                                                                                                                                                                                                                                       Peelman L.J., de Weghe
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92175874;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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InterPro; IPR001023; HSP70.
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                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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Pred. No.
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, nucleotide sequence and expression hsp70 gene.";
Biochim. Biochips. Acta 1219:64-72(1994).
-!- FUNCTION: IN COOPERATION WITH OTHER CHAPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
"CDNA cloning and expression of stress-inducible rat hsp70 in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00012; HSP70; 1. PRINTS; PR00301; HEATSHOCK70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94368874; PubMed-8086479;
Lisowska K., Krawczyk Z., Widlak W., Wolniczek P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95012453;
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FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OPROANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
                                                                                                                                                                                             AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        injured rat brain.";
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Sciurognathi; Muridae; Murinae; Rat
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t heat inducible
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RX MEDLINE-9923476; PUBMEGG10216320;

RA OSIPIUK J., Walsh M.A., Freeman B.C., MOTIMOTO R.I., JOACHIMIAK A.;

RA OSIPIUK J., Walsh M.A., Freeman B.C., MOTIMOTO R.I., JOACHIMIAK A.;

RT "Structure of a new crystal form of human hsp70 ATPase domain.";

RL ACTA CLTYSTALLOGY. D 55:1105-1107(1999).

RL ACTA CLTYSTALLOGY. D 55:1105-1107(1999).

CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPBRONES, HSP70S STABILIZE COMERNIST RANGIATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN COC NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN COC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC COMPANIANCE AND DITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR CC PROTEIN TRANSLOCATION WITH HSP90. THEY PARTICIPATE IN ALL THESE COMPONATIONS OF OTHER PROTEINS. THEY PARTICIPATE IN ALL THESE COMPONATIONS OF OTHER PROTEINS. THEY BAND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES COUNTING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING COMPANIANCE CO
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SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
SEQUENCE FROM S., Madan A., Dickhoff R., Dors M., Madan A., Hi
ROWEN L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hi
LOTETZ C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
"Sequence of the human major histocompatibility complex class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drabent B., Genthe A., Benecke B.-J.;
"In vitro transcription of a human hsp 70 heat shock gene by extracts
prepared from heat-shocked and non-heat-shocked human cells.";
Nucleic Acids Res. 14:8933-8949(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hunt C., Morimoto R.I.;
"Conserved features of eukaryotic hsp70 genes revealed with the nucleotide sequence of human hsp70.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heat shock protein HSP70."
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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                   EMBL;
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L; M59828; AAA63226.1; -.
L; M59830; AAA63227.1; -.
L; AF134726; AAAD21816.1; -.
L; AF134726; AAD21815.1; -.
L; M11717; AAA52697.1; -.
L; M27443; AAA59844.1; -.
L; M24744; AAA59845.1; -.
L; X04676; CAA28381.1; -.
L; X04677; CAA28382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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SWISS-2DPAGE; P08107;
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                                                                                         Perry M.D., Aujame L., Shtang S., Moran L.A.;

Perry M.D., Aujame L., Shtang S., Moran L.A.;

"Structure and expression of an inducible HSP70-encoding gene from "structure.";

Gene 146:273-278(1994).

Gene 146:273-278(1994).

Gene 146:273-278(1994).

FREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF UNIVERSE THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE MONATIVE COMPORMATIONS OF OTHROUGH THEIR ABILITY TO RECOGNIZE MONATIVE COMPORMATIONS OF OTHROUGH THEIR ABILITY TO RECOGNIZE MONATIVE COMPORMATION OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94357449; PubMed=8076831; Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization and sequence of expression in mouse cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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A45871;
A25773;
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9; Conserv
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PS00329; HSP70_2; 1.
PS01036; HSP70_3; 1.
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-> S (IN REF. 3; AAD21815).
78F513118C96DE66 CRC64;
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Best Local Similarity
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771_BOVIN STANDARD; PRT; 641 AA.
0 HS71_BOVIN STANDARD; PRT; 641 AA.
0 27975; 027964;
1 01-NOV-1997 (Rel. 35, Created)
1 01-NOV-1997 (Rel. 35, Last sequence update)
1 15-JUL-1999 (Rel. 38, Last annotation update)
1 HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
1 HSP70-1.
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InterPro; | IPR001023; | HSP70. |
Pfam; | PF000102; | HSP70; |
PROSITE; | PS000397; | HSP70_1; |
PROSITE; | PS000329; | HSP70_2; |
PROSITE; | PS000329; | HSP70_3; |
PROSITE; | PS01036; | HSP70_3; |
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between
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"Aginactin, an agonist-regulated F-actin capping activity is associated with an HSC70 in Dictycatelium.";

J. Biol. Chem. 268:23267-23274(1993).

-I- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS OF THE CELL CORTEX AND CELL PROTRUSIONS.

-I- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONCENTRATION.
                        Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Boyidae; Boyinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P36415; DICTY.
DictyDb; DD01078; hspB.
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SEQUENCE FROM N.A.,
                                                                                                       Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Chaperone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                               284 SLFEGIDFYT 293
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                                                      Cetartiodactyla; Ruminantia;
                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
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I -> C (IN REF. 2).
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Pred. No. 0.
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RESULT 11
HS71_HUMAN
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Best Local :
                                    HS71_HUMAN STANDARD; PRT; 641 AA. P08107; P19790; O9UQMO; O9UQL9; O1-AUG-1988 (Rel. 08, Created) O1-FEB-1994 (Rel. 28, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2). (HSPA1A OR HSPA1) AND HSPA1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anim. Genet. 25:196-196(1994).

Anim. Genet. 25:196-196(1994).

PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLTY TO RECCENTIZE MONAFIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00301; HEATSHOCK70.

PROSTTE; PS00297; HSP70_1; 1.

PROSTTE; PS00329; HSP70_2; 1.

PROSTTE; PS01036; HSP70_3; 1.

ATP-binding; Chaperone; Heat shock; Multigene family.

ATP-binding; Chaperone; Heat shock; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
              Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001023; HSP70. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grosz M.D., Skow L.C., Stone R.T.;
"An AluI polymorphism at the bovine 70 kD heat-shock protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95030563; PubMed=7943958;
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Chordata;
Primates;
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Z. A.
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Pred. No. 0.13;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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PROSITE; PS00229; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multig
SEQUENCE 639 AA; 69749 MW;
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Phosphorylation.
INIT_MET 0
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SEQUENCE 638 AA
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Q06248;
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PROSITE;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat)
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions are as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sconzo G., Scardina G., Ferraro M.G.;
"Characterization of a new member of the sea urchin Paracent lividus hsp70 gene family and its expression.";
Gene 121:353-358(1992).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidea; Euechinoidea; Echinocea; Echinoida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X61379; CAA43653.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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SLFEGIDFYT
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PS00329;
PS01036;
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Best Local S
Matches 9
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01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
HSPB OR HSC70.
                                                                                                                                                                                                                                                                                                                                                                                                      HS7C_DICDI
P36415;
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS7A_CAEEL P09446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a converge the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization.";
Gene 64:241-255(1988).
-i- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Caenorhabditis elegans
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01-MAR-1989 (Rel.
01-FEB-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00299; HSP70_1; 1.
PROSITE; PS00329; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Mult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88297155;
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HSP-1 OR HSP70A.
                                         Noegel A.A., Schleicher M.;
"The heat shock cognate protein from Dictyostelium affects actin polymerization through interaction with the actin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M18540; AAA28078.1; PIR; JT0285; HHKW7A.
                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                Haus U.,
                                                                                                                                                               STRAIN=AX3;
                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                         MEDLINE=94008983; PubMed=8404847;
                                                                                                                                                                                                                                    NCBI_TaxID=44689;
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                                                                                                                   Trommler P., Fisher P.R.,
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A PROTEIN A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.2%;
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No.
                                                                                                                     Hartmann H.,
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ene family: a
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HS72_YEAST
P10592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL; X70684; CAA50019.1; ...

EMBL; X70684; CAA50019.1; ...
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Q28222;
01-JUL-1989
01-OCT-1994
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family; MHC SEQUENCE 638 AA; 69920 MW; D55076AOFFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.; "The hsc70 gene which is slightly induced by heat is the main virus inducible member of the hsp70 gene family."; FEBS Lett. 355:282-286(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00301; HEATSHOCK70.
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                                                                                                                                                                                                                                   284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPRETIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE COMPATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBERANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                             1 SLFEGIDLYT 10
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4 SLFEGIDFYT 293
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INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                              Similarity
9; Conserv
(Rel.
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                Length 638;
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InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.

YEPD; 9800; -. SGD; S0003947; SSA2.

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EMBL; X12927; CAA31394.1; -.
EMBL; Z73129; CAA97472.1; -.
EMBL; X97560; CAA66167.1; -.
PIR; S20139; S20139.
HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10592; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-I- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Protein identifications database.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garrels J.I., Futcher B., Kobayashi R., Volpe T., Warner J.R., McLaughlin C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Slater M.R., Craig
"The SSA1 and SSA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Las
HEAT SHOCK PROTEIN SSA2.
SSA2 OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                                                        This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 186-195.
STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C
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                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norbeck J., Blomberg A.; "Protein expression during exponential growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electrophoresis 15:1466-1486(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 91-97 AND 325-341.
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                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: PHOSPHORYLATED. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                      {\tt SWISS-PROT} entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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(APR-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=7895733;
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                                                                                                                                                                                                                              license agreement (See http://www.isb-sib.ch/announce/
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to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heuss-Neitzel D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae.";
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"Onchocerca volvulus heat shock protein 70 is a major immuno amicrofilaremic individuals from a filariasis-endemic area."

MOI. Biochem. Parasitol. 33:229-236(1989).

-i- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC ARE

-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                 SEQUENCE FROM N.A.

SPONENCE FROM N.A.

SPONENCE FROM N.A.

L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;

Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;

Molecular cloning and expression of a Penicillium citrinum

"Molecular cloning and expression of a Penicillium citrinum

allergen with sequence homology and antigenic cross-reactivit;

submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

-i- SIMILARITY: BELIONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PROSITE;
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20-AUG-2001 (Rel. 40, Created)

20-AUG-2001 (Rel. 40, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation updat

HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 1
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HSSP; P19120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penicillium citrinum.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium
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NON_TER 1 1
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PF00012; HSP70; 1.
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9; Conserv
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PS00329; HSP70_2; PARTIAL.
PS01036; HSP70_3; 1.
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322 AA;
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35614 MW;
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pfam; pF00012; HSP70; 1.

pRINTS; pR00301; HEATSHOCK70.

pROSITE; pS00329; HSP70_2; 1.

pROSITE; pS01036; HSP70_3; 1.

ATP-binding; Chaperone; Heat shock; Allergen.

NON_TER 1 1
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Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P08106;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U64207; AAB06397.1; -. HSSP; P19120; 3HSC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-86304452; PubMed-3017985; Morimoto R.I., Hunt C., Huang S.-
                                                                                                                                                                                    PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB
                                                                                                                                                                                                                                                                                                                                   HSSP; P19120; TATR.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J02579; AAA48825.1;
PIR; A25646; A25646.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 261:12692-12699(1986).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Angeletti B., Passarelli F., Orru D., D'Ambrosio E.;

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BOTCHiellini C., Le Parco Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ date EMBL; AF026517; AAC05362.1; -.
HSSP; P08109; ICKR.
InterPro; IPR00103; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00101; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
O44352 PRELIMINARY; PRT; 467 AA.
044352;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
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Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha; Chondrosida; Chondrillidae; Chondrosia.
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HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
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Borchiellini C., Le Parco Y.;

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases

EMBL; AF026520; AAC05364.1; -.

HSSP; P08109; ICKR.
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Pfam; PF00012; HSP70; 1.

PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS01036; HSP70_3; 1.
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Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;
Petrobiona.
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                                                                                                                   DB 5;
                                                                                                                  Length 467;
                                                                                             Indels
                                                                                               0
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0;

90.0%;

Pred. No.

0.19;

Mismatches

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Indels

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PRESULTS
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Best Local S
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                                                                                                                                                                                                                                                                        Q90520 PRELIMINARY; PRT; 278 AA.

Q90520;

Q90520;

Q90520;

Q90520;

Q1-NOV-1996 (TrEMBLrel. 01, Created)

Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)

Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)

Q101-UN-2001 (TrEMBLrel. 17, Last annotation update)

ENAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENY).

ENAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENY).

CONCORDING TROUT TRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
NON_TER 1 1
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the expression of BIP, the major protein chaperon of the ER.";
J. Cell Biol. 119:1059-1076(1992).
I DIUTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93077669; PubMed-1360013; Kuhl D., Kennedy T., Barzilai A., Kar "Long-term sensitization training in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aplysia californica
Eukaryota; Metazoa;
Aplysiidae; Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z15039; CAA78757.1; -. HSSP; P19120; 1BA1.
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Kothary R.K., Jones D., Candido E.P.M.; "70-Kilodalton heat shock polypeptides characterization of cDNA sequences."; Mol. Cell. Biol. 4:1785-1791(1984).
EMBL; K02549; AAA49562.1; -.
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                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=85036330; PubMed=6092938;
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nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLFEGIDFYT 147
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220 AA;
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24684 MW;
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Mollusca; Gastropoda; Opisthobranchia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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in Aplysia leads to an
chaperon of the
                                                                                                                                                                                                                                                                                                                              Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220
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                                                                                                                   rainbow
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ER.";
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Q63718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; Multigene family.
                                                                                                                                                                                                                                                                   Heat shock.
NON_TER
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q98899;
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InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                   InterPro; IPR001023; HSP70.
pfam; pF00012; HSP70; 1.
pRINTS; pR000301; HEATSHOCK70.
pROSITE; pS00297; HSP70_1; 1.
pROSITE; pS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-1996) to the EMBL/GenBank/DDBJ EMBL; Y08578; CAA69892.1; .. HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-TUN-2001 (TrEMBLrel. 17, Last annotation update)
70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
                                Q63718 PRELIMINARY; PRT; 455 AA. Q63718; PRT; 455 AA. Q63718; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation HEAT SHOCK ROTEIN 70 (FRAGMENT). Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSP70-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                  Lim E.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=31033;
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                                                                                                                                                               268
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                                                                                                                                                                                                           Similarity 90.0
9; Conservative
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278 AA;
                                                                                                                                                                                                                                                                    367
367 i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                     AA;
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30327 MW;
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40405
            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%;
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Pred. No.
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Pred. No. 0.
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                                                                                                                                                                                                           core 47; DB red. No. 0.5; Mismatches
                                                                                                                                                                                                                                                                      8CD3DD8DF6E3C2CA
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0.36;
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Query Match
Best Local Similarity
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Best Local
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O9U671;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9U665 PRELIMINARY; PRT; 157 AA.

O9U665 O1-MAY-2000 (TERMBLrel. 13, Created)

O1-MAY-2000 (TERMBLrel. 13, Last sequence update)

O1-JUN-2001 (TERMBLrel. 17, Last annotation update)
                                                                                                                   "Heat-shock genes in the heat-stressed genus Littorina."; Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF191824; AAF12783.1; -. HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191830; AAF12789.1; -.
HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Littorina plena.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                              SEQUENCE
                                                                                           InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                  Hohenlohe P.A.;
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                               PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEAT-SHOCK PROTEIN (FRAGMENT).
                                                           YON TER
                                                                     ON_TER
                                                                                                                                                                                                     CBI_TaxID=31221;
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                                                                                                                                                                                                                                                                                                                                                                                 84
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                                                                                                                                                                                                                                                                                                                                                                                 SLFEGIDFYT 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                similarity
9; Conserv
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157 AA;
                                              158 /
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                                              Α,
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17887 MW;
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Score 47;
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                                              B41E5356A24CAD2F CRC64;
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DB 5;
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01-MAY-2000 (
01-MAY-2000 (
01-JUN-2001 (
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
HEAT-SHOCK PROTEIN (FRAGMENT).
                                NON_TER
                                                                                                                                                                                       Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191839; AAF12788.1; -.
HSSP; P19120; 1BA1.
                                                                                        HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Neotaenioglossa; Lit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=31219;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAT-SHOCK PROTEIN HSC70.
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   SEQUENCE
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9; Conserv
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158 AA;
   158
158 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               oa; Mollusca; Gastropoda; Cae
Littorinoidea; Littorinidae;
   158
17891
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90.0%;
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Pred. No. 0.19
0; Mismatches
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   B41E5356BCECAD2F CRC64;
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Query Match

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SEQUENCE
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094104;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paul S.P., Graves D.C.;
"Phylogeny and sequence analysis of Pneumocystis carinii Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U71151; AAD09565.1; -.
HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; UNKNOWN_1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                        Littorina plena.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caen
Eukaryota; Metazoa; Littorinoidea; Littorinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001023; HSP70.
InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
                                                                                                         SEQUENCE FROM N.A.
Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191828; AAF12787.1; -.
HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                       Q9U667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pneumocystis
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                                                                                                                                                                                                                                                                                          Q9U667;
                                                                                                                                                                                                                                     HSC70
                                                     SEQUENCE
                                                                                     PROSITE; PS01036; HSP70_3; 1
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                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Pred. No. 0.61
1; Mismatches
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         Score
Pred.
                                                      C3F3556A1AF438BB CRC64;
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         DB 5;
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                                                                                                                                                                                                              Caenogastropoda;
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                                                                                                                                                                                                     Littorina
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                     Length 146;
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"Heat-shock genes in the heat-stressed submitted (OCT-1999) to the EMBL/GenBar EMBL; AF191825; AAF12784.1; -. HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID-31221;
                                                NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01036; HSP70_3; 1.
                                                                              InterPro;
PROSITE; F
                                                                                                         "Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191826; AAF12785.1; -.
                                                                                                                                                                  Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID-31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                     HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                  HSSP; P19120; 1BA1.
                                                                                                                                       Hohenlohe P.A.;
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Copyright (c) 1993 - 2000
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044350 chondrosia
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01-MAY-1999 (TrEMBLrel. 10, Last s
01-JUN-2001 (TrEMBLrel. 17, Last s
HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; UNKNOWN_1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification, characterization, and expression of the BiP endoplasmic reticulum resident chaperonins in Pneumocystis carinii."; Infect. Immun. 64:4463-4471(1996).
EMBL; U80967; AAD00455.1; -.
HSSP; P19120; 3HSC.
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Eukaryota; Fungi; Ascomycota; Pneumo
Pneumocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97045128; PubMed=8890193;
Stedman T.T., Buck G.A.;
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                  Heat shock.
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InterPro; IPR000169; Thiolprot_act_site
Pfam; PF00012; HSP70; 1.
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286 SLYEGIDLYT 295
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645 AA;
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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US-08-797-358B-3
US-08-637-763B-8
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US-09-170-354-8
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US-08-487-890A-19
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Query Match 88.2%; Score 45; DB 4; Length 643; Best Local Similarity 80.0%; Pred. No. 0.6; Matches 8; Conservative 1; Mismatches 1; Indels 0; Ga	ESULT 1  Sequence 3, Application US/08797358B  Sequence 3, Application US/08797358B  Patent No. 6368478  GENERAL INFORMATION: INTRACELLULAR VITAMIN D BINDING PROTEIN TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN NUMBER OF SEQUENCES: 9  CORPERAL INFORMATION: INTRACELLULAR VITAMIN D BINDING PROTEIN NUMBER OF SEQUENCES: 9  COMPUTER READABLE FROM:  COUNTRY: 4370 La Jolla Village Drive, Suite 700  STATE: California  COUNTRY: United States  COUNTRY: United States  COMPUTER READABLE FROM:  MEDIUM TIPE: Floppy disk  COMPUTER READABLE FROM:  MEDIUM TIPE: Floppy disk  COMPUTER READABLE FROM:  MEDIUM TIPE: Floppy disk  COMPUTER IBM PC Compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARRE: Detentin Release #1.0, Version #1.25  COMPUTER PAPLICATION NUMBER: US/08/797, 358B  FILING DATE: 11-Feb-1997  FILING DATE: 11-Feb-1997  FILING DATE: 12-FEB-1996  ATTORNEY/ACENT INFORMATION:  NAME: Campbell, Cathryn A.  REFERENCE/DOCKET NUMBER: 31, 815  REFERENCE/DOCKET NUMBER: 3-00/011, 491  FILING DATE: 1619 533-9001  TELEFOMUNICATION INFORMATION:  NAME: Campbell, Cathryn A.  REFIRENCE/DOCKET NUMBER: 9-CE 3165  TELECOMMUNICATION INFORMATION:  REFIRENCE/DOCKET NUMBER: 31, 815  REFERENCE/DOCKET NUMBER: 9-CE 3165  TELECOMMUNICATION INFORMATION:  NAME: Campbell, Cathryn A.  REFIRENCE/DOCKET NUMBER: 9-CE 3165  TELECOMMUNICATION INFORMATION:  TELEPHONE: (619) 533-9001  TELEFOM: 535-901  TELEF	28 33 64.7 913 2 US-08-478-373-5 29 33 64.7 913 3 US-08-474-671-5 30 33 64.7 913 3 US-08-474-671-5 31 33 64.7 913 3 US-08-897-438-5 31 33 64.7 913 3 US-08-997-438-5 32 62.7 230 2 US-08-706-706-18 33 32 62.7 230 2 US-08-706-706-18 34 32 62.7 230 3 US-08-98-692-52 36 32 62.7 494 3 US-08-98-692-52 36 32 62.7 494 3 US-08-98-692-52 38 32 62.7 494 5 US-08-98-692-52 39 32 62.7 494 5 US-08-664-39 39 32 62.7 494 5 US-08-656-664-39 39 32 62.7 495 3 US-08-488-2 40 32 62.7 571 3 US-08-488-2 41 32 62.7 571 3 US-08-656-664-37 42 32 62.7 571 3 US-08-656-664-37 43 32 62.7 571 3 US-08-656-664-37 44 32 62.7 571 3 US-08-656-664-11 45 32 62.7 578 3 US-08-656-664-11 Sequence 11 45 32 62.7 578 3 US-08-656-664-11 Sequence 11
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                                                                                                                                                   Sequence 6, Application US/08637763B Patent No. 5849559 GENERAL INFORMATION:
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Best Local :
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERAE: Patentin Release #1.0, Version #1.25
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 646 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wittrup, Dr. Karl D. APPLICANT: Robinson, Anne S.
                                                                               TITLE OF INVENTION: AI NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
COUNTRY:
                              CITY: Washington
                                                STREET:
                                                ADDRESSEE: Morrison & Foerster STREET: 2000 Pennsylvania Avenue,
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                                                                                                                     VAN DER WOUW, MONIQUE J.A. et al
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80.0%;
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Pred. No. 1.
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RESULT 4
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Best Local Similarity
Thehes 6; Conserve
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TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                    REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: ARABINOXYLAN DEGRADING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0: FILING DATE: 25-AUG-1996 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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    TOPOLOGY:
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|: 332 amino acids
   amino acid
   GY: linear
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66.7%;
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    Mismatches

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RESULT 6
US-09-170-354-8
US-09-170-354-8
; Sequence 8, Application US/09170354
; Patent No. 6066356
; PATENT INFORMATION:
; APPLICANT: VAN DER WOUW, MONIQUE J.A. et al
; APPLICANT: ARABINOXYLAN DEGRADING ENZYME
                                                                                                                                                                                                                                                                                                                                                   ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-170-354-6
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/170,354
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/637,763
FILING DATE:
APPLICATION NUMBER: 08/637,763
FILING DATE:
APPLICATION NUMBER: 08/637,763
FILING DATE:
APPLICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3615-0066.00
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09170354 Patent No. 6066356
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morrison & Foerster STREET: 2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                          2 LFEGIDVYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                      332 amino acids
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Pred. No.
                                                                                                                                                                                                                                                                              Score 34; DB 3; Pred. No. 39;
                                                                                                                                                                                                                                                              Mismatches
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39;
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                                                                                                                                                                                                                                                                                               Length 332;
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                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08727308 Patent No. 6020176 GENERAL INFORMATION:
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TELEFAX: (202) 887-0750
TELEFAX: (202) 887-0750
TELEFAX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
COMPUTER: PC COMPATIBLE
COMPATING SYSTEM: PC COOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/170,354
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/637, FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULASHIGE, Kate H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yuji KAMIYA et al.
TITLE OF INVENTION: KAURENE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                PRIOR APPLICATION DATA:
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CITY: Washington
STATE: DC
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CITY: Washington
STATE: D.C.
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                                                    APPLICATION NUMBER: US/08/727,308 FILING DATE: October 8, 1996
                                   CLASSIFICATION:
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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APPLICATION NUMBER:
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                                                  October 8, 1996
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Pred. No.
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Sequence 19, Application US/08487890A Patent No. 5708149
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GENERAL II
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SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
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TELECOMMUNICATION INFORMATION:
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NAME: Warren M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Murdin, Andrew APPLICANT: Klein, Michel Title OF INVENTION: Trans
                                                  NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                        APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION UMBER: US 08/148,968
APPLICATION UMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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23 SLEPGVDVDT 32
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                                   TELEPHONE:
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linear
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Yang, Yan-Ping
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Harkness, Robin
Schryvers, Anthony
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                                     (416) 595-1155
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70.0%;
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                                                                         1038-466 MIS:jb
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Pred. No. 1e+02;
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; TYPE: amino acid
; STRANDEDNESS: sir
; TOPOLOGY: linear
US-08-487-890A-19
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US-08-478-435-19
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Best Local Similarity
Matches 5; Conserv
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                                                                                         TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/175,116
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                       REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                             FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             APPLICATION NUMBER: US 01 FILING DATE: 29-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 01
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOY-1994
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STREET: Su-
STRY: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                            TYPE: amino acid
STRANDEDNESS: sin
                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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Stewart, Michael 1
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Suite 701, 330 University Avenue
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                                                         36 amino acids
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Yang, Yan-Ping
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Harkness, Robin
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62.5%;
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Pred. No. 5
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Best Local Similarity bz..-
Thes 5; Conservative
                                                     Sequence 19, Application US/08478373 Patent No. 5922841
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Patent No. 59229
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Best Local Similarity
                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I REGISTRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 10
                                                                                                                                    28 FEGVAIYT 35
                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                           LENGTH:
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Suite 701, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                        36 amino acids
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Yang, Yan-Ping
Harkness, Robin
Schryvers, Anth
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Harkness, Robin
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                           Loosmore, Sheena
                                                                                                                                                                                                                                                                      linear
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62.5%;
Anthony
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Pred. No.
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Query Match
Best Local Similarity
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                                                                                                                                                                            Patent No.
                                                                                                                                                                                               Sequence 19,
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FILING DATE: 08-NOV-193
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-463 M
TELECOMMUNICATION INFORMATION:
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LOOSMO
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TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 19:
SEQUENCE CHARACTERISTICS:
I.ENGTHI.
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APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
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FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                  APPLICANT:
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 147
                                 APPLICANT:
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28 FEGVAIYT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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Suite 701, 330 Un
                            Chong, Pele
Gray-Owen, Scott
Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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                                                                                                                               Harkness, Robin
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                                                                                                           Schryvers, Anthony
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IBM PC compatible
                                                                                                                                              Loosmore, Sheena
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Pred. No. 5.
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TOPOLOGY: US-08-474-671-19
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US-08-483-577A-19
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICATION NUMBER: US 08
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 01
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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CITY: Toronto
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP; M5G 1R7
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                                                                                                       UMBER OF SEQUENCES:
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                                                             STREET:
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M5G 1R7
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                             Application US/08483577A
                                                             Suite 701, 330 Unviersity Avenue
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Klein, Michel
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Yang, Yan-Ping
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                                                                             Sim & McBurney
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07-JUN-1995
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                                                                                                                         Transferrin Receptor Genes
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62.5%;
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19,
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                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 07-JUN-199
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
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MEDIUM TYPE: Floppy disk
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                        STATE:
                                                                                                                                                          CITY: Toronto
                                                                                                                                                                      STREET:
                                                                                                                                                                                       ADDRESSEE:
                                                                                                            ZIP: M5G 1R7
                                                                                                                       COUNTRY:
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                                                                                                                                         Ontario
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6th Floor, 330 Un
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Klein, Michel
Klein, Transferrin Receptor Genes
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Yang, Yan-Ping
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Robin
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Pred. No. 5.
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/483,577
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/37,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-720
TELECATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
STRANDEENESS: single
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL T
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PCT-US95-13975-72
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Best Local Similarity 04...
""+" obes 5; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13975
FILING DATE: 26-OCT-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/329,883
FILING DATE: 26-OCT-1994
CLASSIFICATION BATA:
APPLICATION NUMBER: 08/329,883
FILING DATE: 26-OCT-1994
CLASSIFICATION:
RAPELICATION NUMBER: 39118-PCT
REGISTRATION NUMBER: 39118-PCT
TELECOMMUNICATION HUMBER: 39118-PCT
TELECOMMUNICATION 1278-0400
TELEFAX: (212)378-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 72, Application PC/TUS9513975 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cochran, Mark D.
APPLICANT: McDonell, Michael W.
TITLE OF INVENTION: Recombinant Feline Herpes virus
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 FEGIDVYT 10
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28 FEGVAIYT 35
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036
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STREET: 1185 Avenue of the Americas
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62.5%;
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                                                                                        Query Match
Best Local Similarity
Thes 5; Conserve
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Search completed: December Job time: 366 sec
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                       LENGTH:
                                                                             3 FEGIDVYT 10
                                                       FEGLTIYT 8
                                                                                                                                                                                           H: 301 amino acids amino acid
                                                                                                   Conservative
                                                                                                               64.78;
62.58;
           ó
           2001, 07:59:58
                                                                                                               Score 33; DB Pred. No. 54;
                                                                                                    Mismatches
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Minimum DB:
Maximum DB:
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Maximum Match 100%
Listing first 45 summaries
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 Pred. No. score grea and is der
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 0
length: 2000000000
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PIR_68:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219241 seqs, 76174552 residues
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Copyright (c) 1993 - 2000 Compugen Ltd.
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RESULT 2 A44261 dnaK-type molecular chaperone HSP70a - California sea hare (fragment) N;Alternate names: heat shock protein 70 C;Species: Aplysia californica (California sea hare) C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999 C;Accession: A44261 C;Accession: A44261 J. Cell Biol. 119, 1069-1076, 1992 A;Title: Long-term sensitization training in Aplysia leads to an increase in the expr. A;Reference number: A44261; MUID:93077669 A;Reference number: A44261; MUID:93077669 A;Roccession: A44261 A;Status: preliminary; not compared with conceptual translation A;Residues: 1-209 <kuh> A;Note: sequence extracted from NCBI backbone (NCBIP:118951) C;Genetics: A;Gene: HSP70a C;Function:</kuh>	Query Match 90.2%; Score 46; DB 2; Length 208; Best Local Similarity 90.0%; Pred. No. 0.088; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1 SLFEGIDVYT 10                       Db 132 SLFEGIDFYT 141	RESULT 1  B44261  dnaK-type molecular chaperone HSC70 - California sea hare (fragment)  N;Alternate names: heat shock protein 70 homolog HSC70  C;Specles: Aplysia californica (California sea hare)  C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999  C;Accession: B44261  R;Kennedy, T.E.; Barzilai, A.; Kandel, E.R.  J. Cell Biol. 119, 1069-1076, 1992  A;Title: Long-term sensitization training in Aplysia leads to an increase in the e A;Reference number: A44261; MUID:33077669  A;Accession: B44261  A;Status: preliminary; not compared with conceptual translation  A;Molecule type: nucleic acid  A;Note: sequence extracted from NCBI backbone (NCBIP:118950)  C;Genetics: A;Gene: HSC70  C;Function: involved in protein folding and assembling/disassembling of protein  C;Superfamily: heat shock protein 70  C;Keywords: ATP; molecular chaperone	30 46 90.2 647 1 HHXL70  31 46 90.2 647 2 T41121  32 45 88.2 214 2 A03309 dnaK-type molecula  33 45 88.2 379 2 I46588  34 45 88.2 467 2 T45473 heat-shock protein  36 45 88.2 641 2 JN0668  37 45 88.2 641 2 JN0668  38 45 88.2 641 2 JN0668  39 45 88.2 641 2 S09036  40 45 88.2 643 2 S25585 dnaK-type molecula  40 45 88.2 643 2 S09036 dnaK-type molecula  41 42 88.2 651 2 T45517 heat shock protein  42 43 84.3 209 2 S48024  43 84.3 209 2 C44261 dnaK-type molecula  44 43 84.3 209 2 C44261 dnaK-type molecula  45 43 84.3 309 2 A34041  ALIGNMENTS
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A;Description: involved in protein folding and C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
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N;Alternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 21-reb-1997 #sequence_revision 21-Feb-1997
                                                                                                                                                                                                                                                                        R;Rosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Gene 96, 295-300, 1990
A;Title: Sequence of a sea urchin hsp70 gene and its 5' A;Reference number: PQ0138; MUID:91099690
A;Accession: PQ0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: involved in protein folding and assembling/disassembling of protein complC;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: 70-kilodalton heat shock polypeptides A; Reference number: I51344; MUID:85036330 A; Accession: I51344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: I51344
R;Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
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                                                                                              A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                        A;Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                  dnak-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment)
N;Alternate names: heat shock protein 70
C;Species: Paracentrotus lividus (common urchin)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 20-Aug-1999
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A; Residues: 1-278 < KOT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                     A;Gene: hsp70 II
A;Introns: 68/1; 137/1; 188/3; 281/3
                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-372 < ROS>
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Best Local
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Best Local 9
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                          Query Match
Best Local
           Matches
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156 SLFEGIDFYT 165
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nes 9; Conservative
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             Conservative
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                          90.2%;
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Pred. No. 0.08
0; Mismatches
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           Score 46; DB
Pred. No. 0.17
0; Mismatches
             0;
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Pred. No.
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0.12;
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0.089;
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                                              Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Borchiellini, C.; Le Parco, Y. submitted to the EMBL Data Library, A;Reference number: Z22983
A;Accession: T45479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat-shock protein 70 [imported] - Eunicella cavolini (fragment) C; Species: Eunicella cavolini
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A; Residues: 1-467 <BOR>
A; Cross-references: EMBL: AF026517;
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A; Accession: T45477
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                                                                                                  heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment) C;Species: Funiculina quadrangularis C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
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C;Superfamily: heat shock
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                             submitted to the EMBL Data A; Reference number: Z22983 A; Accession: T45476
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C; Superfamily:
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A; Residues: 1-467 <BOR>
A; Molecule
                A;Status:
                                                                                     R; Borchiellini, C
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preliminary;
e type: mRNA
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9; Conservative
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9; Conserv
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                                                                                       Le Parco,
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Pred. No. 0.22
0; Mismatches
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Pred. No. 0.
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                    from GB/EMBL/DDBJ
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heat-shock protein 70 [imported] - Eunicella cavolini (fragment) C;Species: Eunicella cavolini C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change C;Accession: T45478 R;Borchiellini, C.; Le Parco, Y.
                                                                                                                       C;Genetics:
A;Gene: hsc70
A;Note: localized to filopodias and c
A;Note: heat shock protein 70
                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-632 <BOV>
A;Cross-references: EMBL.AF025951;
A;Experimental source: strain AX3
                                                                                                                                                                                                                                                    A; Reference number: Z22980
A; Accession: T45471
                                                                                                                                                                                                                                                                            R; Boves, H.; Mintert, U.; Dittrich, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                             C; Accession:
                                                                                                                                                                                                                                                                                                                     dnak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum) N;Alternate names: heat shock cognate protein 70 C;Species: Dictyostelium discoideum C;Species: Dictyostelium discoideum C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
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A;Residues: 1-469 <BOR>
A;Cross-references: EMBL:AF026518; PIDN:AAC05363
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A; Status: preliminary; translated
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A; Gene: Hsp70
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A; Cross-references: EMB
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dnaK-type molecular chaperone - chicken
N;Alternate names: heat shock protein 70
C;Species: Gallus gallus (chicken)
C;Accession: A25646
C;Accession: A25646
R;Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Baherji, S.S.
J. Biol. Chem. 261, 12692-12699, 1986
A;Title: Organization, nucleotide sequence, and transcription of the chicken HSI
A;Reterence number: A25646; MOID:86304452
A;Accession: A25646
A;Molecule type: DNA
A;Residues: 1-534 <MOR>
A;Residues: 1-534 <MOR>
A;Cross-references: GB:J02579; NID:9211940; PIDN:AAA48825.1; PID:9211941
A;Note: the authors translated the codon TCG for residue 583 as Trp
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.

J. Biol. Chem. 268, 23267-23274, 1993
A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated a A; Reference number: A48872; MUID:94043116
A; Accession: A48872
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-636 <EDD>
A; Cross-references: GB:L22736; NID:9433179; PIDN:AAA33219.1; PID:9433180
A; Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 6
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description:
C; Superfamily: |
C; Keywords: ATP
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C; Superfamily: 1
C; Keywords: ATP
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final content of the process of the content of 
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heat shock protein 70
P; molecular chaperone
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Pagoulatos, G.; Lazaridis,
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R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I. FEBS Lett. 355, 282-286, 1994
A;Title: The hsc70 gene which is slightly induced by heat is A;Reference number: 136927; MUID:95080396
A;Accession: 136927
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Reference number:
A; Accession: S31766
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A; Residues: 1-638 < RES:
A; Cross-references: EMBL: X70684; NID: 922781; PIDN: CAA50019.1;
A; Experimental source: kidney; cell line COS-1
C; Genetics:
A; Gene: hsg70
C; Function:
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dnaK-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
W;Alternate names: heat shock protein YG102; protein L0971; protein YC;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-JuC;Accession: S20139; S64772; S64775; S69383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Sconzo, G.; Scardina, G.; Ferraro, M.G. Gene 121, 353-358, 1992
A;Title: Characterization of a new member of the A;Reference number: JC1391; MUID:93077053
A;Accession: JC1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
N;Alternate names: heat shock protein 70IV; hsp70IV protein
C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-
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C;Genetics:
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C; Function:
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A; Residues: 1-639 <SCO>
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Best Local
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Best Local
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Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein
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Pred. No.
0; Mismatc
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                          07-May-1993 #text_change 20-Jun-2000
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0.31;
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A; Residues: 1-639 <SLA>
A; Cross-references: EMB
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A; Accession: S64772
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                                                                                                                                                                                                                                                                                                                                                             dnak-type molecular chaperone hsp70A - Caenorhabditis elegans N;Alternate names: heat shock protein 70 A C;Species: Caenorhabditis elegans
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A; Cross-references: EMB
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A; Residues: 1-639 < PI
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                                                     A;Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352
A;Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352
A;Note: genomic clones representing six distinct members of the hsp70 gene family wer A;Note: transcripts of hsp70A are abundant in control worms and also increase two- to A;Note: one of the three introns in hsp70A is in a position similar to an intron in D
                                                                                                                                                                                                                                             R;Snutch, T.P.; Heschl, M.F.
Gene 64, 241-255, 1988
A;Title: The Caenorhabditis
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                                 C; Genetics:
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A; Residues: 1-640 <SNU>
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              hsp70A
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elegans hsp70 MUID:88297155

gene

family: a molecular

genetic characteri

22-Jun-1999

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A; Molecule type: DNA
A; Residues: 1-639 <GOF>
A; Residues: 1-639 <GOF>
A; Cross-references: EMBL: Z73129; NID: g1360201; PIDN: CAA97472.1; PID: g1360202; MIPS: YL
A; Cross-references: EMBL: Z73129; NID: g1360201; PIDN: CAA97472.1; PID: g1360202; MIPS: YL
A; Experimental source: strain S288C
A; Experimental source: strain S288C
A; D: Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64775
A; Reference number: S64775
A; Reference S64775
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A;Residues: 72-639 <DUE>
A;Cross-references: EMBL:Z73129; MIPS:YLL024c
A;Cross-references: EMBL:Z73129; MIPS:YLL024c
A;Experimental source: strain S288C
R;Purnelle, B.; Goffeau, A.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals mily and a new ABC transporter homologous to the human multidrug resistance protein.
A;Reference number: S69380
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Nucleic Acids Res. 17, 805-806, 1
A;Title: The SSA1 and SSA2 genes
                                                                                                                            A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
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A; Accession: S20139
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A;Map position: 12L
Conservative
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SSA2 genes of the yeast Saccharomyces
0139; MUID:89128457
                       90.2%;
0;
                    Score 46; DB 2
Pred. No. 0.31;
Mismatches
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  Gaps
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A;Map position: IV
A;Introns: 69/1; 331/3; 558/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comple;Superfamily: heat shock protein 70
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match
Best Local Similarity 90.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1||||||||||||
Db 287 SLFEGIDYT 10
Db 287 SLFEGIDFYT 296

Search completed: December 6, 2001, 07:58:28
Job time: 276 sec
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Title:
Perfect score:
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Listing first 45 summaries
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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51
December 6, 2001, 08:00:52; Search time 50.21 Seconds (without alignments) 7.302 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  3 paracentrot
0 penicillium
6 gallus gall
2 cercopithec
2 saccharomyc
8 paracentrot
6 caenorhabdi
5 dictyosteli
                                               4 sus scrofa
2 ceratitis c
3 drosophila
6 homo sapien
7 sus scrofa
                                                                                                                                        9 rattus norv
1 saccharomyc
5 bos taurus
2 saccharomyc
1 brugia mala
3 oncorhynchu
1 pleurodeles
3 neurospora
7 xenopus lae
0 blastocladie
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0 manduca sex
6 drosophila
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RESULT 2 HS72_PARLI ID HS72_I	Query Mat Best Loca Matches 1 S 1 A 3 S	HSSP; J040 HSSP; P19; InterPro; Pfam; PF00 PROSITE; I PROSITE; I PROSITE; I ATP-bindii NON_TER NON_TER SEQUENCE	his hetw he se se odi nti	SEQUENCE MEDLINE= ROTHSTEIN ROTHSTEIN POnchocea amicrofii Mol. Biod	01-OCT-1989 01-FEB-1996 01-FEB-1996 HEAT SHOCK Onchocerca Eukaryota; Onchocercical (CBI_TaxID=	ESULT 1 870_ONCVO HS70_ P1150		44444 3355 444 543 544 544 544 544 544 5
T 2 PARLI HS72_PARLI	tch al sim. 9; SLFEGII	EMBL; J04006; AAA29 HSSP; P19120; 1ATR. InterPro; IPR001023 Pfam; PF00012; HSP7 PROSITE; PS000329; H PROSITE; PS000329; H PROSITE; PS01036; H ATP-binding; Heat s NON_TER 1 NON_TER 32 SEQUENCE 322 AA;	ween the Swiss Inst European Bioinforma by non-profit in lified and this state ities requires a lice send an email to lice	SEQUENCE FROM N.A.  MEDLINE-99201313; PubMed=2704388  MEDLINE-99201313; PubMed=2704388  Rothstein N.M., Higashi G., Yate  Rothocerca volvulus heat shock  amisorofilaremic individuals from  Mol. Biochem. Parasitol. 33:229-  -!- DISBASE: HEAT SHOCK PROTEIN  MICROFILAREMIC INDIVIDUALS F.  -!- SIMILARITY: BELONGS TO THE H.	01-OCT-1989 (Rel. 01-FEB-1996 (Rel. 01-FEB-1996 (Rel. 01-FEB-1996 (Val. 01-FEB-1996 (Val. HEAT SHOCK 70 KDA Onchocerca volvul Eukaryota; Metazc Onchocercidae; On NCBI_TaxID=6282;	ONCVO		444444444444444444444444444444444444444
STA	larity Conser Conser 11 11 FYT 52	;; AAA29417; 1ATR.; 1ATR. RR001023; HSP70; 1SP70 00297; HSP71 00297; HSP71 01036; HSP71 11036; HSP71 Heat shocl 1 1 1 322 322 322 323	the Swiss I opean Bioinfo non-profit d and this st s requires a an email to	M N.A. )1313; M., Hi volvul mic in para HEAT AREMIC TY: BE	9 (Rel. 12 6 (Rel. 33 6 (Rel. 33 70 KDA PR VOLVULUS. Metazoa; Metazoa; dae; Oncho	STA		888888888888888888888888888888888888888
STANDARD;	90.2 90.0 vative	# HSP ; HSP 0; 1. SSP70_ SSP70_ SSP70_ SSP70_ 322 3561	Institute Institute Iformatics I institut I try is cop	.A. Higashi G., Yate vulus heat shock individuals from arasitol 33:229- AT SHOCK PROTEIN MIC INDIVIDUALS F BELONGS TO THE H	Ce OF	STANDARD;		644 644 644 644 646 646 650
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372 AA	ore 46; DB 1 ed. No. 0.087 Mismatches	81552	it. It is pro dioinformatic tute. There as long as tremoved. ment (See ht ib.ch).	tei tei fil fil (19 (19 X	uence update) iotation update) ioto (FRAGMENT) 70) (FRAGMENT) Chromadorea; Sp	322 AA	ALIGNMENTS	CAN CAN CAN CAN CAN GRA
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20-AUG-2001 (Rel. 4
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HEAT SHOCK 70 KDA F
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01-AUG-1991 (Rel. 19, Last sequence update)
01-UUN-1994 (Rel. 29, Last annotation updat
HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
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Q92260;
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                                                                                                    SEQUENCE FROM N.A.

Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai

"Molecular cloning and expression of a Penicil

allergen with sequence homology and antigenic

a hsp70 human heat shock protein.";
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PROSITE; PS00329; HSP70_2; PARTIAL.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.
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-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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PROSITE; PS0
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                                                   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                        Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                  NCBI_TaxID=5077;
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SWISS-PROT entry is copyright.
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372 AA;
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40, Last sequence update)
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Pred. No. 0.
                                                                                                                                                           Liaw S.F., Tsai J.J., Han S.H.; sion of a Penicillium citrinum
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RESULT 4
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DT 01-AUG
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01-AUG-1988 (Rel. 08, Last sequence update)
01-FBB-1994 (Rel. 28, Last annotation update)
01-FBB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (HSP70).
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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PROSITE; PR00329; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB
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MEDLINE=86304452; PubMed=3017985;
Morimoto R.I., Hunt C., Huang S.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001023; HSP70. Pfam; PF00012; HSP70; 1.
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Pred. No.
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and transcription of t
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                     CRC64;
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Query Match Best Local

Similarity

90.2%; 90.0%;

Score Pred.

46; No.

DB 1; 0.18;

Length 634;

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RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RESULT RE
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1_CERAE STANDARD;
Q28222;
Q28222;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
15-DEC-1998 (Rel. 37, Last ann
HEAT SHOCK 70 KDA PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEMLY TRANSLATED POLYPERTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE CONFORMATIONS OF OTHER PROTEINS. THEY PARTICIPATE IN ALL THESE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PRETIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES STRESS-INDUCED DAMAGE.

1- INDUCTION: BY HEAT SHOCK.

1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                        PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X70684; CAA50019.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.; "The hsc70 gene which is slightly induced by heat is the main virus inducible member of the hsp70 gene family."; FEBS Lett. 355:282-286(1994).
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                                                        SLFEGIDVYT 10
SLFEGIDFYT 293
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9; Conserv
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37, Last sequence update)
37, Last annotation updat
                                                                                                                                        90.2%;
                                                                                                                                                                                                                                                     Heat shock; Multigene fi
20 MW; D55076A0FFAB6AB3
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33 CRC64;
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RESULT

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HS72_YEAST

ID HS72_YEAST

AC PH372_YEAST

AC PH372_YEAST

AC O11-OCT

DT 01-OCT

AC SACCha

OC SACCha

AC STRAIN

RA SLATE

RE SEQUEN

RA STRAIN

RA DUESTE

RI [3]

RP SEQUEN

RA DUESTE

RI [3]

RP SEQUEN

RA DUESTE

RI [4]

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p10592;
01-JUL-1989 (Rel. 11, Creat
01-OCT-1994 (Rel. 30, Last
01-OCT-1996 (Rel. 34, Last
HEAT SHOCK PROTEIN SSA2.
SSA2 OR YLL024C OR L0931.
EMBL; X12927; CAA31394.1; -.
EMBL; Z73129; CAA97472.1; -.
EMBL; X97560; CAA66167.1; -.
PIR; S20139; S20139.
HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10592; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 186-195.
STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garrels J.I., Futcher B., Kobayashi R., Latte Volpe T., Warner J.R., McLaughlin C.S.; "Protein identifications for a Saccharomyces database.";
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Slater M.R., Craig
"The SSA1 and SSA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duesterhoeft A., Floe
Submitted (MAY-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Electrophoresis 15:1466-1486(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95203288; PubMed=7895733;
                                                                                                                                                                                                                                                                                                                                                                                                           PTM: PHOSPHORYLATED. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: CYTOPLASMIC.
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1 (APR-1996)
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EMBL/GenBank/DDBJ
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RESULT 7
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PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

PROSITE; PS01036; HSP70_3; 1.

PROSITE; PS01036; HSP70_3; 1.
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SGD; S0003947; SSA2.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sconzo G., Scardina G., Ferraro M.G.; "Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 gene family and its expression."; Gene 121:353-358(1992).
-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q06248;
Q1-JUN-1994 (Rel. 29, Created)
Q1-JUN-1994 (Rel. 29, Last sequence update)
Q1-JUN-1994 (Rel. 29, Last annotation updat
HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INIT_MET MOD_RES
                                                                                                                                                                                               Pfam; PF00012; HSP70. 1.

PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; x61379; CAA43653.1; -. PIR; JC1391; JC1391. HSSP; P19120; 1NGJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute or Extraction Bioinformatics Institute.
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                                                               Score 46; DB 1;
Pred. No. 0.18;
0; Mismatches
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01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN A.
HSP-1 OR HSP70A.
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P09446;
01-MAR-1989
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__DICDI STANDARD; PRT; 640 AA P36415;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1997 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
HSPB OR HSC70.
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Gene 64:241-255(1988).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00299; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
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NCBI_TaxID-6239;
                                                                                                                                                                                                                          Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
NCBI_TaxID=44689;
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MEDLINE=94008983; PubMed=8404847; Haus U., Trommler P., Fisher P.R.,
                                                                                           SEQUENCE FROM N.A. STRAIN=AX3;
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"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Pred. No. 0.18;
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    Hartmann H., Lottspeich F.,
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HS71_BOVIN STAN

Q27975; Q27964;

Q1-NOV-1997 (Rel. 3

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15-JUL-1999 (Rel. 3

HEAT SHOCK 70 KDA P
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J. Biol. Chem. 268:23267-23274(1993).
II FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN BINDING PROTEIN CAP32/34, ACTS AS A CHAPERONE BY STIMULATING THE REPOLDING OF DENATURATED CAP32 AND CAP34.
STIMULATING THE REPOLDING OF DENATURATED CAP32.
II SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS OF THE CELL CORTEX AND CELL PROTRUSIONS.
II SUBCELLULAR STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
IN STATILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P36415; DICTY.
D1ctyDb; DD01078; hspB.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The near shock cognate protein from Dictyostelium affects actin polymerization through interaction with the actin-binding protein cap 32/34.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01326; HSP70_3; 1.
ATD-hinding; Charcono.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X75263; CAA53039.1; -. EMBL; L22736; AAA33219.1; -. PIR; S37394; S37394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94043116; PubMed-8226849; Eddy R.J., Sauterer R.A., Condeelis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF
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                                                                                                                                                       Local Similarity
mes 9; Conserv
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64 64
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70499 MW;
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     35, Created)
35, Last sequence update)
38, Last annotation update)
PROTEIN 1 (HSP70-1).
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IHHHINGNAWVVESGPVSEVLSFN (IN RR
N -> T (IN REF. 2).
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R -> A (IN REF. 2).
S -> A (IN REF. 2).
V -> A (IN REF. 2).
V -> A (IN REF. 2).
V -> P (IN REF. 2).
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Pred. No.
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RESULT 11
HS71_HUMAN
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AC P08107
DT 01-AUG
DT 01-FEB
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HS71_HUMAN S
P08107; P19790;
01-AUG-1988 (Rel
01-FEB-1994 (Rel
20-AUG-2001 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An Alui polymorphism at the bovine 70 kD heat-shock protein-1 (HSP70-1) locus.";
Anim. Genet. 25:196-196(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Chaperone; SEQUENCE 641 AA; 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U09861;
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MEDLINE=95126904; PubMed=7826329;
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                                                                                                                                                                                                                                              286 SLFEGIDFYT 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEMLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABLILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURKING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRESS-INDUCED DAMAGE.
INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
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; AAA03450.1; -.
; INGC.
                                                                            STANDARD; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one; Heat shock; Multigene family. 70250 MW; 6D548263E98780F9 CRC64;
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90.0%;
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Pred. No.
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(Rel. 08, Created)
(Rel. 28, Last sequence update)
(Rel. 40, Last annotation update)

InterPro; IPR001023; HSP70.

603012 140550

PROSITE; PS00297; HSP70\_1; 1.
PROSITE; PS00329; HSP70\_2; 1.
PROSITE; PS01036; HSP70\_3; 1. Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70 

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AS OSIPLIK J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

(Siplik J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

(T "Structure of a new crystal form of human hsp70 ATPase domain.";

(L Acta Crystallogr. D 55:1105-1107(1999).

(C -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

(C -1- FUNCTION: IN COOPERATION WITH OTHER CYTOSOL AS WELL AS WITHIN

(C ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC

(C RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR

(C RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR

(C PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION

(C PROTEIN TRANSLOCATION WITH HSP90. THEY PARTICIPATE IN ALL THESE

(C COMPORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEDTIDE

(C COMPORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEDTIDE

(C SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES

(C DURING TRANSLATION AND MEMBERANE TRANSLOCATION, OR FOLLOWING
EMBL; M59828; AA
EMBL; M59830; AA
EMBL; AF134726; AE
EMBL; AF134726; AF13472
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MEDLINE-91055806; PubMed=1700760;

Milner C.M., Campbell R.D.;

"Structure and expression of the three MHC-linked
Immunogenetics 32:242-251(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (HSPAlA AND HSPAlB).
ROWEN L., Qin S., Madan A., Dickhoff R., Dors M.,
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Conserved features of eukaryotic hsp70 genes revealed with the nucleotide sequence of human hsp70."; Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.; "Human major histocompatibility complex contains gene heat shock protein HSP70.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-36 AND 360-424 FROM N.A. MEDLINE-89184548; PubMed=2538825;
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Mammalia; Eutheria;
                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "In vitro transcription of a human hsp 70 heat shock gene by prepared from heat-shocked and non-heat-shocked human cells.' Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence of the human major histocompatibility complex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382
MEDLINE=99234376; PubMed=10216320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87066768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drabent B., Genthe A., Benecke B.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                             INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRESS-INDUCED DAMAGE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morimoto R.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acad. Sci. U.S.A. 86:1968-1972(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
                                                                  AAA63226.1; -.
AAA63227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=3786141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    databases
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SLFEGIDFYT

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MOUSE

HS71\_MOUSE STANDARD; PRT; 641 AA.
p17879; Q61689;
01-x0G-1990 (Rel. 15, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 35, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN 1 (HSF70.1) (HSF70-1/HSF70-2).
HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1.

Mus musculus (Mouse). Eukaryota; Metazoa; C

Query Match Best Local S Matches 9

Similarity 9; Conserv

90.2%;

Score 46; Pred. No.

0.18; DB 1;

Length 641

Conservative

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Mismatches

Indels

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Gaps

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CONFLICT CONFLICT CONFLICT CONFLICT

7 110 370 469

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N

AAD21816).

7 110 370 469 499 70052 1

CONFLICT ATP-binding;

3D-structure.

Chaperone;

Heat shock;

Multigene

family;

MHC III;

SEQUENCE

641 AA;

MW;

z

-> S (IN REF. 3; AAD21815). 78F513118C96DE66 CRC64;

MISSING (IN REF.

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Perry M.D., Aujame L., Shtang S., Moran L.A.;

"Structure and expression of an inducible HSP70-encoding gene from Mus musculus.";

Gene 146:273-278(1994).

Gene 146:273-278(1994).

Gene 146:273-278(1994).

OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OFF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZED. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PETTIDE SEGMENTS WITH A NET HURROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEDITARY BY THE PROPERTY OF THE PROPERTY OF THE PROTEINS. THEY BIND EXTENDED PETTIDES DURING TRANSLATION AND MEDITARY BY THE PROPERTY OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization and sequence of a mouse hsp70 gene and expression in mouse cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
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01-FEB-1994 (Rel.
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M35021; AAA37864.1; EMBL; M76613; AAA57233.1;
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                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                      the European Bioinformatics Institute. The second of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
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InterPro; IPR001023; HSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bouquet Y.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peelman L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92175874; PubMed=1339404;
Peelman L.J., de Weghe A.R., Copp
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                                                                                                                                                                                                                                                                                                                                                      PUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
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                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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                                                                                                                                                                                                  the Swiss Institute of Bioinformatics
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28, Last sequence update)
35, Last annotation update)
PROTEIN 1 (HSP70.1).
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00299; HSP70_3; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Chaperone; Heat shock; Multigene fa SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33
                                                                                                                BIOCHIM. Biophys. Acta 1219:64-72(1994).

-i- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
-i- FUNCTION: IN COOPERATION WITH GAGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPETIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-LEW.1W/GUN;
MEDLINE-95012453; PubMed-7927536;
Walter L., Rauh F., Guenther E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
Massa S.M., Sharp F.R.;
"cDNA cloning and expression of stress inducible rat hsp70 in normal
and injured rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00012; HSP70;
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                                                                                                                                                                                                                                                      STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94096443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
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                                                                                                                                                                                                                       MEDLINE-94368874; PubMed-8086479;
Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     "Comparative analysis of the three major histocompatibility complex-
linked heat shock protein 70 (Hsp70) genes of the rat."; [mmunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                           nsp70 gene.
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                                                                                                                                                                                                         Cloning, nucleotide sequence and expression
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                             SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                      THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
                                          AND MEMBRANE TRANSLOCATION, OR INDUCTION: BY HEAT SHOCK.
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S., Narasimhan P
                                                                                                                                                                                                                                                                                                                                                                                                                        36:325-335(1993)
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Rodentia;
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90.0%;
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Pred. No. 0.18
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P., Zhang J.S.,
                                                         FOLLOWING
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33 CRC64;
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REVISIONS TO Slater M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST STANDARD; PRT; 641 AA P10591; O1-JUL-1989 (Rel. 11, Created) O1-OCT-1994 (Rel. 30, Last sequence update) O1-OCT-1996 (Rel. 34, Last annotation update) O1-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Chaperone; Heat shock; Multigene family; CONFLICT 7: Rr -> H(IN REF. 3). CONFLICT 227 227 D -> H(IN REF. 2 AND 3). CONFLICT 408 408 G -> A(IN REF. 3).
                                                                                                                                                                                                                                                                    MEDIINE-89128457; PubMed-2644626;
Slater M.R., Craig E.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                           HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100). SSA1 OR YAL005C.
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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                                                                       MEDLINE=85087943; PubMed=6096826;
Ogden R.C., Lee M.-C., Knapp G.;
"Transfer RNA splicing in Sacchar
                                                                                                                                                          Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B., Belaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H., Sequencing of chromosome I of Saccharomyces cerevisiae: analysis the 42 kbp SPO7-CENI-CDC15 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                             STRAIN=S288C / AB972;
MEDLINE=95028152; PubMed=7941740;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                               Nucleic Acids
                                                                                                                    SEQUENCE OF 590-641 FROM N.A.
                                                                                                                                              Yeast 10:535-541(1994).
                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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PF00012; HSP70; 1.
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X77208;
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641 AA;
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                    207;
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CAA54423.1; -.
                                               12:9367-9382(1984).
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70163 MW;
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in Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to the SWISS-PROT data bank.

-I- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE
ATP-DEPRUBENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC.
-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Protein expression during exponential Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 186-195.
STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed-8935650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garrels J.I., Futcher B., Kobayashi R., Volpe T., Warner J.R., McLaughlin C.S., "Protein identifications for a Saccharon
                                                                                                                                Heat shoc
INIT_MET
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                                                                                                                                                                                                                                                                                                                       PIR; S25438; HHBYA1.
PIR; S42164; S42164.
HSSP; P19120; 1ATR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases [5]
                                                                                                                                                                                                                                                                                             SWISS-2DPAGE; P10591; YEAST YEPD; 9788; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 91-97 AND
                                                                                                                                                                                       Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEMS Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norbeck J., Blomberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electrophoresis 15:1466-1486(1994).
                                                                                                                                                                                                                                                               InterPro; IPR001023;
                                                                                                                                                                                                                                                                              SGD; S00000004; SSA1.
   282
1 SLFEGIDVYT
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| SLFEGIDFYT
                                                                                                                                                                         shock;
                                                                                                                                                                                                                                                                                                                                                                  X12926; CAA31393.1;
L22015; AAC04952.1;
                                                           Similarity 90.0
9; Conservative
                                                                                                                                  641 AA;
                                                                                                                                                                          ATP-binding; Multigene family;
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   291
                                                                                                                                  69526
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Pred. No.
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Result
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Maximum Match 100%
Listing first 45 summaries
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Match
SPTREMBL_17:*
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sp_organelle:*
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sp_unclassified:*
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Q9u665 littorina p
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P81157 aplysia cal
P81157 aplysia cal
Q90520 oncorhynchu
Q90889 fugu rubrip
Q63718 rattus norv
Q44350 chondrosia
Q44350 getrobiona
Q94351 guancha lac
Q44351 eunicella c
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Q9uvml rhizopus st	094104 pneumocysti	O94106 pneumocysti	Q9nlu2 saguinus oe	Q9uvm0 rhizopus st	073922 oreochromis	Q9gpm5 monosiga ov	044347 petrosia fi	O44346 asbestoplum	Q9u9b4 mytilus edu	Q24952 geodia cydo	Q9xzj2 crassostrea	Q94805 trichoplusi	P93937 ascophyllum		Q9zs55 arabidopsis	059855 schizosacch	Q9ngk9 wuchereria	Q9njb7 wuchereria	£O.	Q9qwj5 mus musculu	Q63256 rattus norv	093240 paralichthy	Q93601 caenorhabdi	Q9i8f9 oryzias lat	Q98900 fugu rubrip

## ALIGNMENTS

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RESULT
Q9U670
ID Q9
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Best Local Similarity 90.0
Matches 9; Conservative
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SEQUENCE
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Q9U667; Q1-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q9U670 PRELIMINARY;
Q9U670;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                    HSSP; P19120; 1BA1.
InterPro; IPR001023; HSP70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                   Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191828; AAF12787.1; -.
                                                                                                                                                                                                                                                                                                                        Littorina plena.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                    1 SLFEGIDVYT 10
                                                                                        SLFEGIDFYT
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146 AA;
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16607 MW;
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90.0%;
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Last sequence update)
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                                   153
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01-JUN-2001
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Q9069;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
upam-shock profess (FRAGMENT).
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SEQUENCE
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SEQUENCE
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"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191825; AAF12784.1; -.
HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBL_TaxID-31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191826; AAF12785.1; -.
HSSP; P19120; 1BA1.
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Eukaryota; Metazoa; Mollusca; Ga
Neotaenioglossa; Littorinoidea;
NCBI_TaxID=31221;
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                                                                                                 Q9U665
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PROSITE; PS01036; HSP70_3; 1.
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PROSITE; PS01036; HSP70_3; 1.
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153 AA;
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155 AA;
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17352 MW;
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17676 MW;
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a; Littorinidae; Littorina.
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  Q9U668 PRELIMINARY;
Q9U668;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
NON_TER 1
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Q9U671;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Littorina plena.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Littorina scutulata.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001023; HSP70.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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                                                                                                                                                                                                                     1 SLFEGIDVYT
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                                                                                                                                                                                                                                                                                       similarity 90.0
9; Conservative
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9; Conservative
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158 AA;
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157 AA;
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17887
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17834 MW;
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90.0%;
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90.0%;
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    Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                       Score 46; DB Pred. No. 0.35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                          B41E5356A24CAD2F
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35;
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0.35;
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                                                                                                                                                                                                                                                                                                                                   Length 158;
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Best Local Similarity
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Q90666;
01-MAY-2000
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NON_TER
SEQUENCE
                                P81159
P81159;
   01-JUN-1998
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Heat-shock genes in the heat-stressed genus I "Heat-shock genes in the heat-stressed genus I Submitted (OCT-1999) to the EMBL/GenBank/DDBJ EMBL; AF191829; AAF12788.1; -. HSSP; P19120; 1BA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEAT-SHOCK PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                         SLFEGIDFYT 94
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158 AA;
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(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                 PRELIMINARY;
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; 17891 MW;
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17868 MW;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 5
Pred. No. 0.35;
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                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B41E5356BCECAD2F CRC64;
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                                                                                                                                                                                                                                                                                                                                                   Mismatches
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J databases.
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J databases.
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Best Local S
Matches 9
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NON_TER
SEQUENCE
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SEQUENCE
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221
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the expression of BiP, the major protein chaperon of the ER.";
J. Cell Biol. 119:1069-1076(1992).
-i- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
-i- SIMILARTY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; Z15039; CAA78757.1; -.
HSSP; P19120; IBBAL.
InterPro: TDDACCO.
                                                                                                                                                                                                                                                                                                                                                                                                                         P81157;
01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
HEAT SHOCK 70 KDA PROTEIN A
                                                                                                                      the expression of BiP, the major protein chaperon of the C. Cell Biol. 119:1069-1076(1992).

-i- INDUCTION: BY HEAT SHOCK.

-i- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY EMBL; Z15037; CAA78755.1;

-INTERPROJUCIA; HSP70.

Pfam: PF00012; HSP70; 1.
                                                                  PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93077669; PubMed=1360013;
Kuhl D., Kennedy T., Barzilai A., Kar
"Long-term sensitization training in
                                                                                                                                                                                                                                                                                                                                                       Aplysia californica
Eukaryota; Metazoa;
Aplysiidae; Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aplysia californica
Eukaryota; Metazoa;
Aplysiidae; Aplysia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
                                 Heat shock; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00329; HSP70_2; 1. PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat shock; Multigene family
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0012; HSP70; 1.
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220 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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AA;
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24684 MW;
221
24404 MW;
                                                                                                                                                                                                                                                                                                                                                                           Mollusca;
                                                                                                                                                                                                                                                                                                                                                                                           (California sea hare).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                 70_2; 1.
70_3; 1.
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2%;
                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
(HSP70A) (FRAGMENT).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                         Gastropoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FA8557F2BB85C37A CRC64;
853F794106E83CC9 CRC64;
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Best Local
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Q90520;
Q90520;
Q90520;
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 01, Last sequence update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q98899 PRELIMINARY; PRT; 367 AA.
Q98899;
Q1-FEB-1997 (TrEMBLrel. 02, Created)
O1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0301; HEATSHOCK70.
PRINTS; PRO03029; HSP70_2; 1.
PROSITE; PS00329; HSP70_3; 1.
Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kothary R.K., Jones D., Candido E.P.M.; "70-Kilodalton heat shock polypeptides characterization of cDNA sequences."; Mol. Cell. Biol. 4:1785-1791(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-85036330; PubMed-6092938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q90520
                                                              Submitted (OCT-1996) to the EMBL; Y08578; CAA69892.1; HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                              Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K02549; AAA49562.1; -. HSSP; P08109; 1CKR.
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                                                                                                                                                                                                          Lim E.H.;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSP70-3
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              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                            Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156
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9; Conservative
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278 AA;
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; 30327 MW;
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 13; Length 278; Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E4C745DE5484C17A CRC64;
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Query Match
Best Local S
Matches 9
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Best Local :
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q63718 PRELIMINARY; PRT; 455 AA. Q63718; Q1-NOV-1996 (TERMBLrel. 01, Created) 01-NOV-1996 (TERMBLrel. 01, Last sequence update) 01-JUN-2001 (TERMBLrel. 17, Last annotation update)
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAT SHOCK RÖTEIN 70 (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Cra
Mammalia; Eutheria; Rodentia; Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 227118; CAA81642.1; -
HSSP; P08107; 1HJO.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angeletti B., Passarelli F., Orru D., D'Ambrosio E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat shock.
                                                                                                                          044350 PRELIMINARY; PRT; 467 AA. 044350; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                         Chondrosia reniformis.
Eukaryota; Metazoa; Porifera; Demospongiae; Chondrosida; Chondrillidae; Chondrosia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
SEQUENCE FROM N.A. Borchiellini C., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat shock.
                                           NCBI_TaxID=68574;
                                                                                                                                                                                                                                                                                    1 SLFEGIDVYT 10
||||||| ||
254 SLFEGIDFYT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 SLFEGIDFYT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SLFEGIDVYT
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 455
455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                     Conservative
 Le
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40405 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   455
50404 MW;
 Parco
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 1
Pred. No. 1.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; D
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0F45F12CBA1E2971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8CD3DD8DF6E3C2CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pascale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 367;
D.95;
                                                                                                                                            update)
on update)
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                                                                                 Tetractinomorpha;
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E
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                                                                                                                                                                                                                                                                                                                                                                                      Length 455
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                                                                                                                                                                                                                                                                                                                                                          Indels
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT
044352
ID 044
AC 044
DT 01:
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Q9NJ92
ID Q9NJ92
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DE HEAT S
OS GUACHO
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RP SEQUEN
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PRINTS: PRO0301: HSP70: 1.

PROSITE: PRO0301: HEATSHCK70.

PROSITE: PS01030: HSP70_2: 1.

PROSITE: PS01036: HSP70_3: 1.

NON_TER 1 1

NON_TER 467 467

SEQUENCE 467 A7
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Best Local Similarity
Thes 9; Conservat
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Best Local Similarity
Matches 9; Conserv
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS01036; HSP70_3; 1.
NON_TER 1 1 1
NON_TER 467 467
SEQUENCE 467 AA; 51458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O44352 PRELIMINARY; PRT; 467 AA.
O44352;
O1-JUN-1998 (TremBLrel. 06, Created)
O1-JUN-1998 (TremBLrel. 06, Last sequence update)
O1-JUN-2001 (TremBLrel. 17, Last annotation update)
HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
                                                                                                                                         Q9NJ92 PRELIMINARY; PRT; 467 AA.
Q9NJ92;
Q1-Q7-2000 (TrEMBLrel. 15, Created)
Q1-Q7-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                          Eukaryota; Metazoa; Porifera;
Clathrinidae; Guancha.
                                                                                                                            Guancha lacunosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Borchiellini C., Le Parco Y.;

Submitted (SEP-197) to the EMBL/GenBank/DDBJ databases.

EMBL; AF026520; AAC05364.1; -.

HSSP; P08109; ICKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF026517; AAC05362.1; -. HSSP; P08109; lCKR.
                                  NCBI_TaxID=115120;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Petrobiona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=68578;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petrobiona massiliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||||| ||
252 SLFEGIDFYT 261
                                                                                                                                                                                                                                                                                                                                                                                                            252 SLFEGIDFYT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLFEGIDVYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
51458 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 5; Pred. No. 1.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 5; Length 467; Pred. No. 1.3; 0; Mismatches 1; Indels
                                                                                                    Calcarea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23EB28FFD1873DA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ODBE6920F2E6EA96 CRC64;
                                                                                               Calcinea; Clathrinida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcaronea; Petrobionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 467;
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SEQUENCE FROM N.A.

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δÃ
                                                                                                                                                                                  Search completed:
Job time: 182 sec
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                                                                                                                Query Match
Best Local S
Matches 9
                                                                                                                                                                             Borchiellini C., Le Parco Y.;

"Sponges paraphyly and the origin of Metazoa.";

L Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF182195; AAF61297.1;

R InterPro; IPR001023; HSP70.

R Pfam; PF00012; HSP70; 1.

R PRINTS; PR00301; HEATSHOCK70.

R PRINTS; PR003029; HSP70_2; 1.

R PROSITE; PS00329; HSP70_3; 1.

T NON_TER PS01036; HSP70_3; 1.

T NON_TER 467 467

SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;
                                                               Local Similarity 90.1 tes 9; Conservative
                                                                                      1 SLFEGIDVYT 10
             December
                                                               261
                                                                                                                              90.2%;
            6
            2001, 07:56:54
                                                                                                                Score 46; DB 5
Pred. No. 1.3;
0; Mismatches
                                                                                                                   0;
                                                                                                                                          5.
                                                                                                                                          Length 467;
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